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RESEARCH ARTICLE

Sheath rot in rice: Morphological, molecular characterization - *Sarocladium oryzae* (Sawada) and genotypic response

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Abstract

Rice is one of the vital staple food crops worldwide and it is affected by many fungal diseases. Among these, sheath rot disease caused by *Sarocladium oryzae* is emerging as a severe threat, leading to yield losses ranging from 10–85 %. Sheath rot disease of rice affects all the stages of the crop, but the disease is utmost critical in booting stage. It damages the boot leaf sheath that protects developing panicles, which delays or prevents panicle emergence. Grain production and quality are severely reduced. Discoloured, chaffy and sterile grains produced in the infected panicles. Survey was conducted in Thoothukudi district of Tamil Nadu during the period 2022 – 23. Ten isolates of *S. oryzae* were isolated using the infected samples collected. The isolate (So 5) obtained from Peikulam village of Sathankulam block (Lat. 8.51° N, Long. 77.85° E) was found to be the most virulent isolate. Morphological studies showed that the isolate So 5 recorded the maximum mycelial growth of 7.70 cm diameter after 20 days of inoculation in PDA medium. The pathogen produced white cottony aerial mycelial growth and cylindrical shape of conidia. The pathogen was molecularly confirmed as *S. oryzae* by comparing the similarities with the NCBI database (Accession No. OR298274). Screening of genotypes is essential to identify the resistant sources. One hundred rice genotypes were screened under natural and artificial conditions. The genotypes *viz*., Aryan 1102, Aryan 1203, Dhalaheera, Kattanoor, Navara black, Purpleputtu, Salem senna, Swarna and Varaprabha showed resistance in both conditions.

Keywords: resistant varieties; rice genotypes; *Sarocladium oryzae*; screening; sheath rot

Introduction

Rice (*Oryza sativa*) is the world's most important cultivated food crop, serving as main food for 90 % of the people in the world. Asia accounts for 90 % of global output. Rice is cultivated in varied agroecological zones in tropical and semi tropical regions (1). Growth, yield and the quality of rice are affected by many fungal infections. At present, sheath rot of rice caused by the pathogen *Sarocladium oryzae* [(Sawada) W. Gams & D. Hawksw.] is an endemic disease in Thoothukudi district of Tamil Nadu. Sheath rot disease affects rice plants in all growth stages, but the disease is most destructive in the booting stage, before panicle emergence. It mostly damages the boot leaf sheath that protects developing panicles, which delays or prevents panicle emergence and slows down the movement of nutrients from foliage to panicle. Grain production and quality are severely reduced because of the discoloured and sterile seeds produced in the infected panicles which causes 10-85 % yield loss (2).

This pathogen produces distinctive greyish brown lesions on the flag leaf sheath and causes the discolouration of grains, glumes and seeds with additional effects of reduced seed germination and poor grain filling. Three pathogens associated with sheath rot viz., *Fusarium oxysporum, F. equiseti* and *Phoma sorghina* have an endophytic (latent) stage in pathogen life cycles until the plant undergoes stress before infecting it (3). *S. oryzae* is mostly seed borne and disperses conidia by wind.

Sheath rot of rice cannot adequately be prevented by chemical control measures because they do not kill the fungi inside the glume (4). In addition, the use of fungicides to treat diseases has several negative effects *viz.,* resistance to pathogens, residual toxicity, environ mental pollution, etc. Sheath rot of rice can be managed by crop improvement measures which include the identification of resistant genotypes through screening and subsequent use of resistant sources in breeding programmmes which is more environmentally friendly than chemical control measures. Hence, the current research is focused on genotypic screening.

Isolation of the pathogen

Rice plants with sheath rot symptoms were collected during the year 2022-2023 from major rice cultivating areas in Thoothukudi district, Tamil Nadu, India. By using the single hyphal tip technique, the sheath rot causal organism was isolated under sterilized conditions from the collected ten samples (flag leaf of the diseased rice plants) (5).

Identification of virulent isolate of S. oryzae

9 mm mycelial discs from actively developing *S. oryzae* isolates of five days old cultures were shifted to Petri plates comprising Potato Dextrose Agar media. The plates were kept at 28 ± 2 °C, replicated thrice and maintained for observation. The radial growth of the mycelium was measured in all the isolates when the mycelium completely covered the plates in any one of the isolates (after 20 days) (6). Based on the growth and pathogenicity test, virulent isolate of *S. oryzae* was identified.

Morphological and molecular characterization

The morphology of the conidia and mycelium was examined under BLISCO BLS-114 Trinocular compound microscope (10 X). The colour of the mycelia and conidia, as well as the presence of septation in the mycelia, were also observed. The isolates of the pathogen were identified as *S. oryzae,* based on morphological and cultural characteristics (7).

