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Performance of Gene Introgressed Lines against Blast Disease under Different Agro Climatic Locations of Chhattisgarh and Telangana

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ABSTRACT

Rice blast disease incited by the fungus Pyricularia oryzae is considered as a major limiting factor in the global rice production because of its wide distribution and destructiveness under favourable conditions its cause severe yield losses upto 80-100%. The present study was conducted in four different agro-climatic regions viz., IIRR Hyderabad, KVK Dhamatari (C.G.), RMDCARS Ambikapur (C.G.) and SGCARS Jagdalpur (C.G.) during Rabi 2017 and Kharif 2017. In this experiment sixteen introgressed lines i.e., MSP-1, MSP-2, MSP-3, MSP-4, MSP-5, MSP-6, MSP-7, MSP-8, MSP-9, MSP-10, MSP-11, MSP-12, MSP-13, MSP-14, MSP-15 and MSP-16 (developed by ICAR-IIRR, Hyderabad) are evaluated along with donor parents, recurrent parents, resistant and susceptible checks. These lines were gene pyramided with board spectrum of blast resistant genes i.e., Pi1, Pi2 and Pi54. The results confirmed that, MSP-1 and MSP-7 (Pi1), MSP-3, MSP-9, MSP-14 and MSP-16 (Pi54), MSP-6 and MSP-12 (Pi1, Pi2 and Pi54), MSP-8 and MSP-13 (Pi2) and MSP-11 (Pi1 and Pi54) lines were showed resistant reaction to blast disease at four locations. While MSP-4 (Pi1 and Pi2), MSP-10 (Pi1 and Pi2), MSP-15 with (Pi2) genes were moderately resistant at KVK Dhamtari. Similarly MSP-2 (Pi2) at SGCARS Jagdalpur and MSP-5 (Pi2 and Pi54) at RMDCARS Ambikapur and IIRR, Hyderabad showed moderately resistant reaction respectively.

Key words: *Rice blast, Resistance genes and Introgressed lines.*

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important staple food that feed more than half of the world's population[13], it is cultivated in an area about 160.74 million hectares with production of 486.57 million metric tonnes and productivity 4.51 metric tonnes in 2016-17[20]. In India, Rice is cultivated on an area of 433.88 lakh hectares with a total production of 104.32 million tonnes with 2404 kg productivity in 2016-2017 (Annual report 2016-17). India is one of the world's largest producers of white rice and brown rice, accounting for 20% of all world rice production.

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In Chhattisgarh rice occupied average of 3.6 million ha with 6322.1 thousand tonnes production and 1.2 to 1.6 t/ha productivity. Rice crop suffers from many diseases caused by fungi, bacteria, viruses, phytoplasma, nematodes and other non-parasitic disorders. Among the fungal diseases, blast caused by *Pyricularia oryzae* Cavara [synonym *Pyricularia grisea* Sacc. the anamorph of *Magnaporthe grisea* (Herbert) Yaegashi and Udagawa], is considered as a major threat to rice production because of its wide spread distribution and its destructiveness under favorable conditions. This disease was recorded from 85 countries[8] and it is estimated to cause 14-18% grain yield losses worldwide[15]. The yield losses due to pests and diseases are estimated to be around 37%[11] of which, blast accounts to 14-18 per cent. Resistance to the pathogen is a classic gene-for-gene system, where a major resistance gene is effective against *Pyricularia oryzae* strains containing the corresponding avirulance gene[17]. Twenty resistant genes have been identified by extensive genetic studies[5,14,23]. *Pi-b* and *Pi-ta*, two major resistance genes, introgressed from indica cultivars, have recently been molecularly characterized[4,9,21]. Both *Pi-b* and *Pi-ta* encode predicted nucleotide binding site type proteins that are characteristic of products of major resistance genes[4,21,22]. Several management strategies have been proposed and evaluated to minimize the blast disease incidence. Cultural practices, host plant resistance and the use of synthetic fungicides are the three strategies adopted to control rice blast[7,10]. Although the use of resistant cultivars is known to be the most effective control strategy. Therefore, the use of resistant varieties with multiple genes (gene pyramiding) is thought to be one of the most economically and environmentally efficient ways to avoid frequent breakdown of resistance and controlling the blast severity. Thus here we tried to evaluate the introgressed lines in different agro climatic regions with respect to their resistant and susceptible reaction.

