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Evaluation of Donor and Advanced Lines for Blast Resistance Across Agroclimatic Zones of Andhra Pradesh and Telangana

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Abstract

Rice blast, caused by the fungal pathogen *Pyricularia oryzae*, is a major threat to rice production worldwide. As *P. oryzae* is a highly evolving and dynamic pathogen and adapting host plant resistance is the most significant way of managing the blast disease. The present study aims to assess the performance of rice genotypes across different locations to understand their adaptability and also to monitor the virulence patterns of the blast pathogen population. A multi-location trail was carried out with 39 cultivars consisting of near-isogenic lines, international differentials, donors and commercial cultivars possessing different genes for blast resistance by adopting Uniform Blast Nursery (UBN) at six locations in different agroclimatic zones of Andhra Pradesh and Telangana during *Kharif* 2023. There was significant variation in disease pressure among locations, with ARS, Nellore exhibiting the highest Location Severity Index (LSI) of 4.44 and ARS, Uttukur showing the lowest LSI of 2.76. The susceptibility Index (SI) 7.45 was recorded highest in the susceptible check (HR-12) while the resistant check Tetep showed the lowest SI of 2.16. Several genotypes carrying the *Pi-1*, *Pi-12*, *Pi-z+Pi-a+Pi-i*, *Pi-54*, *Pi-9* and *Pi-kh+* genes demonstrated consistent resistance across different locations. The study highlights the importance of considering gene combinations for durable resistance and the need for site-specific adaptation in rice breeding programs to combat rice blast effectively.

Keywords: Agroclimatic zones, Blast disease, Differential lines, Rice, Telangana

Introduction

Rice is one of the most significant edible cereal grains. Rice is a rich source of carbohydrates, which is essential for providing energy. It also contains vitamins and minerals, contributing to a balanced diet and it serves as a primary staple food for more than two-thirds of the world's population (Fukagawa and Ziska, 2019). Although rice output has expanded to meet global demand, productivity has not increased appreciably. One of the major constraints faced by the rice growers for low productivity is biotic stress. Among the biotic factors, diseases remain a persistent challenge in rice cultivation. The rice crop suffers

from diseases caused by fungi, bacteria, viruses, phytoplasma, nematodes and other non-parasitic disorders. Among the fungal diseases blast disease is caused by *Pyricularia oryzae* Cavara which is a significant threat to rice production worldwide (Anand Kumar *et al*., 2023). It can cause severe loss in yield to the extent of 70-80% in various rice ecosystems (Aruna *et al*., 2015). *P. oryzae* is constantly evolving and is regarded as a threat to global food security. Management of blast disease is carried out using various strategies, including crop rotation, fungicide application and planting of resistant varieties. Among the various methods for managing plant diseases, genetic resistance is widely regarded as the most effective and sustainable, providing both economic and environmental benefits (Bonman, 1992). Rice blast resistance is a classic gene-for-gene interaction, where a major resistance gene in the host plant effectively counters *P. oryzae* strains carrying the corresponding avirulence gene (Silue *et al*., 1992). Developing rice cultivars with durable resistance to blast is crucial for ensuring food security. This study aimed to evaluate the resistance of various rice genotypes containing of near-isogenic lines, international differentials, donors and commercial cultivars possessing different genes for blast resistance under different agro-climatic conditions in Andhra Pradesh and Telangana, India.

Materials and Methods

The present study was carried out to evaluate blast disease in different agro-climatic regions of Andhra Pradesh and Telangana during *kharif* 2023.These lines were evaluated in Uniform blast nurseries at six different locations *viz.*, IIRR Hyderabad, RARS Maruteru (A.P.), ARS Nellore (A.P.), ARS Ragolu (A.P.), RARS Nandyal (A.P.) and ARS Uttukur (A.P.). The details of the locations were presented in the **Table 1**. Thirty-nine cultivars consisting of near-isogenic lines, international differentials, donors and commercial cultivars possessing different genes for blast resistance including appropriate susceptible (HR-12, Co-39) and resistance (Tetep, Rasi and IR 64) checks were evaluated for blast resistance. The fungus was isolated by tissue segmentation method (Bonman *et al.*, 1987). Single spores were located and picked up microscopically and transferred to fresh sterilized Petri plates containing Oat Meal Agar (OMA) medium. The Petri plates were incubated at 28 °C for 7 days and the fungus was identified following mycological description (Ou, 1985). 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.