Identification and confirmation of the organism at the species level is done by molecular characterisation. The DNA was extracted from the virulent isolate So 5 of *S. oryzae* by the CTAB method (8). The ITS rDNA regions were amplified by using the primer pairs ITS1/ITS4. PCR rea-ction was carried out by a total volume of 10 µL containing 1µL of suspended DNA, 1µL of forward primer and reverse primer, 4 µL of PCR master mix and 4 µL of distilled water. The following conditions were adopted for polymerase chain reaction: initial denaturation at 94 °C for 2 min, followed by 30 cycles of denaturation at 94 °C for 1 min, annealing at 55 °C for 1 min, extension at 72 °C for 2 min, final extension at 72 °C for 7 min and storage at 4 °C. Agarose gel electrophoresis was carried out using 1 % agarose gel in 1X TAE buffer to identify the banding pattern (9). DNA sequencing was done in Eurofins Analytical Services India Private Limited, Bengaluru and the ITS rDNA gene sequence obtained was compared with gene bank sequences by using NCBI BLAST. The primer pairs used for ITS region amplification were:

ITS1 - 5′ TCCGTAGGTGAACCTGCGG 3′ (forward primer)

ITS4 - 5′ TCCTCCGCTTATTGATATGC3′ (reverse primer)

Screening of rice genotypes

Screening of rice genotypes under artificial conditions

The study was conducted in the glasshouse of the Department of Plant Pathology at V.O. Chidambaranar Agricultural College and Research Institute (VOC AC & RI), Killikulam (Lat. 8.69° N, Long. 77.86° E), using a Completely Randomized Block Design (CRBD). A total of 100 rice genotypes, sourced from the Department of Genetics and Plant Breeding, V.O.C AC & RI, Killikulam, were used for the screening study, along with ADT 49 as the resistant check and ADT 37 as the susceptible check (10). All genotypes were grown in mud pots, watered periodically and maintained under appropriate conditions.

Paddy grain was used for the mass multiplication of the pathogen (10). Once the mycelial growth had completely colonized the grains, a single myceliated grain was retrieved from the flask and placed between the unemerged panicle and the flag leaf sheath of each plant. Fifteen days after inoculation, disease incidence on the mature flag leaf sheath was assessed using a 0-9 scale (Table 1), as described by IRRI (1) and recorded. A standard formula was used to calculate the Percent Disease Index (PDI) (11). The genotypes were grouped for their varietal reaction based on the PDI values (Table 2).

$$PDI = \frac{\text{Sum of all disease ratings}}{\text{Total no. of samples observed} \times \text{maximum disease rating}} \text{ X } 100$$

Screening of rice genotypes under natural conditions

In a raised nursery bed, seeds of 100 rice genotypes, ADT 49 and ADT 37 were sown. After 21 days, the seedlings were transplanted into the main field at a spacing of 20 × 15 cm in three rows per meter. This trial was conducted during Kharif 2022 in the B - Block of V.O.C. AC & RI, Killikulam, Vallanad, under irrigated conditions (Lat. 8.69° N, Long. 77.86° E) using a Randomized Block Design (RBD). During the study, all standard agronomic practices were followed. After the heading stage, all genotypes were evaluated for sheath rot disease resistance based on symptom development. Observations on sheath rot disease incidence were recorded on the mature flag leaf sheath of individual plants using a 0–9 scale (Table 1) (12). PDI was calculated using a standard formula (11). The genotypes were grouped for their varietal reaction based on the calculated PDI values (Table 2).

Table 1. Standard rating scale for sheath rot of rice (IRRI, 2002).

S.No		Description	Grade
1.	No incidence	No sheath rot symptom	0
2.	Less than 1 %	Small brown lesions on boot leaf sheath and panicle emergence on normal	1
3.	1–5 %	Lesions enlarge or coalesce and cover about 5 percent of the leaf sheath and panicle emergence normal	3
4.	6–25 %	Lesions cover about 6–25 percent of the leaf sheath area and 75 percent of panicle exerted	5
5.	26–50 %	Lesions cover about 26–50 per cent of the leaf sheath area and 50 percent of panicle exerted	7
6.	51–100 %	Lesions cover more than 50 percent of the leaf sheath area and 75 percent of panicle emergence completely affected or only about 25 percent of panicle exerted	9

Table 2. Varietal reaction based on PDI.

PDI	Varietal reaction (VR)
0	Immune
1–10	Resistant
11–25	Moderately resistant
26–50	Moderately susceptible
51–75	Susceptible
76–100	Highly susceptible

Results and Discussions

Collection of samples and isolation

Ten infected samples were collected from various paddy growing areas of Thoothukudi district in Tamil Nadu. From these samples, ten sheath rot isolates of *S. oryzae* were derived and named So 1 to So 10. All *S. oryzae* isolates were grown in PDA medium and observed after 20 days for the mycelial growth (cm) and dry weight (g) illustrated in Fig. 1. Among the ten isolates of *S. oryzae*, isolate So 5 recorded the maximum mycelial growth of 7.70 cm diameter in PDA medium and the isolate So 1 had the least mycelial growth of 6.00 cm (Table 3).

