Research Article
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MULTILOCATION EVALUATION FOR IDENTIFICATION OF SOURCES OF RESISTANCE TO BLAST AND BACTERIAL LEAF BLIGHT IN RICE

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ABSTRACT

Rice (*Oryza sativa* L.) is a principal staple food crop sustaining more than half of the global population. However, its productivity is significantly constrained due to occurrence of blast (*Magnaporthe oryzae)* and bacterial leaf blight (*Xanthomonas oryzae* pv. *oryzae)*. Although chemical control is commonly used, the effectiveness is often limited due to high input cost, environmental concerns, emergence of pathogen resistance and inconsistent reaction under field conditions. Moreover, chemical control of BLB is generally less effective. While, several resistant varieties have been developed, durability of resistance is frequently compromised due to the evolution of new races and pathotypes. Therefore, continuous identification of novel resistance sources and systematic screening of advanced breeding materials are essential. A Multiple Resistance Screening Trial (MRST– PJTAU) comprising up of 147 germplasm lines including MLT lines, advanced breeding lines and hybrids along with checks were evaluated against blast and BLB at each three locations during *kharif*, 2024 and *rabi*, 2025-26 under artificial inoculations conditions. Two entries, namely, KPS-12657 and RDR-4914, exhibited resistance against leaf blast, whereas, seven rice genotypes, namely, KNM 12466, WGL 1957, RDR 4621, RNR 37910, RNR 44035, WGL 1790, and WGL 1792 demonstrated highly resistant reaction to neck blast. Further, three entries (WGL 2042, RNR 41714 and WGL 1790) exhibited consistent resistance to BLB across multiple locations providing valuable resources for durable resistant rice breeding. Notably, WGL 1790 also demonstrated resistance to neck blast and BLB, indicating potential donor for multiple disease resistance.

Keywords: Host plant resistance, BLB, Blast, Multi-location screening, Sources of resistance

Rice (*Oryza sativa* L.) constitutes a foundational food crop globally, with over ninety per cent of its global production and consumption concentrated within the Asian continent. Concomitant with sustained growth in the global population, a nearly 14.5% escalation in global rice consumption is projected by 2030 (Yuan *et al*., 2021). However, the realization of this objective, however, presents substantial challenges, primarily attributable to the considerable impact of various biotic stressors upon rice productivity, particularly insect-pests and pathogenic diseases (Simon *et al*., 2023). Among the diseases affecting the rice crop, blast (*Magnaporthe oryzae*) and bacterial leaf blight (BLB) (*Xanthomonas oryzae* pv. *oryzae*) constitute the major diseases posing a substantial threat due to their wide distribution and potential damage under favorable conditions (Alam *et al*., 2024). Blast infection may occur across various growth stages of the crop and is associated with potential yield losses, which can range 10 – 30% annually (Pedrozo *et al*., 2025). The severity of the disease is heightened in both upland and lowland ecosystems, particularly under propitious environmental conditions (Asibi *et al*., 2019). Conversely, BLB may induce systemic infection during the maximum tillering stage, potentially resulting in 20 – 40% yield loss (Alam *et al.,* 2024). Susceptible rice cultivars may experience yield losses potentially approaching cent per cent, contingent upon factors such as prevailing meteorological conditions, varietal characteristics, the regime of nitrogen fertilizer application, and the timing of onset of infection (Kanipriya *et al*., 2023).

Although chemical control measures including fungicides against blast and bactericides against BLB are commonly used by the farmers, their efficacy is frequently constrained by factors including elevated input costs, pressing environmental considerations, the emergence of pathogen resistance, and inconsistent field performance (Salleh *et al*., 2022). Furthermore, the chemical control measures for BLB appears generally attenuated under field conditions and no effective bactericides commercially available (Javeedvali *et al*., 2024). Consequently, the deployment of host plant resistance (HPR) typically represents the most economical, ecologically sound, environmentally safe and sustainable strategy for the management of both diseases (Ramprasad *et al*., 2024).