Uniform Blast Nursery (UBN) was a 10x1 m bed. The soil was pretreated with FYM, NPK and commercial sulphuric acid before tilling to distribute the manure uniformly in the soil. Highly susceptible variety (HR 12) was sown as a border row on either side of the bed and between the test material rows. After every 10 rows of test materials HR 12 was planted which acts as spreader rows. Test material was sown in 50 cm rows perpendicular to the border row with 10 cm spacing between the rows (**Figure 1**).

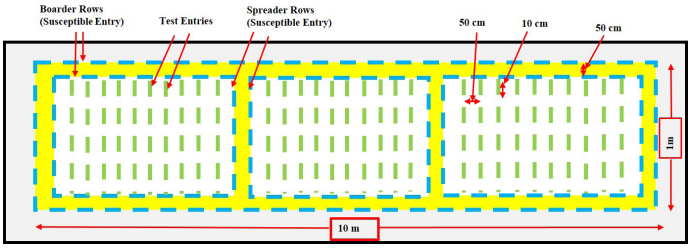


Figure 1: Layout of Uniform Blast Nursery

25 days after sowing these nursery beds were sprayed with spore suspension of local blast isolate using a hand-operated atomizer. Relative humidity was maintained by sprinkling water as mist with

30 min time interval depending on the intensity of temperature. The UBNs were covered with polythene sheets during night to maintain the humidity to build up more spore load and in turn to increase the disease pressure on the varieties. Scoring was done after 10-15 days of post infection depending on the severity of the infection on the susceptible check using SES scale (IRRI, 1996) (**Table 2**). Scoring was done after 10-15 days of inoculation depending on the severity of the infection on the susceptible check using SES scale (IRRI, 1996). The data thus obtained from field experiments in a Randomized Block Design were analyzed statistically by Two-way ANOVA (Gomez and Gomez, 1984).

Table 1: Details of different locations of Andhra Pradesh and Telangana

Agro climatic zone	Location	Research Station/ Institute	State	Latitude	Longitude	Ecosystem
Godavari Zone	Maruteru	Regional Agricultural Research Station (RARS)	Andhra Pradesh	16.6299° N	81.7457° E	Irrigated, Lowland
Southern Zone	Nellore	Agricultural Research Station (ARS)	Andhra Pradesh	14.4303° N	79.9987° E	Irrigated, Lowland
North coastal Zone	Ragolu	Agricultural Research Station (ARS)	Andhra Pradesh	18.16412°N	83.5010° E	Irrigated, Lowland
Scarce rainfall Zone	Nandyal	Regional Agricultural Research Station (RARS)	Andhra Pradesh	15.4786° N	78.4831° E	Rainfed, Upland
Southern Zone	Uttukur	Agricultural Research Station (ARS)	Andhra Pradesh	14.4373° N	78.8050° E	Rainfed, Upland
Southern Telangana Zone	Hyderabad	Indian Institute of Rice Research (ICAR-IIRR)	Telangana	17.3871° N	78.4916° E	Irrigated, Lowland

Results and Discussions

The results revealed that the intensity of rice blast disease incidence varied at different test locations. Among the locations, the Location Severity Index (LSI) was recorded high at ARS, Nellore (4.44) located in the Southern region of the agroclimatic zone of Andhra Pradesh followed by RARS, Maruteru (3.70) located in the Godavari zone and the least disease incidence was recorded at ARS, Uttukur (2.76) located in the Southern region of the agroclimatic zone of Andhra Pradesh (**Figure 2**). HR-12 showed susceptibility to blast in all the regions (**Plate 1a** and **1b**). HR-12 showed highest susceptibility index (7.31) and resistant check Tetep recorded lowest susceptibility index (2.06) while, Rasi and IR-64 recorded an average score of 2.95 and 3.10 respectively (**Table 2**).