Morphological and cultural identification of S. oryzae

The mycelial colony of *S. oryzae* appeared as white, cottony, aerial growth. An orange tinge was observed at the base of the colony corresponding to the top side of the culture. Upon continuous exposure to light, the colony developed shades of orange coloration (13). The hyphae appeared as septate and sparsely branched. Conidiophores were thicker than vegetative hyphae. Conidia were single-celled, smooth, hyaline, cylindrical to fusiform and occasionally curved (Fig. 2). *S. oryzae* has been isolated from infected flag leaf sheaths of rice and morphologically identified by previous researchers (14).

Molecular characterization and identification of *S. oryzae*

PCR products were visualized on agarose gel (1 %) stained with ethidium bromide, appearing as single bands of approximately 550 bp in length (Fig. 3). The PCR products were sequenced and the Internal Transcribed Spacer (ITS) region of *S. oryzae* was obtained and searched against the NCBI nucleotide database (Fig. 4). The results showed that the sequences matched existing *S. oryzae* entries in the NCBI database (Accession No. OR298274).

Fig. 1. Growth of different isolates of *Sarocladium oryzae* on PDA.

Table 3. Cultural characteristics of *Sarocladium oryzae* isolates.

S. No	Isolates	Colour of mycelium	Type of mycelium	Conidial shape	Colony diameter (cm) (20 DAI)
1	So 1	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	6.00^{d}
2	So 2	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	7.41^{a}
3	So 3	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	7.62^{a}
4	So 4	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	6.51^{bc}
5	So 5	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	7.70^{a}
6	So 6	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	7.41^{a}
7	So 7	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	6.42^{cd}
8	So 8	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	6.70^{bc}
9	So 9	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	6.60^{bc}
10	So 10	White, cottony, aerial growth	Hyaline, septate and branched	Cylindrical	6.91^{b}
			CD (P = 0.05)		0.442
			SE (d)		0.149

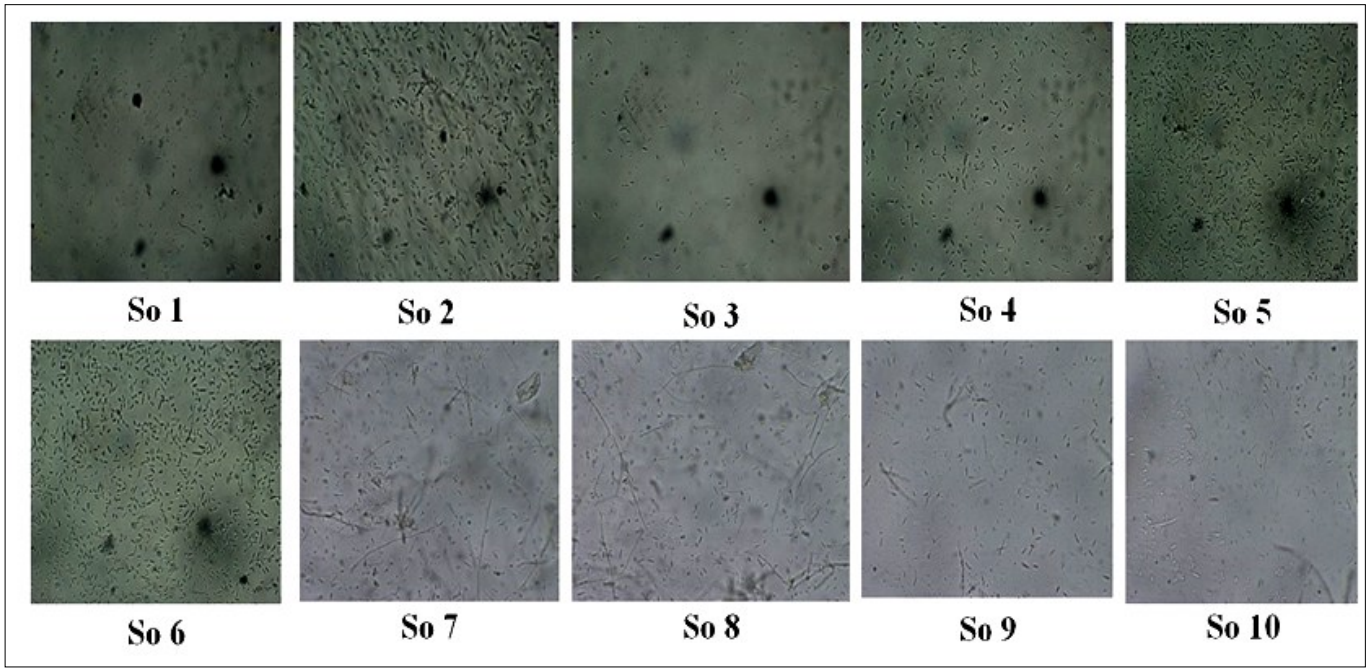

Fig. 2. Morphological characters of *Sarocladium oryzae* isolates.