As of now, 46 BLB resistance genes and 102 rice blast resistance genes (R-genes) have been

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reported (Fiyaz *et al*., 2022; Thulasinathan *et al*., 2023). Among these, three genes for BLB (*xa5, xa13* and *Xa21*) and two genes for blast (*Pi1* and *Pi54*) have been widely used in marker-assisted breeding for development of varieties suitable for major rice growing regions of India (Sharma *et al*., 2012; Joseph *et al*., 2004). While numerous resistant varieties have been successfully developed *via* conventional breeding and gene introgression programs (Ramprasad *et al*., 2024), the durability of this resistance is frequently compromised by the ongoing evolution of novel pathogen races and pathotypes (Alam *et al*., 2024). Consequently, the continuous identification of novel resistance sources and the systematic screening of advanced breeding materials constitute essential endeavors. In this context, the present investigation sought to evaluate 147 rice genotypes for their resistance against blast and BLB under artificial inoculation conditions through multi-location testing. The primary objective involved the identification of stable resistant genotypes amenable for utilization as donor parents within breeding programs, thereby facilitating the development of durable, disease-resistant rice varieties.

MATERIAL & METHODS

Plant Materials

The experiment was conducted under the Multiple Resistance Screening Trial (MRST-PJTAU) to identify sources of resistance against blast and bacterial leaf blight (BLB) during *kharif*, 2024 and *rabi*, 2024-25 across various rice research centres of PJTAU. A total of 147 rice genotypes comprising of multi-location trial (MLT) lines, advanced breeding lines, hybrids, resistant and susceptible checks (Table 1) were evaluated for BLB and blast resistance under field and UBN conditions. Across the locations, the screening trial was conducted with Randomized Completely Block Design (RCBD) with resistant and susceptible checks and the disease wise location details were presented in Table 2. The locations tested for blast and BLB are the hot-spot locations. Artificial inoculation was employed to ensure adequate disease pressure under both field and UBN conditions for BLB and blast. The genotypes were nominated from various rice research centres of PJTAU and centre wise distribution of rice genotypes nominated by rice breeders were presented in Table 3.

Table 1. Category of rice genotypes used in this study:

Planting materials	Genotypes
Advanced breeding material	83
MLT lines	37
Introgressed lines	2
Hybrids	20
Checks	5
Total	**147**

Table 2. Locations tested under this study

S.No.	Name of the disease	Location of the Screening	Season
1.	Bacterial Leaf Blight	Rice Research Unit (RRU), ARI, Rajendranagar Regional Agricultural Research Station, Warangal Regional Sugarcane and Rice Research Station, Rudrur	*Kharif*, 2024
2.	Leaf Blast	Regional Agricultural Research Station, Polasa, Jagtial Regional Agricultural Research Station, Warangal Regional Sugarcane and Rice Research Station, Rudrur	*Rabi*, 2024-25
3.	Neck Blast	Rice Research Unit (RRU), ARI, Rajendranagar	*Kharif*, 2024

Table 3. Centre distribution of rice genotypes nominated for MRST-PJTAU trial

S.No.	Name of the Centre	No. of entries
1.	RRU, Rajendranagar (Hybrids)	21
2.	RRU, Rajendranagar (Varieties)	18
4.	RARS, Jagtial	16
5.	ARS, Kunaram	12
6.	RS&RRS, Rudrur	10
7.	RARS, Warangal	19
8.	ARS, Kampasagar	07
9.	Multi-location testing (MLTs) entries	37
10.	Checks	7
	Total	**147**

Phenotyping of MRST-PJTAU rice cultures for leaf blast resistance under Uniform Blast Nursery (UBN)

The UBN is a widely used screening system to evaluate rice germplasm, breeding lines, and checks for leaf blast resistance under high and uniform disease pressure. The phenotypic screening for leaf blast resistance was conducted during rabi, 2024-25 using the Uniform Blast Nursery (UBN) method. Each test entry was sown in a single row of 50 cm length with 10 cm spacing between rows. The highly susceptible check (TN-1) and resistant check (NLR 34449) were sown at every 10 test entries as infector row and the nursery was bordered on all sides by two rows of TN-1 (AICRPR, ICAR-IIRR). For artificial inoculation, a local Rajendranagar virulent isolate of Magnaporthe oryzae was mass multiplied on oat meal agar (OMA). Conidia was harvested and a spore suspension was prepared at a concentration of 1 × 10u spores ml{ ¹. To this suspension, Tween-20 was added and sprayed on 15-day-old seedlings using a hand atomizer to enhance disease development. To ensure severe leaf blast pressure, an additional inoculum was added to UBN plot to drive natural infection. The highly susceptible check (TN-1) was sown 20 days prior to the test entries in UBN and inoculated to create leaf blast to serve as inoculum. The diseased samples from TN-1 collected, chopped them into pieces of 3-6 cm long and scattered across the nursery. To create conducive weather conditions, the high humidity was maintained in the UBN after inoculation by running the misting unit during 11.00 AM to 03.00 PM at one hour interval for 15 days post inoculation. Disease severity was recorded using the Standard Evaluation System (SES) scale for rice (IRRI, 2014), where immune (0 score), resistant (1.0-3.0), moderately resistant (3.1-5.0), susceptible (5.1–7.0) and highly susceptible (7.1–9.0) were assigned to the test entries, respectively.