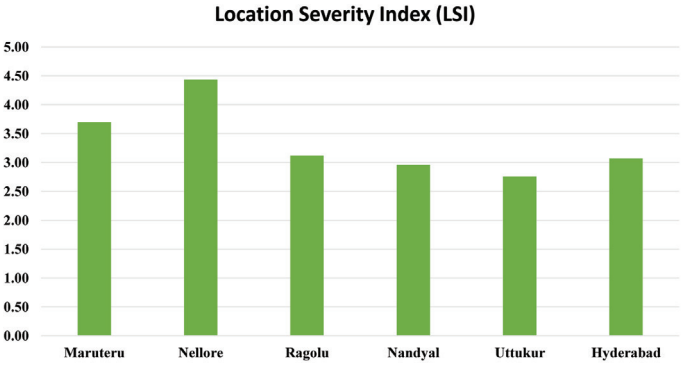


Figure 2: Location Severity Index (LSI) of different test locations

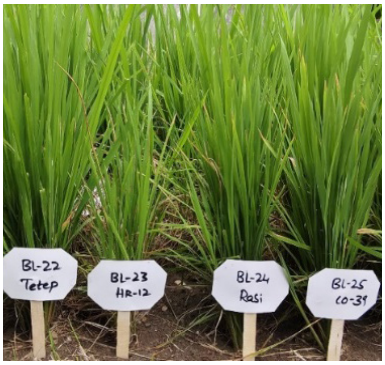
The differential lines RP Biopatho-3 (*Pi-2*), RP Biopatho-4 (*Pi-54*) and PRS-59 (*Pi-9*) showed resistant

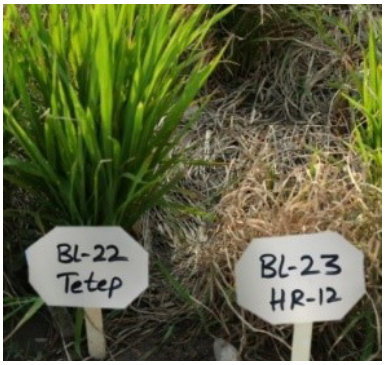



RARS, Maruteru **ARS, Nellore** **ARS, Ragolu**

Plate 1a: Multilocation evaluation of differential lines carrying different blast resistant genes





RARS, Nandyal **ARS, Uttukur** **IIRR, Hyderabad**

Plate 1b: Multilocation evaluation of differential lines carrying different blast resistant genes

reaction (<3) to blast disease in all the locations. PRS-17 (*Pi-9*+*Pi-54*) exhibited resistant reaction (<3) in four locations, whereas at IIRR, Hyderabad and ARS, Uttukur it showed moderately resistant reaction of 3.15 and 3.52, respectively. Differentials with combinations of genes BL-122 (*Pi-1*+*Pi-2*) and A57 (*Pi-1*+*Pi-2*+*Pi-4*) showed resistant reaction in all the locations except at RARS, Maruteru and ARS, Nellore. Differential line Zenith (*Pi-z*+*Pi-a*+*Pi-i*) showed resistant reaction in all the locations except in ARS, Nellore. C104 PKT (*Pi-3*) recorded susceptible reaction in RARS, Maruteru, ARS, Nellore and ARS, Ragolu. Tadukan (*Pi-ta*) showed susceptible reaction only in ARS, Nellore and it showed resistant reaction in all other locations.

The susceptible check (HR-12) succumbed to blast in all the locations except at ARS, Uttukur it showed moderately resistant reaction (5.04). The resistant check Tetep (*Pi-k*$^{h+}$) showed resistant reaction (<3) to blast disease in all the test locations. Resistant check IR 64 was found resistant (<3) only at RARS, Nandyal, while it showed moderately resistant reaction in the remaining locations. Another resistant check Rasi showed resistant reaction (<3) in four locations and at ARS, Nellore and IIRR, Hyderabad it exhibited moderately resistant reaction. The susceptible check Co-39 showed resistant reaction (<3) at ARS, Ragolu and ARS, Uttukur while it exhibited moderately resistant reaction at RARS, Nandyal and IIRR, Hyderabad. It exhibited a moderately resistant reaction at RARS, Maruteru and susceptible reaction at ARS, Nellore.

Table 2: Details and performance of the differential lines to *Pyricularia oryzae* under different agro climatic regions during *kharif* -2023