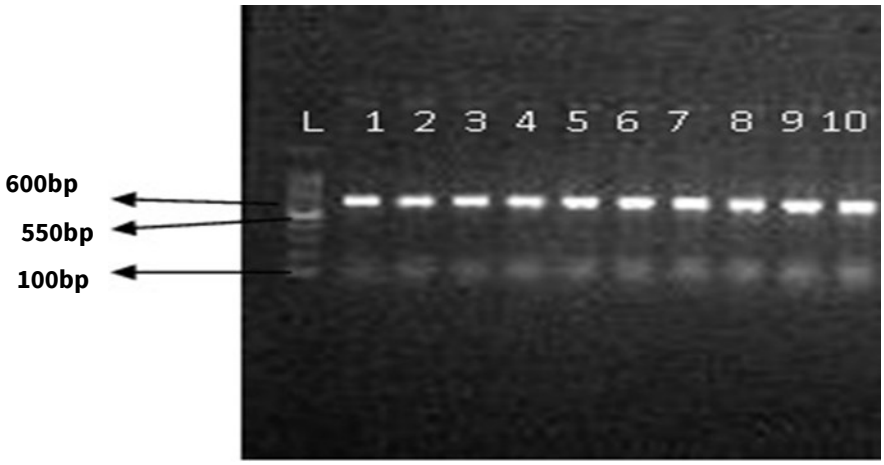

Fig. 3. Amplification of internal transcribed spacer (ITS) region of *Sarocladium oryzae.*

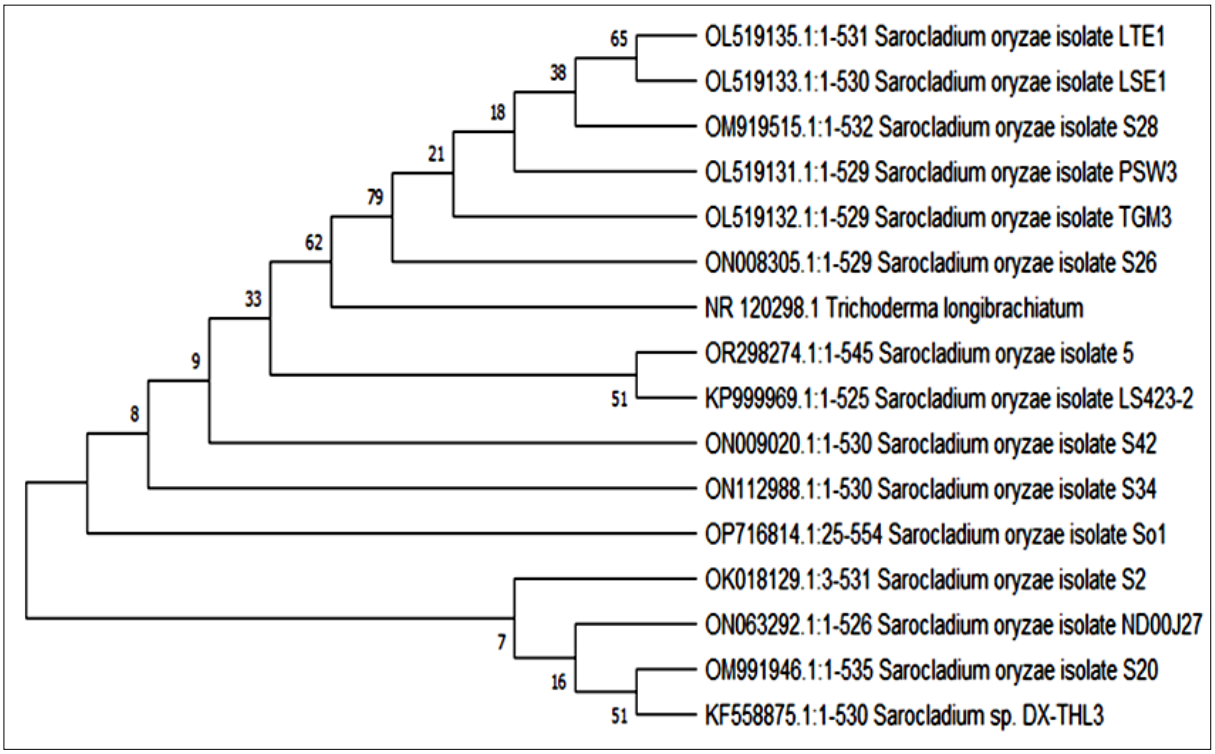

Fig. 4. Phylogenetic tree of *Sarocladium oryzae* with closely related species from NCBI database.