Phenotyping of rice germplasm lines for neck blast resistance under field conditions

Each test entry was planted in two rows of 1.5 m length, with 10 hills per row at a spacing of 20 × 15 cm. The highly susceptible variety TN-1 was used as a check. Artificial inoculation was performed at the booting stage using a conidial suspension of M. oryzae with a concentration of 1×10u conidia ml^{-1}. The severity of the disease was graded on a 0–9 scale (IRRI, 2014), with 0 = no lesion or one or two tiny lesions on the panicles; 1 = symptom on several pedicels or secondary branches; 3 = lesions on a few primary branches or the middle part of panicle axis; 5 = moderate infection with lesions covering half of the node or the uppermost internode or the lower part of panicle axis; 7 = heavy infection, lesions abundant on the panicle base or uppermost inter-node or panicle axis near the base with more than 30% of filled grains; 9 = very heavy infection, around the panicle base or uppermost internode or the panicle axis near the base with less than 30% of filled grains. Disease severity was assessed at physiological maturity. Based on the disease score, entries were categorized as highly resistant (0), resistant (1-3) moderately resistant (4–5) and susceptible (6–9).

Phenotyping of rice germplasm lines for BLB disease resistance under field conditions

Screening for BLB resistance was conducted using the leaf clipping method described by Kauffman et al. (1973). Artificial inoculation was carried out at 40–45 days after transplanting (maximum tillering stage) using a virulent isolate of Xanthomonas oryzae pv. oryzae. In each genotype, 10 plants were selected and 12–15 fully expanded leaves were clipped using sterilized scissors dipped in bacterial suspension. Disease severity was recorded based on the IRRI Standard Evaluation System (2014) using a 0–9 scale, where disease reactions ranged as highly resistant (1), resistant (3), moderately resistant (5), susceptible (7) and highly susceptible (9) depending on the percentage of diseased leaf area.

RESULTS AND DISCUSSION

Phenotyping of rice germplasm lines for leaf blast and neck blast resistance

One hundred & forty-eight Multiple Resistant Screening Trial rice genotypes were evaluated for resistance to leaf blast and neck blast diseases under multi-location field and uniform blast nursery conditions. The results revealed substantial genotypic variation in resistance levels, highlighting the ongoing challenge of pathogen evolution that frequently undermines varietal resistance (Alam et al., 2024). The location severity for leaf blast ranging from 3.0 to 6.3 score on 0–9 rating scale and neck blast (4.5) clearly showing the successful screening at respective locations (Table 4).

The ensuing results indicated that substantial variation in resistance levels among the genotypes. Among the tested lines, two entries, namely, KPS-12657 and RDR-4914, exhibited resistant reaction against leaf blast across the locations (Table 5). For neck blast disease, seven genotypes, namely, KNM 12466, WGL 1957, RDR 4621, RNR 37910, RNR 44035, WGL 1790, and WGL 1792 demonstrated highly resistant reaction (Fig. 1). However, the variation in reaction against blast displayed by the genotypes across locations, highlighting the limited durability of resistance due to ongoing pathogen evolution and the need for continuous screening for novel sources of resistance Ragulakollu et al., 2025; Sharma et al., 2023)

Phenotyping of rice germplasm lines for BLB disease resistance

Significant variation was additionally observed among the genotypes examined concerning their reaction to Bacterial Leaf Blight. The Location Severity Index of BLB ranging from 4.2 to 8.4 score on 0 – 9 SES rating scale clearly indicating that sufficient disease pressure and successful screening across the locations (Table 4). None of the genotypes were found highly resistant to BLB across the locations tested. Among the 148 evaluated genotypes, three genotypes ((WGL 2042, RNR 41714 and WGL 1790) consistently exhibited resistant to resistant reaction across all three testing locations such as Rice Research Unit, ARI, Rajendranagar; RARS, Warangal; and RS&RRS, Rudrur during kharif, 2024 (Table 5 & Fig. 1). Notably, WGL 1790 also demonstrated resistance to neck blast, indicating potential donor for multiple disease resistance for future breeding programmes. The stable performance of these genotypes under artificial inoculation with a virulent isolate of Xanthomonas oryzae pv. oryzae suggests possession of effective resistance genes against the BLB pathogen (Ramprasad et al., 2024), positioning them as promising donors for breeding programs aimed at durable resistance.