S. No.	Desig-nation	Entry No.	Resistance Gene	Disease reaction to blast 0-9 Scale (IRRI, 1996)*												
				Maruteru	R/S	Nellore	R/S	Ragolu	R/S	Nandyal	R/S	Uttukur	R/S	Hyderabad	R/S	SI**
1	BL1	C101 LAC	*Pi-1*	2.80	R	5.53	MS	3.43	MR	2.43	R	3.22	MR	3.45	MR	3.48
2	BL2	C101 A51	*Pi-2*	3.69	MR	5.61	MS	3.18	MR	3.50	MR	3.01	MR	3.88	MR	3.81
3	BL3	C104 PKT	*Pi-3*	5.37	MS	4.87	MS	5.10	MS	3.17	MR	3.21	MR	3.58	MR	4.22
4	BL4	C101 TTP	*Pi-4b*	4.91	MS	5.62	MS	2.35	R	2.25	R	2.35	R	2.78	R	3.38
5	BL5	RIL - 10	*Pi-12*	2.74	R	5.48	MS	2.14	R	3.50	MR	3.11	MR	2.65	R	3.27
6	BL6	RIL - 29	*Pi-7*	5.31	MS	3.61	MR	3.54	MR	3.63	MR	2.28	R	3.60	MR	3.66
7	BL7	O. minuta	*Pi-9*	3.63	MR	4.82	MS	2.30	R	3.77	MR	2.10	R	2.27	R	3.15
8	BL8	BL-122	*Pi-1 + Pi-2*	4.07	MS	4.12	MS	2.69	R	3.12	MR	3.36	MR	2.26	R	3.27
9	BL9	BL-245	*Pi-2 + Pi-4*	4.25	MS	3.62	MR	2.27	R	3.21	MR	3.04	MR	3.07	MR	3.24
10	BL10	A 57	*Pi-1 + Pi-2 + Pi-4*	4.60	MS	5.22	MS	2.17	R	2.57	R	2.15	R	2.53	R	3.21
11	BL11	C101 PKT	*Pi-4a*	3.87	MR	4.56	MS	3.24	MR	3.22	MR	3.23	MR	2.07	MR	3.36
12	BL12	Raminad-STR-3	-	3.32	MR	5.68	MS	3.47	MR	2.53	R	3.02	MR	2.76	R	3.46
13	BL13	Zenith	*Pi-z + Pi-a + Pi-i*	2.75	R	4.43	MS	2.67	R	2.16	R	2.22	R	2.42	R	2.77
14	BL14	NP - 125	-	2.28	R	5.91	MS	3.48	MR	3.32	MR	3.02	MR	3.20	MR	3.54
15	BL15	USEN	*Pi-a*$^{+}$	3.47	MR	3.97	MR	3.57	MR	3.15	MR	3.10	MR	4.89	MS	3.69
16	BL16	Dular	*Pi-k*$^{a+}$	3.28	MR	3.88	MR	2.88	R	2.22	R	3.31	MR	2.63	R	3.03
17	BL17	Kanto - 51	*Pi-k*	5.21	MS	4.64	MS	2.18	R	2.80	R	3.14	MR	2.79	R	3.46
18	BL18	Shi-tia-tao	*Pi-k*^{s}	5.44	MS	3.92	MR	2.42	R	2.25	R	2.30	R	5.30	MS	3.60
19	BL19	Calaro	*Pi-k*^{s}	5.22	MS	3.78	MR	2.48	R	3.23	MR	2.37	R	3.17	MR	3.37
20	BL20	Tadukan	*Pi-ta*	3.69	MR	5.66	MS	2.82	R	2.20	R	2.20	R	2.77	R	3.22
21	BL21	IR - 64	Resistant	3.85	MR	3.89	MR	3.05	MR	2.22	R	3.12	MR	3.05	MR	3.20
22	BL22	Tetep	*Pi-k*$^{h+}$	2.47	R	2.97	R	2.71	R	1.97	HR	1.83	HR	1.02	HR	2.16