MATERIAL AND METHODS

Multilocation evaluation of resistant lines were conducted for sixteen introgressed lines *viz.*, MSP-1, MSP-2, MSP-3, MSP-4, MSP-5, MSP-6, MSP-7, MSP-8, MSP-9, MSP-10, MSP-11, MSP-12, MSP-13, MSP-14, MSP-15 and MSP-16 possessing blast resistance genes with recurrent parents *i.e.*, BPT5204, Improved Samba masuri, Swarna and IR-64, donar parent (C101LAC, C101A51 and Tetep) with susceptible check (Co-39 and HR-12) and resistant check (Rasi) were these lines evaluated against blast disease in different agro climatic regions of Chhattisgarh and Telangana during *Rabi* 2017 and *Kharif* 2017. The details of Sixteen introgressed lines and blast resistance genes are given below in Table 1 and 2. These lines were evaluated in Uniform blast nurseries at four different locations *viz.*, IIRR Hyderabad, KVK Dhamatari (C.G.), RMDCARS Ambikapur (C.G.) and SGCARS Jagdalpur (C.G.). The fungus was isolated by tissue segmentation method[3]. Single spores were located and picked up microscopically and transferred to fresh sterilized Petri plates containing OMA medium. The Petri plates were incubated at 28^0C for 7 days and the fungus was identified following mycological description given by Ou[18]. After 14 days of incubation at 28°C, petri plates (90 mm) of *P. oryzae* isolate was washed with 20 ml of sterile distilled water to produce spore suspension. The concentration of the conidial suspension was adjusted to 1×10^5 conidia ml^{-1} using a haemocytometer. Each row in the nursery bed representing one isogenic line. Susceptible variety (HR-12) were sown around the nursery beds to maintain the blast disease. After 25 days these nursery beds were sprayed with sporulation of local blast isolate using a hand operated atomizer. Data was collected from nursery beds by using 0-9 scale after 15 days of spraying[6], (Table 1& 2 and Figure 1&2). Therefore multi-location introgressed trials

were conducted in different agro- climatic locations of major rice growing areas.

RESULTS AND DISCUSSION

In Chhattisgarh and Telangana multi-location trials were conducted during *Kharif*-2016-17 and *Rabi* 2017. The introgressed lines which are having resistance genes in BPT5204, Improved Samba mahsuri, Swarna and IR-64 background were collected from the IIRR, Rajendranagar. These lines were screened for blast reaction at four different locations. Phenotypic screening of the selected lines was performed during *Rabi* 2017 and *Kharif* 2017 in different agro climatic locations *viz.*, IIRR Hyderabad, KVK Dhamatari (C.G.), RMDCARS Ambikapur (C.G.) and SGCARS Jagdalpur (C.G.). Selected lines with target genes and HR-12 susceptible check were screened for blast resistance. These results indicated that MSP-1 (BPT5204//C101LAC), MSP-3 (BPT5204//Tetep), MSP-6 (BPT5204//C101LAC//C101A5//Tetep), MSP-7 (Swarna//C101LAC), MSP-8 (Swarna//C101A51), MSP-9 (Swarna//Tetep), MSP-11 (Swarna//C101LAC//Tetep), MSP-12 (Swarna //C101LAC//C101A5//Tetep), MSP-13 (IR64//C101A51), MSP-14 (IR64//Tetep) and MSP-16 (Improved Samba mahsuri//Tetep) showed complete resistance reaction (0-3) to blast disease at four regions and susceptible parent as a control check, which had the maximum disease incidence (7-9). MSP-2 (BPT5204//C101A51) showed resistance at IIRR, Hyderabad and KVK, Dhamtari, highly resistance at RMDCARS, Ambikapur and moderate resistance at SGCARS, Jagdalpur. MSP-4 (BPT5204//C101LAC//C101A51) showed resistance at IIRR Hyderabad, RMDCARS, Ambikapur and SGCARS, Jagdalpur (C.G.), while moderate resistance at KVK, Dhamtari. MSP-5 (BPT5204//C101LAC//Tetep) showed moderate resistance at IIRR Hyderabad and RMDCARS, Ambikapur, while resistance showed at SGCARS, Jagdalpur and highly resistance showed at KVK, Dhamtari. MSP-10 (Swarna //C101LAC//C101A51) and MSP-15 (Improved Samba mahsuri//C101A51) showed resistance at IIRR Hyderabad and SGCARS, Jagdalpur while highly resistance showed at RMDCARS, Ambikapur and moderate resistance showed at KVK, Dhamtari (Table 1 & 2 and Figure 1). The significant effect of genotype and environment interaction might suggest that genotypes possess different resistant genes and structures of the population, in terms of virulence genes and varied across different locations[12]. Similar trial was also conducted by Muralidharan *et al*[16] and evaluated rice genotypes carrying resistance genes to blast disease in multi-environment tests (METs) Tadukan carrying resistance gene *Pi-ta* showed small lesions infecting <2% leaf area indicating a very high level of durable resistance to blast disease. The METs clearly demonstrated the expression of a high degree of resistance in A57 carrying three resistance genes (*Pi-1*, *Pi-2* and *Pi-4*). A57 was identified as the best line that exhibited resistance to blast across the country in all rice growing environments irrespective of ecosystems. Abamu *et al.*[1] studied effects and Multiplicative Interaction Models which are widely used for analyzing main-effects and genotype by-environment (G×E) interactions in multilocation variety trials to gain insight into G×E in rice blast, and identify genotypes with high and stable resistance to the disease. Ramesh Babu *et al.*,[19] verified the introgressed lines for blast resistance studies revealed that, the introgressed lines (ILM-16 and ILM-29) with gene pyramiding of three genes (*Pi1*, *Pi2* and *Pi54*) showed complete resistant reaction at all different locations. The introgressed lines (ILM-10, ILM-11, ILM-15 and ILM-30-4) with two resistance genes (*Pi1* and *Pi2*) showed moderately resistant reaction. The introgressed line (ILM-30) with two resistance genes (*Pi2* and *Pi54*) showed moderately resistant reaction at three different locations.