Table 4. The disease wise promising lines along with location severity index in the present study

S.No.	Name of the disease	No. of promising entries	Designation	Range of Location Severity Index (LSI)
1.	Leaf Blast	2	KPS-12657 and RDR-4914	6.3 (JGL), 3.0 (KPS)
2.	Neck Blast	7	KNM 12466, WGL 1957, RDR 4621, RNR 37910, RNR 44035, WGL 1790 and WGL 1792	4.5 (RNR)
3.	Bacterial Leaf Blight	2	RNR 41714 and WGL 1790	4.2 (RDR),6.5 (RNR), 8.3 (WGL)

Note: The LSI is range of incidence across the locations.

Table 5. Disease data along with Pedigree of rice genotypes tested under MRST-PJTAU trial

S. No.	Genotype	Pedigree	Collection	LB Pooled	NB	BLB Pooled
1	KNM 14319	JGL 11727 x MUT NS1//JGL 17004	Advanced line	2.5	5.0	7.0
2	KNM 13555	MTU 1156 X WGL 1097 // MUT NS1	Advanced line	4.0	1.0	5.7
3	KNM 12362	KNM 1638 X IET 23993 // RNR 15048	Advanced line	4.0	5.0	7.0
4	KNM 14376	KNM 118 x IR 04A 216	Advanced line	4.0	3.0	7.7
5	KNM 15970	WGL 962 X KNM 1638 // KNM 1638 X IET 23993	Advanced line	3.5	3.0	6.3
6	KNM 15736	WGL 962 X KNM 1638 // KNM 1638	Advanced line	4.0	1.0	5.7
7	KNM 15692	BPT 5204 X IR 09 N 251 // WGL 962 X WGL 1119	Advanced line	2.5	3.0	5.7
8	KNM 14283	BPT 5204 X MUT NS1	Advanced line	3.5	3.0	6.3
9	KNM 16056	IRTON 117 X PUSA 44 // KNM 118	Advanced line	5.5	5.0	5.7
10	KNM 16036	IRTON 117 X KNM 118	Advanced line	3.0	5.0	6.3
11	KNM 16006	IR 71033 X KNM 118 // IRTON 113	Advanced line	5.0	5.0	5.7

Cond.