Screening of rice genotypes

Artificial condition

In the one hundred rice genotypes, disease scoring was recorded based on disease grades (Fig. 5). The percent disease index and varietal reactions were calculated and are presented in Table 4 and Fig. 6. Among the 100 rice genotypes evaluated, 9 were identified as resistant, 23 exhibited moderate resistance, 35 were moderately susceptible, 29 were susceptible and 4 were highly susceptible (Table 5). The resistant genotypes were Aryan 1102, Aryan 1203, Dhalaheera, Kattanoor, Navara black, Purple puttu, Salem senna, Swarna and Varaprabha. The genotypes viz., Dhalaheera, Swarna and Kattanoor were resistant against sheath rot disease (15). In an earlier study, twenty-two aromatic rice varieties were screened against *S. oryzae* using the grain inoculation method and a disease index of 5.36 % was recorded (16).

Natural condition

The varietal reactions and the percent disease index are presented in Table 4. Among the one hundred genotypes screened under natural field conditions, 12 were found to be resistant, 33 showed moderate resistance, 29 were found to be moderately susceptible, 22 were susceptible and 4 were highly susceptible (Table 6, Fig. 7).

The resistant genotypes were Aryan-1102, Aryan-1203, Navara black, Dhalaheera, Molikarumbu, Swarna, Kattanoor, Kichali samba, Kothamalli samba, Purple puttu, Salem senna and Varaprabha.

An earlier study screened 57 rice entries against *S. oryzae* under field conditions (17). Among these, 32 entries were moderately susceptible, 10 were moderately resistant, 14 were susceptible and one was highly susceptible. 43 rice genotypes were screened under natural conditions and it was reported that the genotypes viz., Dhalaheera, Swarna and Kattanoor were resistant against sheath rot disease and can be used for further development of resistant varieties (15). In an experiment conducted in field conditions eighty genotypes were screened and three genotypes were found to be resistant (18). In addition, 44 rice germplasm materials were screened under natural conditions with susceptible check variety IET-19396 (19).

Asha, Sabri, Usha, Madhuri and Dibraj were the commercial rice varieties that showed resistance to the sheath rot pathogen (20). Sheath rot incidence in various tall and dwarf varieties revealed that dwarf varieties were more susceptible to the disease, likely due to the reduced internodal length (21, 10). In contrast, tall rice cultivars have been found to inherit resistance to *S. oryzae* (14, 22).

57 rice entries were screened against *S. oryzae* under field conditions and among these, 32 entries were found to be moderately susceptible, 10 entries showed moderate resistance, 14 lines exhibited susceptibility and 4 lines were found to be highly susceptible (17).

Conclusion

In the present study, the most virulent isolate, so 5, was identified from Peikulam village in the Sathankulam block of Thoothukudi district. The pathogen was confirmed as *Sarocladium oryzae* based on cultural, morphological and molecular analyses (Accession No. OR214953). In screening experiments, the genotypes Aryan 1102, Aryan 1203, Dhalaheera, Kattanoor, Navara Black, Purpleputtu, Salem Senna, Swarna and Varaprabha exhibited resistance under both natural and artificial conditions. These resistant genotypes can be utilized in breeding programmes to develop improved rice varieties with enhanced resistance to sheath rot disease.

Fig. 5. Disease grades of sheath rot symptom.

Table 4. Screening of rice genotypes for sheath rot disease resistance.

