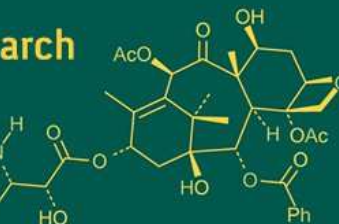
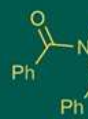
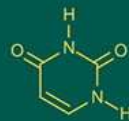
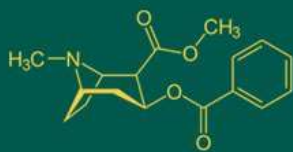


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Assessment of rice germplasm for resistance to bacterial leaf blight under laboratory conditions

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Abstract

A study was conducted during 2025-2026 at university lab at Coimbatore, to evaluate 100 rice genotypes for resistance to bacterial leaf blight (BLB) under artificial inoculation conditions. The pathogen was isolated and purified using standard microbiological techniques, and inoculation was performed using the leaf clipping method. Disease severity was assessed based on lesion length and percentage of diseased leaf area following the IRRI Standard Evaluation System. Significant variation in disease response was observed among the genotypes. The resistant check, Improved Samba Mahsuri, recorded the lowest disease incidence (4.17%), confirming its strong resistance, while the susceptible check Jyothi exhibited severe infection (69.07%). Among the tested genotypes, only one genotype was classified as resistant, and one genotype (Chakhao Poireiton) showed moderate resistance. Twenty genotypes were categorized as moderately susceptible, whereas the majority (64 genotypes) were susceptible, and fifteen genotypes were highly susceptible. The results indicate the scarcity of strong resistance sources among the evaluated germplasm. This study highlights the importance of identifying and utilizing resistant genotypes like Improved Samba Mahsuri in breeding programs to develop BLB-resistant rice varieties for sustainable crop production.

Keywords: Bacterial leaf blight, Kressek, rice, leaf clipping method

Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the world and serves as the staple food for nearly half of the global population. It is a major source of carbohydrates and contributes significantly to nutritional security, particularly in developing countries [1-3]. Rice plays a central role in the agricultural economy of India, with its production on a large scale, which provides millions of farmers with their means of livelihood. It plays a crucial part in food security because a significant percentage of the population is relying on rice as a main element of the diet [4]. The adaptability of rice to diverse agro-climatic conditions and continuous breeding efforts aimed at improving yield potential, nutritional quality, and stress tolerance have sustained its importance under changing climatic scenarios (5, 6). Furthermore, rice cultivation contributes substantially to rural employment and socio-economic stability, particularly in Asia [7]. The availability of wide genetic diversity and ongoing research on disease resistance and abiotic stress tolerance further enhance the sustainability of rice production systems [8-10].

Although rice plays a crucial role, its productivity faces significant limitations due to various biotic stresses, such as diseases caused by fungi, bacteria, and viruses, in addition to insect pests and weeds. Among these, bacterial leaf blight (BLB) is one of the most devastating diseases affecting rice cultivation across major rice-growing regions. BLB is caused by the bacterium *Xanthomonas oryzae* pv. *oryzae* (Xoo) and is capable of causing yield losses ranging from 20 to 50 percent under moderate infection, with losses reaching up to 75 percent under severe epidemic conditions (11-13). The disease is particularly destructive in irrigated and rainfed lowland ecosystems, where favorable environmental conditions promote rapid pathogen multiplication.

Bacterial leaf blight develops when the pathogen enters the rice crop through natural openings such as hydathodes or through wounds and subsequently colonizes the vascular tissues, especially the xylem vessels.

The pathogen interferes with water and nutrient transport, leading to typical symptoms such as water-soaked lesions, yellowing, leaf drying, and wilting ^[14, 15]. The bacterium produces virulence factors, including transcription activator-like effectors, which manipulate host gene expression and suppress plant defense mechanisms, thereby facilitating disease progression ^[8, 16]. In severe cases, systemic infection results in a condition known as “Kressek,” characterized by rapid wilting and death of young plants.

The severity and impact of bacterial leaf blight largely depend on the growth stage at which infection occurs. Seedling-stage infection is particularly damaging, as it adversely affects early plant vigor, root and shoot development, and tiller initiation. Early infection can lead to stunted growth and reduced yield potential, while infection at later stages such as maximum tillering, panicle initiation, and booting results in significant yield and grain quality losses ^[17, 18]. Disease severity has been shown to negatively correlate with grain weight, yield, and grain quality parameters ^[17]. Several studies have emphasized the importance of managing bacterial leaf blight from the early growth stages to minimize losses and sustain productivity ^[19, 20].