S. No.	Genotype	Pedigree	Collection	LB Pooled	NB	BLB Pooled
12	KNM 13584	MTU 1156 X WGL 1097 // IR 10A 199	Advanced line	5.0	7.0	7.0
13	KNM 12466	(BPT 5204 x RNR 15048) x JGL 11727	Advanced line	3.5	0.0	6.3
14	TN-1	-	Check	3.0	7.0	7.0
15	ISM	-	Check	4.0	5.0	6.3
16	MTU 1001	-	Check	5.0	7.0	7.7
17	JGL 24423	-	Check	5.5	7.0	7.7
18	NLR 34449	-	Check	3.0	3.0	7.7
19	KPS 10329	Akshyadhan X RNR-15048	Advanced line	4.5	7.0	7.0
20	KPS 14341	AK Dhan x NLR-145	Advanced line	5.0	5.0	7.0
21	KPS14785	NDR359 x MTU 1010	Advanced line	4.5	5.0	7.0
22	KPS14625	HKR-0862 x RNR-15048	Advanced line	4.0	5.0	7.7
23	KPS14920	PAU 3832-79-4-3-1 x RNR-15048	Advanced line	5.0	5.0	7.0
24	KPS14758	HKR08425 x RNR-15048	Advanced line	2.5	5.0	6.3
25	KPS14515	JGL-17004 x BM-71	Advanced line	4.0	1.0	7.0
26	KPS 14932	PAU 3832-79-4-3-1 x RNR-15048	Advanced line	3.5	5.0	7.0
27	WGL 1880	RNR 15048/MTU 1156	Advanced line	4.5	7.0	7.0
28	WGL 1969	MTU 1010/BR-89-3812-C3	Advanced line	3.5	5.0	7.0
29	WGL 1972	MTU 1010/(MTU 1081/WGL 1143)	Advanced line	6.0	5.0	7.0
30	WGL 1977	KPS 3018/NLR 3354	Advanced line	2.5	5.0	7.0
31	WGL 2000	KNM 1638/WGL 1127	Advanced line	5.0	5.0	7.0
32	WGL 2001	KNM 1638/WGL 1127	Advanced line	5.0	5.0	7.0
33	WGL 2013	WGL 962/WGL 1196	Advanced line	3.5	5.0	7.0
34	WGL 2019	NLR 34449/WGL 1191	Advanced line	4.5	5.0	7.0
35	WGL 2024	IR 04A 216/CR dhan 201	Advanced line	6.0	5.0	7.0
36	WGL 2025	IR 04A 216/DRR dhan 44	Advanced line	5.0	5.0	7.0
37	WGL 2027	HHZ-26-SAL-Y1-Y1/MAS-946-1	Advanced line	5.0	3.0	6.3
38	WGL 2034	HHZ-26-SAL-Y1-Y1/DRR dhan 44	Advanced line	6.0	3.0	6.3
39	IBT-WGL -17	MTU -IL-1/RMSGM 3	Advanced line	5.0	5.0	5.7
40	IBT-WGL-26	MTU -IL-1/RMSGM 3	Advanced line	6.5	7.0	6.3
41	WGL 1927	WGL 962/MIL 12//WGL 962/BM 71	MAS derived lines	5.0	7.0	7.0
42	WGL 1931	WGL 962/MIL 12//WGL 962/BM 71	MAS derived lines	4.0	7.0	7.7
43	WGL 1942	(Siddi ×MIL-12) × (Siddi × BM71)	MAS derived lines	6.5	5.0	6.3
44	WGL 1957	(Siddi ×MIL-12) × (Siddi × BM71)	MAS derived lines	6.0	0.0	5.7
45	WGL 2042	KNM 118/BM 71//KNM 118/MIL 12	MAS derived lines	4.5	5.0	3.0
46	RDR 2742	KNM-110/MTU-1164	Advanced line	3.5	5.0	4.3
47	RDR 2747	(MTU-1164/GL-283)//CSA-43	Advanced line	5.0	7.0	5.7
48	RDR 4644	(JGL1798 /MUTNS1) // NLR40054 / MUTNS1)	Advanced line	4.0	7.0	7.0
49	RDR 4642	KNM1638 /MUTNS1	Advanced line	3.5	5.0	6.3
50	RDR 4626	MTU1156 /MUTNS1	Advanced line	5.0	7.0	4.3
51	RDR 4621	KNM118 X MUTNS1	Advanced line	4.0	0.0	7.0
52	RDR 5773	(HKR-08-83/WGL1131)//(RAMAPPA/ WGL1121)	Advanced line	4.5	5.0	5.7
53	RDR 5288	MTU1010/BR-89-382-C3	Advanced line	4.5	5.0	6.3
54	RDR 4927	(MTU1156 /MUTNS1)//JGL24423	Advanced line	5.5	1.0	6.3
55	JGL 46164	(IRTON 270 X RNR 15048) X NLR 34449	Advanced line	6.0	7.0	6.3
56	JGL 46210	(IRTON 270 X RNR 15048) X JGL 27356	Advanced line	4.0	7.0	6.3
57	JGL 46224	IR 71604-4-1-4-4-4-2-2-2R X JGL 20779	Advanced line	5.0	7.0	7.0

Cond.