S. No	Genotypes	Artificial condition			Natural condition		
		Disease severity (PDI)	Scale	Varietal reaction	Disease severity (PDI)	Scale	Varietal reaction
1.	IR 64	58.73	7	S	55.55	7	S
2.	CO 39	55.56	7	S	58.73	7	S
3.	Abiyan	36.50	5	MS	15.87	3	MR
4.	Adukan	90.47	9	HS	80.95	9	HS
5.	Aman	58.73	7	S	36.50	5	MS
6.	Anjali	61.90	7	S	65.07	7	S
7.	Annada	33.33	5	MS	39.68	5	MS
8.	Aryan 917	46.03	5	MS	34.92	5	MS
9.	Aryan 1023	49.20	5	MS	39.68	5	MS
10.	Aryan 1102	7.93	1	R	9.52	1	R
11.	Aryan 1203	6.34	1	R	6.34	1	R
12.	Aryan 5532	33.33	5	MS	20.63	3	MR
13.	Aryan 6333	19.04	3	MR	24.39	3	MR
14.	Bharathi	61.90	7	S	17.46	3	MR
15.	Chandaikar	23.80	3	MR	23.80	3	MR
16.	Chemban 986	68.25	7	S	20.63	3	MR
17.	Chembavu 5599	42.85	5	MS	42.85	5	MS
18.	Chembavu 4331	33.33	5	MS	36.50	5	MS
16.	Chennellu 5590	65.07	7	S	49.20	5	MS
20.	Chennellu 4735	52.38	7	S	30.15	5	MS
21.	Chenkayamma 5523	22.22	3	MR	19.04	3	MR
22.	Chinapunchan	58.73	7	S	43.85	5	MS
23.	Chiruchitteni 882	23.80	3	MR	23.80	3	MR
24.	Chithiraikar	20.63	3	MR	17.46	3	MR
25.	Chitteni 1123	39.68	5	MS	55.55	7	S
26.	Chitteni 5520	36.50	5	MS	42.85	5	MS
27.	Chitteni 5525	74.60	7	S	55.56	7	S
28.	Chitteni 7256	30.15	5	MS	42.85	5	MS
29.	Chomala	46.03	5	MS	20.63	3	MR
30.	Company thavalaikannan	36.50	5	MS	15.87	3	MR
31.	Dhalaheera	4.76	1	R	7.93	1	R
32.	Gowri	61.90	7	S	22.22	3	MR
33.	Iilupaipoosamba	17.46	3	MR	20.63	3	MR
34.	Jaya	80.95	9	HS	84.12	9	HS
35.	Jaisreeram	30.15	5	MS	22.22	3	MR
36.	Kaivara samba	47.61	5	MS	34.92	5	MS
37.	Kalinga	46.03	5	MS	36.50	5	MS
38.	Kaloondaikar	68.25	7	S	17.46	3	MR
39.	Kalyani	42.85	5	MS	49.20	5	MS
40.	Karnellu	12.69	3	MR	20.63	3	MR
41.	Karukot	19.04	3	MR	46.03	5	MS
42.	Karuthanavara	61.90	7	S	68.25	7	S
43.	Karuvalli	25.39	5	MS	12.69	3	MR
44.	Karsamba	49.20	5	MS	42.85	5	MS
45.	Kattanoor	7.93	1	R	4.76	1	R
46.	Kattisamba	34.92	5	MS	17.46	3	MR
47.	Kayamma	71.42	7	S	71.42	7	S
48.	Keralagandasala	11.11	3	MR	19.04	3	MR
49.	Kichali samba	15.87	3	MR	7.93	1	R
50.	Kodaikannan	74.60	7	S	30.15	5	MS
51.	Kotara samba	46.03	5	MS	22.22	3	MR
52.	Kothamalli samba	12.69	3	MR	7.93	1	R
53.	Krishnahemavathy	14.28	3	MR	17.46	3	MR
54.	Kuliyadichan	30.15	5	MS	23.80	3	MR
55.	Kullkar	71.42	7	S	39.68	5	MS
56.	Kunjukunju 1811	41.26	5	MS	14.28	3	MR
57.	Kunjukunju 6974	74.60	7	S	36.50	5	MS
58.	Kunjukunju 7168	65.07	7	S	68.25	7	S
59.	Kuruvaikalanjium	55.56	7	S	33.34	5	MS
60.	Mallikar	71.42	7	S	30.15	5	MS