Table 1: Details of different hot-spot locations of Chhattisgarh and Telangana

S. No.	Location	University/ Institute	State	Latitute	Longitute	Ecosystem	Elevation (in ft.)
1	Ambikapur	Rajmohini Devi College of Agriculture and Research Station (IGKV)	Chhattisgarh	23.696°N	82.216°E	Irrigated, Uplands	1878
2	Dhamtari	Krishi Vigyan Kendra (IGKV)	Chhattisgarh	20.709°N	81.550°E	Irrigated, Midland	1063
3	Hyderabad	Indian Institute of Rice Research (ICAR-IIRR)	Telangana	17.320°N	78.393°E	Irrigated, Lowland	1696
4	Jagdalpur	S. G. College of Agriculture and Research Station (IGKV)	Chhattisgarh	19.002°N	81.046°E	Irrigated, Lowland	1798

Table 2: Performance of rice cultivar BPT5204, ISM, Swarna and IR-64 introgressed lines carrying blast resistance genes under different agro climatic regions of Chhattisgarh and Telangana during *Rabi* 2017 and *Kharif* 2017

SN	Designation	Cross Combination	Genes	Disease reaction to blast 0-9 Scale (IRRI, 1996)*							
				Ambikapur	DR	Jagdalpur	DR	Dhamtari	DR	Hyderabad	DR
1	MSP-1	BPT5204 X C101LAC	*Pi1*	3.33±0.58	R	3.67±0.58	R	3.00±0.00	R	3.00±0.00	R
2	MSP-2	BPT5204 X C101A51	*Pi2*	1.67±0.58	HR	4.00±0.00	MR	2.00±0.00	R	2.50±0.58	R
3	MSP-3	BPT5204 X TETEP	*Pi54*	3.67±0.58	R	3.33±0.58	R	1.67±0.58	HR	3.50±0.58	R
4	MSP-4	BPT5204 X C101LAC X C101A51	*Pi1 and Pi2*	3.67±0.58	R	2.33±0.58	R	4.67±0.58	MR	3.00±0.00	R
5	MSP-5	BPT5204 X C101LAC X TETEP	*Pi1 and Pi54*	4.00±0.00	MR	3.00±0.00	R	1.67±0.58	HR	4.00±0.00	MR
6	MSP-6	BPT5204 X C101LAC X C101A51 X TETEP	*Pi1, Pi2 and Pi54*	2.67±0.58	R	2.33±0.58	R	1.00±0.00	HR	2.50±0.58	R
7	MSP-7	SWARNA X C101LAC	*Pi1*	1.00±0.00	HR	3.33±0.58	R	1.00±0.00	HR	1.50±0.58	HR
8	MSP-8	SWARNA X C101A51	*Pi2*	3.67±0.58	R	3.67±0.58	R	1.00±0.00	HR	2.50±0.58	R
9	MSP-9	SWARNA X TETEP	*Pi54*	1.00±0.00	HR	3.33±0.58	R	1.67±0.58	HR	2.00±0.00	R
10	MSP-10	SWARNA X C101LAC X C101A51	*Pi1 and Pi2*	1.33±0.58	HR	2.67±0.58	R	4.67±0.58	MR	3.00±0.00	R
11	MSP-11	SWARNA X C101LAC X TETEP	*Pi1 and Pi54*	3.67±0.58	R	2.33±0.58	R	3.00±0.00	R	1.50±0.58	HR
12	MSP-12	SWARNA X C101LAC X C101A51 X TETEP	*Pi1, Pi2 and Pi54*	3.00±0.00	R	1.67±0.58	HR	2.67±0.58	R	2.50±0.58	R