S. No.	Genotype	Pedigree	Collection	LB Pooled	NB	BLB Pooled
58	JGL 46549	(Pranahitha X ISM(Pi54)) X MTU 1010 NIL (Gna)	Advanced line	2.5	1.0	7.0
59	JGL 46298	JMS 18B X JGL 24423	Advanced line	4.0	5.0	6.3
60	JGL 46211	(NSN 1/95 X RNR 15048) X JGL 27356	Advanced line	5.0	7.0	7.0
61	JGL 47849	JGL 11118 X IR 14K 642	Advanced line	3.5	1.0	6.3
62	JGL 47870	(NLR 34449 X IET 23993) X (JGL 28545	Advanced line	4.0	1.0	7.0
		X Rathuheenathi)				
63	JGL 47877	(WGL 915 X PTB 33) X JGL 24423	Advanced line	4.0	3.0	7.0
64	JGL 47949	JGL 24423 X MTU 1010 NIL	Advanced line	3.0	5.0	7.0
65	JGL 46239	IR 71604-4-1-4-4-4-2-22R X JGL 20779	Advanced line	5.5	5.0	6.3
66	JGL 46429	JGL 24423 X MTU 1010 NIL	Advanced line	4.5	5.0	6.3
67	JGL 47951	JGL 24423 X MTU 1010 NIL	Advanced line	2.5	5.0	6.3
68	JGL 47973	(Pranahitha X ISM) X MTU 1010 NIL	Advanced line	5.0	5.0	6.3
69	JGL 47861	JGL 26965 X Aganni	Advanced line	4.5	1.0	7.0
70	JGL 44139	(MUT NS1 X NLR 34449) X MTU 1010	Advanced line	4.5	3.0	6.3
71	JGLH 489		Hybrid	3.5	5.0	6.3
72	JGLH 518		Hybrid	4.5	5.0	6.3
73	JGLH 490		Hybrid	4.5	5.0	6.3
74	JGLH 514		Hybrid	6.0	5.0	6.3
75	JMS 24B		Hybrid	5.5	5.0	6.3
76	RNRH 139	CMS 46A x SN 923	Hybrid	5.0	3.0	5.7
77	RNRH 290	CMS 46A x SN 1407	Hybrid	6.0	3.0	6.3
78	RNRH 310	RMS 1A x SN 1606	Hybrid	5.0	1.0	5.7
79	RNRH 315	RMS 1A x SN 1666	Hybrid	5.0	1.0	6.3
80	RNRH 320	RMS 1 x SN 1692	Hybrid	5.5	1.0	6.3
81	RNRH 246	RMS 2 x SN 1692	Hybrid	5.0	3.0	5.7
82	RNRH 329	CMS 46A x SN 1774	Hybrid	6.0	5.0	6.3
83	RNRH 334	CMS 46A x SN 1808	Hybrid	5.0	7.0	6.3
84	RNRH 427	CMS 46A x SN 1972	Hybrid	6.0	7.0	7.0
85	RNRH 408	CMS 52A x SN 2347	Hybrid	6.0	7.0	6.0
86	RNRH 414	CMS 52A x SN 2455	Hybrid	5.5	7.0	6.3
87	RNRH 417	RMS 1 x SN 2479	Hybrid	5.0	1.0	7.0
88	RNRH 418	RMS 2 x SN 2479	Hybrid	3.5	3.0	6.3
89	RNRH 419	RMS 1 x SN 2499	Hybrid	5.0	1.0	7.0
90	RMS 9 B	-	Hybrid	5.5	5.0	7.0
91	RNR 48755	IBTGM14 x YPB46	Advanced line	4.5	5.0	6.0
92	RNR 44199	IET 23993 x JGL 28454	Advanced line	3.0	5.0	5.7
93	RNR 44060	JGL 30090 x IRBPH (K-17)-146	Advanced line	5.5	3.0	6.3
94	RNR 44059	JGL 30090 x IRBPH (K-17)-146	Advanced line	5.0	7.0	7.0
95	RNR 51329	(ISM 390-4 x JGL 13595) x (SYE 503-78-34-2 x BPT 5204 Pi1, Pi2)	Advanced line	4.0	5.0	6.3
96	RNR 51436	(ISM 390-4 x JGL 13595) x (SYE 503-78-34-2 x BPT 5204 Pi1, Pi2)	Advanced line	3.5	7.0	6.3
97	RNR 51447	(ISM 390-4 x JGL 13595) x (SYE 503-78-34-2 x BPT 5204 Pi1, Pi2)	Advanced line	2.5	7.0	7.0
98	RNR 51464	(ISM 390-4 x JGL 13595) x (SYE	Advanced line	5.5	5.0	6.3
		503-78-34-2 x BPT 5204 Pi1, Pi2)				
99	RNR 51493	[(ISM 390-4 x JGL 13595) x (SN 345 x BPT 5204 Pi1, Pi2)]	Advanced line	4.5	3.0	6.3

Cond.