61.	Mapillai samba	42.85	5	MS	49.20	5	MS
62.	Maranellu	23.80	3	MR	42.85	5	MS
63.	Mattai	19.04	3	MR	23.80	3	MR
64.	Meikuruvai	46.03	5	MS	52.38	7	S
65.	Molikarumbu	23.80	3	MR	6.34	1	R
66.	Mulampuchan	84.12	9	HS	90.47	9	HS
67.	Navara 957	14.28	3	MR	20.63	3	MR
68.	Navara 5571	74.60	7	S	65.07	7	S
69.	Navara 6263	22.23	3	MR	14.28	3	MR
70.	Navara black	9.52	1	R	9.52	1	R
71.	Noothipattu	19.04	3	MR	19.04	3	MR
72.	Norungan	44.44	5	MS	22.23	3	MR
73.	Palkudavazhai	46.03	5	MS	14.28	3	MR
74.	Pattani	58.73	7	S	71.42	7	S
75.	Poonkar	65.07	7	S	55.56	7	S
76.	Purple puttu	6.34	1	R	4.76	1	R
77.	Pusa basmati	49.20	5	MS	55.56	7	S
78.	Rajalakshmi	17.46	3	MR	57.14	7	S
79.	Salem senna	3.17	1	R	6.34	1	R
80.	Shadabahar	52.38	7	S	52.38	7	S
81.	Shabahidhan	71.42	7	S	58.73	7	S
82.	Seeraga samba	39.68	5	MS	46.03	5	MS
83.	Sivappumalli	33.33	5	MS	19.04	3	MR
84.	Soorakkuruvai	17.46	3	MR	22.23	3	MR
85.	Srilanka	46.03	5	MS	52.38	7	S
86.	Swarna	6.34	1	R	6.34	1	R
87.	Swarnamalli	23.80	3	MR	65.07	7	S
88.	Swarnamagari	52.38	7	S	58.73	7	S
89.	Thamarai	39.68	5	MS	17.46	3	MR
90.	Thondi	58.73	7	S	42.85	5	MS
91.	Thuyamalli	42.85	5	MS	39.68	5	MS
92.	Uma	90.47	9	HS	77.78	9	HS
93.	Vattan 5052	46.03	5	MS	31.74	5	MS
94.	Varakunanellu	23.80	3	MR	23.80	3	MR
95.	Varaprabha	6.34	1	R	7.93	1	R
96.	Vasanaisamba	22.22	3	MR	22.23	3	MR
97.	Veethiruppu	39.68	5	MS	33.34	5	MS
98.	Virendra	55.55	7	S	61.90	7	S
99.	White ponni	52.38	7	S	58.73	7	S
100.	White sanam	49.20	5	MS	36.50	5	MS
ADT 49 (Resistant check)		7.93	1	R	6.34	1	R
ADT 37 (Susceptible check)		90.47	9	HS	80.95	9	HS

R - Resistant, **MR** - Moderately resistant, **MS** - Moderately susceptible, **S** - Susceptible and **HS** - Highly susceptible.

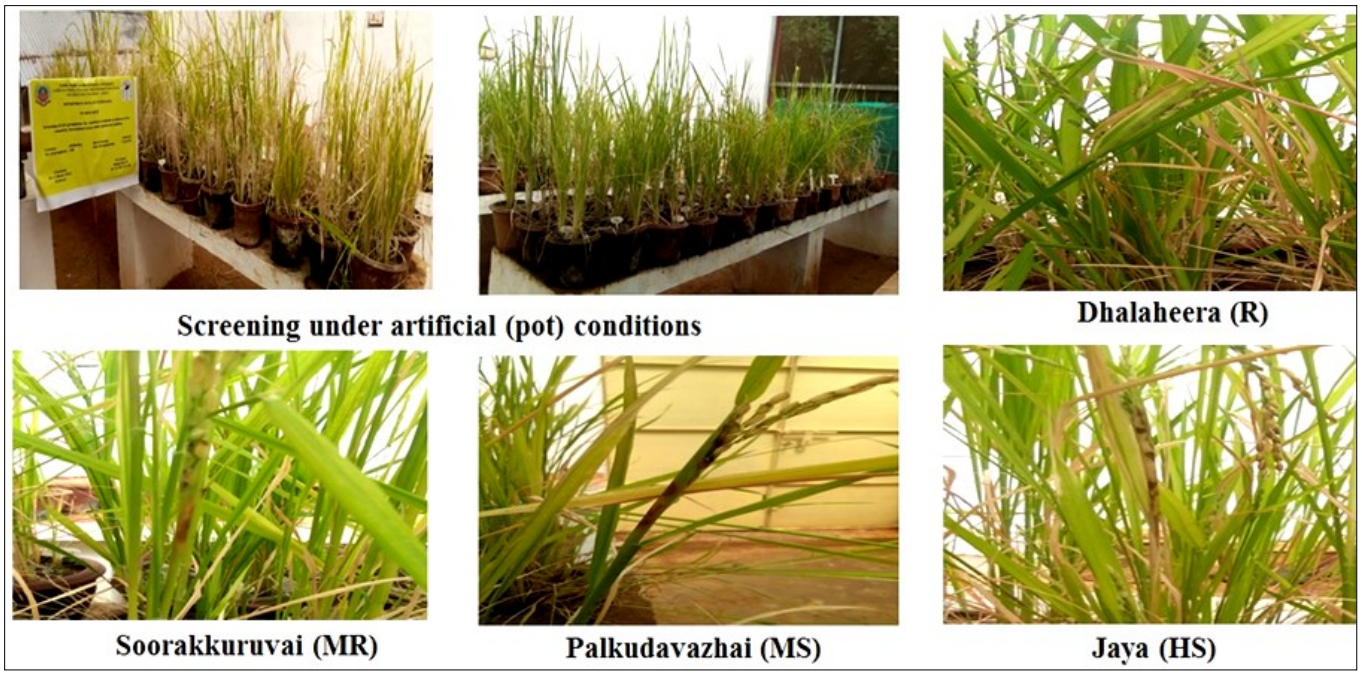

Fig. 6. Screening of rice germplasm for sheath rot resistance under artificial conditions.