Among the various strategies available for managing bacterial leaf blight, the use of host-plant resistance is considered the most economical, environmentally safe, and sustainable approach. Although chemical and biological control measures offer partial protection, their effectiveness is limited without the support of resistant cultivars ^[11, 21]. Screening rice genotypes at the seedling stage under artificial inoculation conditions provides an efficient and reliable method for identifying resistant and susceptible genotypes. Early-stage screening enables rapid elimination of highly susceptible lines, reduces resource expenditure, and accelerates breeding programmes aimed at developing durable resistance ^[22, 23]. Integration of phenotypic screening with molecular approaches targeting major resistance genes further enhances the accuracy of selection ^[14].

In view of the economic importance of rice and the significant yield losses caused by bacterial leaf blight, the present investigation was undertaken to screen rice genotypes at the seedling stage for resistance to bacterial leaf blight. The identification of resistant and tolerant genotypes at an early growth stage will facilitate their effective utilization in rice breeding programmes for the development of bacterial leaf blight-resistant varieties.

Materials and Methods

The screening study was conducted under laboratory conditions during 2025-2026 at the Division of Genetics and Plant Breeding, School of Agricultural Sciences, Karunya

Institute of Technology and Sciences, Coimbatore, Tamil Nadu, India. The artificial inoculation of plants was performed at 21 days post-sowing using the leaf clipping method as detailed by ^[24]. Disease severity was assessed according to the 0-9 scoring scale set forth by the Standard Evaluation System (SES) of IRRI (2013) and classified as outlined in Table 1. This methodological approach allows for an accurate evaluation of plant response to bacterial leaf blight in controlled experiments.

$$\text{Percent Diseased Leaf Area} = \frac{\text{Total lesion length}}{\text{Total leaf area}} \times 100$$

Results and Discussion

The screening of 100 rice genotypes for bacterial leaf blight (BLB) resistance under artificial inoculation revealed a wide variation in disease response among the genotypes are given in Table 2 and 3. The resistant check, G43, recorded a disease leaf area of 4.17%, confirming its resistance under the present study conditions. In contrast, the susceptible check G46 exhibited a very high disease leaf area of 69.07%, indicating severe susceptibility to BLB. Based on disease leaf area percentage and BB scoring, the genotypes were categorized into different reaction groups. Among the evaluated genotypes, only one genotype (G43) showed a resistant (R) reaction with minimal lesion development. A total of twenty genotypes were classified as moderately susceptible (MS), showing intermediate disease symptoms with disease leaf area ranging approximately from 13-25%. These genotypes include G10, G18, G33, G36, G37, G44, G47, G54, G58, G77, G79, G80, G85, G86, G89, and others. The majority of the genotypes, sixty-four genotypes, were grouped under susceptible (S) category, exhibiting disease leaf area between 26-50%, indicating moderate to high infection levels. These include widely cultivated varieties such as G3, G6, G25, G19, G38, G45, G66, G100, and G95. Further, fifteen genotypes were identified as highly susceptible, recording disease leaf area exceeding 50%, indicating severe infection and extensive lesion spread. Notable among them are G2 (70.37%), G8 (78.89%), G97 (80.00%), G46 (69.07%), G87 (69.79%), G45 (62.07%), and G17 (59.76%). Among all the genotypes evaluated, the minimum disease leaf area was observed in G43 (4.17%), while the maximum disease severity was recorded in G97 (80.00%), followed by G8 (78.89%) and G2 (70.37%).

The results clearly indicate that most of the tested genotypes were susceptible to BLB, and only a very limited number showed any level of tolerance. This finding is in agreement with earlier reports that highlight the scarcity of resistant sources for BLB in rice germplasm.

Table 1: Disease scoring scale for bacterial leaf blight in rice as per Standard Evaluation System (SES), IRRI, (2013).