S. No.	Genotype	Pedigree	Collection	LB Pooled	NB	BLB Pooled
100	RNR 51569	[(ISM 390-4 x JGL 13595) x (SN 345 x	Advanced line	5.5	5.0	7.0
		BPT 5204 Pi1, Pi2)]				
101	RNR 51668	[(ISM 390-4 x JGL 13595) x (SN 345 x BPT 5204 Pi1, Pi2)]	Advanced line	4.5	7.0	7.0
102	RNR 35008	HKR 08-01 x MTU 1001	Advanced line	5.0	7.0	7.0
103	RNR 37910	HHZ-Y3-T10 X MTU 1001	Advanced line	4.0	0.0	7.0
104	RNR 41653	NLR 34449 x (HMT Sona x RNR 10291)	Advanced line	3.5	5.0	7.0
105	RNR 41714	(RNR 15048 x ZGY-1) x (JGL 24423 x	Advanced line	3.5	5.0	2.3
		NLR 3513)				
106	RNR 44197	IET 23993 x JGL 28454	Advanced line	3.5	3.0	6.3
107	RNR 44035	KJT 20-1-7-14-9 x HMT Sona	Advanced line	5.0	0.0	4.3
108	RNR 44177	IET 23993 x KMP 223	Advanced line	5.0	5.0	7.0
109	M – 78		MLT-Medium line	5.0	5.0	7.0
110	RNR 51484	{(ISM 390-4 x JGL 13595) x (HMT Sona X BPT Pi1, Pi2)} (SERB)	MLT-Medium line	4.0	5.0	7.0
111	JGL 44230	JGL 21002 X HHZ1-DT4 (ATGC)	MLT-Medium line	5.0	7.0	5.7
112	WGL 1745	MTU 1061/RNR 15048	MLT-Medium line	4.5	7.0	5.7
113	KNM 15812	BPT 5204 X IR 09 251//WGL 962 X MUT NS 1	MLT-Medium line	5.5	5.0	4.3
114	RNR 44139	YPR – 19 x HMT Sona	MLT-Medium line	4.5	5.0	7.0
115	RNR 44304	NPT 14-5 x RNR 31479	MLT-Medium line	6.0	5.0	5.7
116	WGL 1957	Siddi derivative	MLT-Medium line	4.5	7.0	5.7
117	RNR 28361	-	Check	7.0	5.0	6.3
118	RNR 44060	JGL 30090 x IRBPH (K17)-146	MLT-Medium line	6.5	1.0	5.7
119	RNR 51260	{(ISM 390-4 x JGL 13595) x (HMT Sona X BPT Pi1, Pi2)}	MLT-Medium line	5.0	5.0	5.0
120	RNR 44199	IET 23993 x JGL 28454 (ATGC)	MLT-Medium line	5.0	3.0	4.3
121	RDR 5288	MTU-1010 X BR-89-383-C3	MLT-Medium line	6.0	5.0	7.0
122	JGL 44092	JGL 20779 X IR 71604-4-1-4-4-4-2-22R	MLT- Early line	5.0	7.0	6.3
123	KNM 15236	BPT 5204 x MUT NS1// KNM 1638	MLT- Early line	5.5	7.0	6.3
124	RNR 37927	RNR 11718 x NLR 34449	MLT- Early line	2.5	1.0	7.0
125	WGL 1865	UPR 3667-2-1-7/WGL 1121	MLT- Early line	4.0	5.0	6.3
126	RDR 2757	RDR-1144/ (MTU-1153 X Tellahamsa)	MLT- Early line	5.5	5.0	6.3
127	JGL 44230	JGL 21002 X HHZ 1- DT4- LI1-LI1	MLT- Early line	2.5	1.0	6.3
128	KNM 15138	WGL 962 x JGL 11727	MLT- Early line	4.5	7.0	6.3
129	RNR 42664	JGL 24423 x JGL 17004	MLT- Early line	5.0	5.0	5.7
130	WGL 1868	RNR 15048/WGL 1145	MLT- Early line	3.5	7.0	6.3
131	JGL 43093	KNM 118 X MTU 1010 NIL (Gna1)	MLT- Early line	5.0	5.0	6.3
132	KNM 16057	IRTON 117 x Pusa 44 // KNM 118	MLT- Early line	7.5	7.0	5.0
133	RNR 41664	NLR 34449 x (HMT Sona x RNR 10291))	MLT- Early line	5.0	5.0	6.3
134	RNR 44169	IET 23993 x KMP 223	MLT- Early line	6.0	7.0	6.3
135	RNR 15048	-	MLT- Early line	5.5	3.0	7.0
136	JGL 42713	NSN 1-296-2016 X JGL 24423	MLT- Early line	4.5	5.0	4.3
137	KPS 12531	Akshaydhan X NLR-34449	MLT- Early line	7.0	1.0	7.0
138	RNR 51541	{(ISM 390-4 x JGL 13595) x (HMT Sona X BPT Pi1, Pi2)} (SERB)	MLT- Early line	4.0	3.0	5.7
139	WGL 1875	RNR 15048/MTU 1156	MLT- Early line	5.5	5.0	5.0
140	WGL 1877	RNR 15048/MTU 1156	MLT- Early line	4.5	1.0	4.0

Cond.