Table 5. Grouping of rice genotypes based on artificial screening.

S.No	Description	No. of genotypes	Name of the genotypes
1.	Resistant	9	Aryan 1102, Aryan 1203, Dhalaheera, Kattanoor, Navara black, Purple puttu, Salem senna, Swarna and Varaprabha
2.	Moderately resistant	23	Aryan 6333, Chandaikar, Chenkayamma 5523, Chiruchitteni 882, Chithiraikar, Illupaipoosamba, Karnellu, Karukot, Kerakagandasala, Kichali samba, Kothamalli samba, Krishahemavathy, Maranellu, Mattai, Molikarumbu, Navara 957, Navara 6263, Noothipattu, Rajalakshmi, Soorakkuruvai, Swarnamalli, Varakunanellu and Vasanai samba
3.	Moderately susceptible	35	Abiyan, Annada, Aryan 917, Aryan 1023, Aryan 5532, Chembavu 5599, Chembavu 4331, Chitteni 1123, Chitteni 5520, Chitteni 7256, Chomala, Company thavalaikannan, Jaisreeram, Kaivara samba, Kalinga, Kalyani, Karuvalli, Karsamba, Kattisamba, Kotara samba, kuliyadichan, kunjukunju 1181, Mapillai samba, Meikuruvai, Norungan, Palkudavazhai, Pusa basmati, Seeraga samba, Sivappumalli, Srilanka, Thamarai, Thuyamalli, Vattan 5052, Veethiruppu and White sanam
4.	Susceptible	29	IR 64, CO 39, Aman, Anjali, Bharathi, Chemban 986, Chennellu 5590, Chennellu 4735, Chinapunchan, Chitteni 5525, Gowri, Kaloondaikar, Karuthanavara, Kayamma, Kodaikannan, Kullkar, Kunjukunju 6974, Kunjukunju 7168, Kuruvaikalanjiyam, Mallikar, Mulampuchan, Navara 5571, Pattani, Poonkar, Shadabahar, Shabahidhan, Swarnamagari, Thondi, Virendra and White ponni
5.	Highly susceptible	4	Adukan, Mulampunchan, Jaya and Uma

Table 6. Grouping of rice genotypes based on field screening.

S.No	Description	No. of genotypes	Name of the genotypes
1.	Resistant	12	Aryan-1102, Aryan-1203, Navara black, Dhalaheera, Molikarumbu, Swarna, Kattanoor, Kichali samba, Kothamalli samba, Purple puttu, Salem senna and Varaprabha
2.	Moderately resistant	34	Abiyan, Aryan 5532, Aryan 6333, Bharathi, Chomala, Chandaikar, Chemban 986, Chenkayamma 5523, Chiruchitteni 882, Chithirikar, Company thavalaikannan, Gowri, Illupaipoosamba, Jaisreeram, kaloondaikar, karnellu, karuvalli, kattisamba, keralakandasala, kotara samba, Krishna hemavathy, kuliyachichan, kunjukunju 1811, mattai, Navara 957, Navara 6263, Noothipattu, Norungan, Palkudavazhai, Sivappumalli, Soorakkuruvai, Thamarai, Varakunanellu and Vasanai samba
3.	Moderately susceptible	29	Aman, Annada, Aryan 917, Aryan 1023, Chembavu 5599, Chembavu 4331, Chennellu 5590, Chennellu 4735, Chinapunchan, Chitteni 5520, Chitteni 7256, Kaivara samba, Kalinga, Kalyani, Karukot, Karsamba, Kodaikannan, Kullkar, Kunjukunju 6974, Kuruvaikalanjiyam, Mallikar, Mappilai samba, Maranellu, Seeraga samba, Thondi, Thuyamalli, Vattan 5052, Veethiruppu and White sannam
4.	Susceptible	21	IR 64, CO 39, Anjali, Chitteni 1123, Chitteni 5525, Karuthanavara, Kayamma, Kunju kunju 7168, Meikuruvai, Navara 5571, Pattani, Poonkar, Pusa basmati, Rajalaakshmi, Shadabahar, Shabahidhan, Srilanka, Swarnamalli, Swarnamagari, Virendra and White ponni
5.	Highly susceptible	4	Adukan, Jaya, Mulampuchan and Uma

Fig. 7. Screening of rice germplasm for sheath rot resistance under natural condition.

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Authors' contributions

MB conducted the research work and drafted the manuscript. JS supervised the research. MAP and SMPK contributed expertise and provided critical review on breeding aspects. The manuscript was revised and finalized by JS, NR and MT. MP provided the initial guidance and CK assisted in reviewing the final version of the manuscript.

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Declaration of generative AI and AI-assisted technologies in the writing process

The Grammarly AI tool was used with caution to improve the language and readability of the manuscript.

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