Disease score	Lesion area percentage (%)	Disease reaction
1	1-5%	Resistant (R)
3	6-12%	Moderately resistant (MR)
5	13-25%	Moderately susceptible (MS)
7	26-50%	Susceptible (S)
9	51-100%	Highly Susceptible

Table 2: Disease scoring and the reaction of the rice genotypes to bacterial blight

S. No	Genotype Name	Disease leaf area %	BB score	Disease reaction
1	G1	21.18	5	Moderately susceptible (MS)
2	G2	70.37	9	Highly Susceptible
3	G3	32.26	7	Susceptible (S)
4	G4	38.82	7	Susceptible (S)
5	G5	55.56	9	Highly Susceptible
6	G6	41.11	7	Susceptible (S)
7	G7	28.72	7	Susceptible (S)
8	G8	78.89	9	Highly Susceptible
9	G9	34.38	7	Susceptible (S)
10	G10	18.75	5	Moderately susceptible (MS)
11	G11	29.89	7	Susceptible (S)
12	G12	31.33	7	Susceptible (S)
13	G13	29.41	7	Susceptible (S)
14	G14	52.22	9	Highly Susceptible
15	G15	51.58	9	Highly Susceptible
16	G16	36.59	7	Susceptible (S)
17	G17	59.76	9	Highly Susceptible
18	G18	16.84	5	Moderately susceptible (MS)
19	G19	40.00	7	Susceptible (S)
20	G20	44.44	9	Highly Susceptible
21	G21	16.67	3	Moderately resistant (MR)
22	G22	31.33	7	Susceptible (S)
23	G23	30.61	7	Susceptible (S)
24	G24	26.74	7	Susceptible (S)
25	G25	31.87	7	Susceptible (S)
26	G26	58.76	9	Highly Susceptible
27	G27	40.23	7	Susceptible (S)
28	G28	32.63	7	Susceptible (S)
29	G29	34.48	7	Susceptible (S)
30	G30	35.56	7	Susceptible (S)
31	G31	34.88	7	Susceptible (S)
32	G32	32.61	7	Susceptible (S)
33	G33	24.21	5	Moderately susceptible (MS)
34	G34	35.42	7	Susceptible (S)
35	G35	29.67	7	Susceptible (S)
36	G36	18.89	5	Moderately susceptible (MS)
37	G37	26.32	5	Moderately susceptible (MS)
38	G38	37.78	7	Susceptible (S)
39	G39	30.30	7	Susceptible (S)
40	G40	35.00	7	Susceptible (S)
41	G41	47.83	7	Susceptible (S)
42	G42	39.47	7	Susceptible (S)
43	G43	4.17	1	Resistant (R)
44	G44	13.95	5	Moderately susceptible (MS)
45	G45	62.07	9	Highly Susceptible
46	G46	69.07	9	Highly Susceptible
47	G47	24.10	5	Moderately susceptible (MS)
48	G48	27.91	7	Susceptible (S)
49	G49	13.33	5	Moderately susceptible (MS)
50	G50	53.76	9	Highly Susceptible
51	G51	55.43	7	Susceptible (S)
52	G52	46.00	7	Susceptible (S)
53	G53	40.22	7	Susceptible (S)
54	G54	17.39	5	Moderately susceptible (MS)
55	G55	26.53	7	Susceptible (S)
56	G56	45.36	7	Susceptible (S)
57	G57	36.36	7	Susceptible (S)
58	G58	18.39	5	Moderately susceptible (MS)
59	G59	40.48	7	Susceptible (S)
60	G60	26.74	7	Susceptible (S)
61	G61	32.10	7	Susceptible (S)
62	G62	33.33	7	Susceptible (S)
63	G63	31.82	7	Susceptible (S)
64	G64	50.53	9	Highly Susceptible
65	G65	26.67	7	Susceptible (S)
66	G66	53.01	9	Highly Susceptible

67	G67	30.34	7	Susceptible (S)
68	G68	38.10	7	Susceptible (S)
69	G69	46.91	7	Susceptible (S)
70	G70	60.71	9	Highly Susceptible
71	G71	47.06	9	Highly Susceptible
72	G72	54.55	7	Susceptible (S)
73	G73	11.83	7	Susceptible (S)
74	G74	52.69	7	Susceptible (S)
75	G75	21.59	5	Moderately susceptible (MS)
76	G76	41.86	7	Susceptible (S)
77	G77	25.51	5	Moderately susceptible (MS)
78	G78	37.35	7	Susceptible (S)
79	G79	21.51	5	Moderately susceptible (MS)
80	G80	23.26	5	Moderately susceptible (MS)
81	G81	30.11	7	Susceptible (S)
82	G82	24.71	7	Susceptible (S)
83	G83	43.37	7	Susceptible (S)
84	G84	50.00	7	Susceptible (S)
85	G85	25.00	5	Moderately susceptible (MS)
86	G86	15.00	5	Moderately susceptible (MS)
87	G87	69.79	9	Highly Susceptible
88	G88	44.71	7	Susceptible (S)
89	G89	14.58	5	Moderately susceptible (MS)
90	G90	23.91	7	Susceptible (S)
91	G91	39.02	7	Susceptible (S)
92	G92	38.37	7	Susceptible (S)
93	G93	30.85	7	Susceptible (S)
94	G94	47.62	7	Susceptible (S)
95	G95	36.26	7	Susceptible (S)
96	G96	53.13	9	Highly Susceptible
97	G97	80.00	9	Highly Susceptible
98	G98	30.00	5	Moderately susceptible (MS)
99	G99	12.20	5	Moderately susceptible (MS)
100	G100	40.91	7	Susceptible (S)