S. No.	Genotype	Pedigree	Collection	LB Pooled	NB	BLB Pooled
141	RNR 51643	{(ISM 390-4 x JGL 13595) x (HMT	MLT- Early line	5.0	7.0	5.0
		Sona X BPT Pi1, Pi2)} (SERB)				
142	WGL 1939	WGL 962/MIL 12//WGL 962/BM 71	MLT- Early line	4.5	7.0	5.7
143	WGL 1924	WGL 962/MIL 12//WGL 962/BM 71	MLT- Early line	4.0	5.0	7.0
		(ATGC)				
144	JGL 42646	JGL 24423 X IR04A-216	MLT- Early line	5.5	3.0	5.7
145	WGL 1789	WGL 1100/JGL 19618	Advanced breeding line	6.0	1.0	5.7
146	WGL 1790	WGL 1100/JGL 19618	Advanced breeding line	6.0	0.0	3.0
147	WGL 1792	WGL 1100/JGL 19618	Advanced breeding line	5.5	0.0	4.0

MLT – E: Multi-location Testing Genotypes – Early duration group;
MLT – M: Multi-location Testing Genotypes – Medium duration group

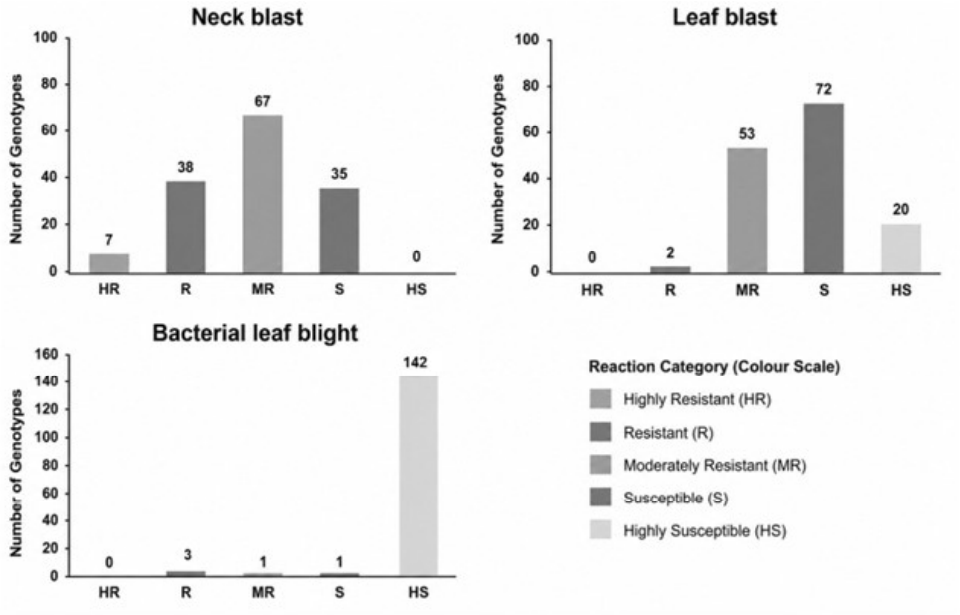

Fig. 1. Reaction of rice germplasm lines to leaf, neck blast and bacterial leaf blight under multi-location screening during 2024-25

CONCLUSION

The identification of resistant sources against both blast and BLB is crucial for developing durable disease-resistant rice varieties (Ramprasad et al., 2024). The promising genotypes identified herein may potentially be utilized within breeding programs as donor lines for the transference of resistance traits into high-yielding cultivars. The elite cultivars identified from this pool, which performed well for yield, yield contributing traits, and multiple disease resistance, advanced in subsequent generations and proposed for release through CVRC or SVRC for the benefit of the farming community. These lines were evaluated under diverse environmental conditions and against multiple pathotypes or races. Given that pathogen population's exhibit high variability and resistance breakdown frequently occurs (Ragulakollu et al., 2025), continuous screening of germplasm across multiple environments is demonstrably essential for the identification of stable resistance sources (Sharma et al., 2023). Consequently, the resistant lines identified in the present study may substantially contribute to prospective pre-breeding and resistance breeding programs, particularly those aimed at the development of improved rice varieties possessing durable resistance to major diseases. In addition, detailed characterization of the prevailing pathotypes or lineages of M. oryzae and X. oryzae pv. oryzae would help to elucidate the spectrum of resistance expressed by these genotypes against locally prevalent pathogen populations.

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