23	BL23	HR - 12	Susceptible	7.98	S	8.69	HS	7.44	S	6.54	S	5.04	MS	9.00	HS	7.45
24	BL24	Rasi	Resistant	2.87	R	3.95	MR	2.78	R	2.14	R	2.22	R	3.67	MR	2.94
25	BL25	Co - 39	Susceptible	4.25	MS	6.92	S	2.35	R	3.12	MR	2.43	R	3.18	MR	3.71
26	BL26	RP Patho-1	*Pi-1*	2.70	R	4.73	MS	2.64	R	2.37	R	3.10	MR	2.33	R	2.98
27	BL27	RP Patho-2	*Pi-2*	3.90	MR	4.96	MS	3.46	MR	3.05	MR	2.07	R	2.69	R	3.36
28	BL28	RP Patho-3	*Pi-54*	2.54	R	3.80	MR	2.32	R	3.12	MR	3.05	MR	3.66	MR	3.08
29	BL29	RP Patho-7	*Pi-1*	2.70	R	3.60	MR	3.48	MR	3.57	MR	3.01	MR	2.45	R	3.14
30	BL30	RP Patho-8	*Pi-2*	3.60	MR	3.78	MR	3.78	MR	2.48	R	2.35	R	2.53	R	3.09
31	BL31	RP Patho-9	*Pi-54*	3.73	MR	5.67	MS	3.50	MR	3.73	MR	3.07	MR	2.22	R	3.65
32	BL32	RP Biopatho-1	*Pi-2*	3.96	MR	4.69	MS	4.58	MS	2.67	R	2.14	R	2.13	R	3.36
33	BL33	RP Biopatho-2	*Pi-54*	2.59	R	3.86	MR	2.82	R	3.11	MR	3.15	MR	2.66	R	3.03
34	BL34	RP Biopatho-3	*Pi-2*	2.62	R	2.90	R	2.88	R	2.28	R	2.13	R	2.71	R	2.59
35	BL35	RP Biopatho-4	*Pi-54*	2.77	R	2.47	R	2.85	R	2.42	R	2.08	R	2.56	R	2.52
36	BL36	PRS-17	*(Pi-9 + Pi-54)*	2.49	R	2.65	R	2.50	R	2.98	R	3.52	MR	3.15	MR	2.88
37	BL37	PRS-50	*Pi-54*	3.74	MR	2.80	R	3.69	MR	3.44	MR	2.15	R	3.67	MR	3.25
38	BL38	PRS-58	*Pi-9*	2.71	R	2.75	R	3.44	MR	3.87	MR	3.22	MR	2.47	R	3.08
39	BL39	PRS-59	*Pi-9*	2.93	R	3.02	R	2.85	R	2.12	R	2.12	R	2.59	R	2.60
	Location Severity Index (LSI)			**3.70**		**4.44**		**3.12**		**2.96**		**2.76**		**3.07**		

*Blast scale (IRRI, 1996), 0- HR, 1-R, 2 to 3-MR, 4 to 5-MS, 6 to 7-S, 8 to 9-HS; R/S- Resistant/Susceptible, HR-Highly Resistance, R-Resistance, MR-Moderate resistant, MS- Moderate Susceptible, S- Susceptible, HS- Highly Susceptible, ** SI-Severity Index

Statistical analysis was carried out using Two way Anova (RBD), the results obtained are presented in the **Table 3**.

Table 3: LSD of test lines and locations

LSD	Differential lines	Locations
C.D.	0.81	0.32
SE(m)	0.29	0.11
SE(d)	0.41	0.16
C.V.	10.07	10.07

The difference in disease reaction scores of susceptible and resistant checks reveals the shift in the pathogen population. The results also reveal that the disease severity and the performance of genes varied in different agroclimatic zones. Apex and minimal disease severity were recorded in the southern zone alone due to varied climatic conditions. Similar trial was also conducted by Muralidharan *et al*., (2004) 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*). A 57 was identified as the best line that exhibited resistance to blast across the country in all rice growing environments irrespective of ecosystems.

Similar results were observed by Jahaar *et al*., (2018) screened 23 Near Isogenic Lines (NILs) at four different agroclimatic locations and reported that NILs with combination of resistant genes *i.e*., BPT5204×C101LAC×C101A5×Tetep (*Pi-1*, *Pi-2* and *Pi-54*), Swarna×C101LAC×Tetep (*Pi-1* and *Pi-54*) and Swarna×C101LAC×C101A5×Tetep (*Pi-1*, *Pi-2* and *Pi-54*) showed complete resistance to blast disease in all the locations.

In the same way, Abamu *et al*., (1998) 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. Divya *et al*., (2013) also reported that lines with gene combinations *Pi-1+Pi-2+Pi-33+Pi-54* and *Pi-1+Pi-2+Pi-33* were highly resistant to blast disease than those with single genes indicating that these non-allelic genes have a complementary effect.

The present study offers valuable insights into the genetic factors underlying blast resistance in rice. The Southern Zone saw the highest and lowest LSI values at ARS, Nellore and ARS, Uttukur, respectively, reflecting changes in pathogen virulence and environmental factors. The resistant genes *Pi-1*, *Pi-12*, *Pi-z* + *Pi-a* + *Pi-i*, *Pi-54* and *Pi-9* and the demonstrated effectiveness of combining these genes provide promising avenues for breeding programs to develop cultivars that are more resilient to this devastating disease.

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