Table 3: Classification based on response to bacterial blight

Name of the Genotype	Affected lesion area (%)	Category	Number of Genotype
G43	1–5	Resistant (R)	1
G21	6–12	Moderately resistant (MR)	1
G10, G18, G33, G36, G37, G44, G47, G49, G54, G58, G75, G77, G79, G80, G85, G86, G89, G99, G98	13–25	Moderately susceptible (MS)	19
G3, G4, G6, G7, G9, G11, G12, G13, G16, G19, G22, G23, G24, G25, G27, G28, G29, G30, G31, G32, G34, G35, G38, G39, G40, G41, G42, G48, G51, G52, G53, G55, G56, G57, G59, G60, G61, G62, G63, G65, G67, G68, G69, G72, G73, G74, G76, G78, G81, G82, G83, G84, G90, G91, G92, G93, G94, G95, G100	26–50	Susceptible (S)	64
G2, G5, G8, G14, G15, G17, G20, G26, G45, G46, G50, G64, G66, G70, G71, G87, G96, G97	>50	Highly Susceptible (HS)	15

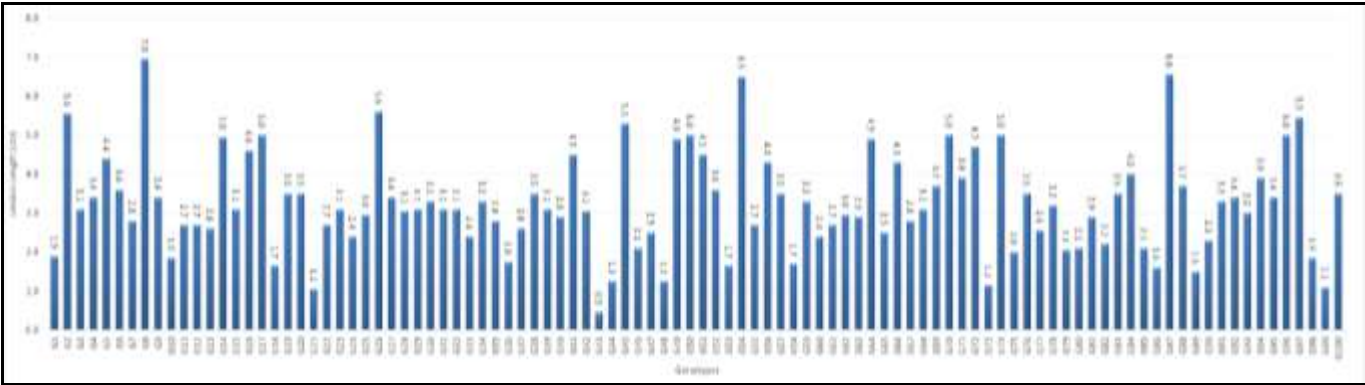


Fig 1: Lesion length of 100 genotypes affected by Bacterial Leaf Blight

Conclusion

The present study clearly demonstrated substantial variability among the 100 rice genotypes in their response to

bacterial leaf blight (BLB) under artificial inoculation. Despite this variability, true resistance was extremely limited, with only the resistant check, G43, exhibiting a

stable resistant reaction with minimal disease severity. The majority of genotypes fell under susceptible and highly susceptible categories, indicating that most of the currently available germplasm lacks effective resistance to BLB. The presence of a small group of moderately susceptible genotypes suggests partial tolerance, which could be useful in breeding programs as intermediate sources of resistance. However, the high disease incidence observed in widely cultivated varieties highlights the vulnerability of existing cultivars to BLB infection. The wide range in disease leaf area from very low in G43 to extremely high in genotypes like G97 and G8 confirms the effectiveness of the screening method and the presence of genetic diversity for disease response. Overall, the findings emphasize the urgent need to identify, conserve, and utilize resistant sources in rice improvement programs. Incorporation of resistance genes from identified tolerant genotypes, along with the use of resistant donors such as G43, will be crucial for developing BLB-resistant, high-yielding rice varieties.

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