13	MSP-13	IR-64 X C101A51	*Pi2*	2.00±0.00	R	3.33±0.58	R	2.67±0.58	R	2.00±0.00	R
14	MSP-14	IR-64 X TETEP	*Pi54*	1.00±0.00	HR	3.33±0.58	R	1.00±0.00	HR	3.00±0.00	R
15	MSP-15	ISM X C101A51	*Pi2*	1.00±0.00	HR	2.67±0.58	R	5.67±0.58	MR	3.00±0.00	R
16	MSP-16	ISM X TETEP	*Pi54*	1.00±0.00	HR	2.33±0.58	R	1.67±0.58	HR	2.50±0.58	R
18	BPT 5204	Recurrent parent	-	7.33±0.58	S	7.33±0.58	S	5.67±0.58	MR	7.50±0.58	S
17	SWARNA	Recurrent parent	-	8.67±0.58	HS	8.33±0.58	HS	6.33±0.58	S	8.50±0.58	HS
19	ISM	Recurrent parent	-	7.00±0.00	S	7.00±0.00	S	5.67±0.58	MR	7.50±0.58	S
20	IR-64	Recurrent parent	-	2.67±0.58	R	3.33±0.58	R	4.67±0.58	MR	3.00±0.00	R
21	C101LAC	Donor parent	*Pi1*	3.00±0.00	R	5.33±0.58	MR	1.00±0.00	HR	3.00±0.00	R
22	C101A51	Donor parent	*Pi2*	4.00±0.00	MR	4.67±0.58	MR	1.00±0.00	HR	3.00±0.00	R
23	TETEP	Donor parent	*Pi54*	1.00±0.00	HR	2.67±0.58	R	1.00±0.00	HR	1.00±0.00	HR
24	RASI	Resistant check	-	1.00±0.00	HR	2.33±0.58	R	1.00±0.00	HR	3.00±0.00	R
25	CO-39	Susceptible check	-	7.67±0.58	S	8.67±0.58	HS	5.00±0.00	MR	9.00±0.00	HS
26	HR-12	Susceptible check	-	9.00±0.00	HS	9.00±0.00	HS	6.33±0.58	S	9.00±0.00	HS

*****Mean and Standard deviation; 0 to 1- Highly Resistance (HR), 2 to 3- Resistance (R), 4 to 5- Moderate resistant (MR), 6 to 7- Susceptible (S), 8 to 9- Highly Susceptible (HS); ISM-Improved Samba Mahsuri, DR-Disease Reaction

Fig. 1: A. Pure Culture of *P. oryzae* and inoculation by hand atomizer, B. Evaluation of introgressed lines on UBN method

CONCLUSION

The present study revealed that multi-location evaluation trials of MSP-1, MSP-3, MSP-6, MSP-7, MSP-8, MSP-9, MSP-11, MSP-12, MSP-13, MSP-14 and MSP-16 with resistant genes (*Pi1*, *Pi2* and *Pi54*) showed complete resistance reaction (0-3) to blast disease at four locations. While MSP-4 (*Pi1* and *Pi2*), MSP-10 (*Pi1* and *Pi2*), MSP-15 with (*Pi2*) genes were moderately resistant at KVK Dhamtari. Similarly MSP-2 (*Pi2*) at SGCARS Jagdalpur and MSP-5 (*Pi2* and *Pi54*) at RMDCARS Ambikapur and IIRR, Hyderabad showed moderately resistant reaction respectively.

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