Host Plant Resistance Studies on Rice Cultivars against Sheath Rot Caused by *Sarocladium oryzae* (Sawada) Gams and Hawksworth

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Rice sheath rot caused by the fungus *Sarocladium oryzae*, has become a highly destructive rice disease with a high variability in yield loss levels. Therefore, sheath rot disease can be effectively managed through crop improvement strategies *viz.,* discovery of resistance sources from varieties,

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germplasm, landraces, wild genetic resources and further deploying them in breeding programmes. In this study, we evaluated 338 NSN-1 rice cultures for their resistance to sheath rot at ZARS V.C. farm Mandya during *Kharif* 2023with HR-12 as a susceptible check under natural and artificially inoculated conditions and disease severity was assessed using a 0-9 disease scoring scale. Our results revealed considerable variations in sheath rot resistance among the NSN-1 rice cultures. Several lines exhibited different levels of resistance, Out of 338, seven NSN-1 cultures were found immune with no disease (*viz.,* NSN-1-4612, NSN-1-4628, NSN-1-4502, NSN-1-4304, NSN-1-5310, NSN-1-4138 and Rasi). One NSN-1-5815 line showed resistance reaction with less than one per cent disease, suggesting their potential for deployment in breeding programs aimed at developing sheath rot resistant rice varieties. These findings contribute to the ongoing efforts to enhance the resistance of rice cultivars to sheath rot, thereby ensuring the sustainability of paddy cultivation.

1. INTRODUCTION

Rice is one of the most important and widely cultivated food crops of the world and the majority of rice (90 per cent) is being produced in Asian countries, China and India being the major producers. Rice suffers from many of the diseases caused by fungi, bacteria, viruses, phytoplasma, nematodes and other non-parasitic disorders. Among them sheath rot has become more prevalent in recent decades. The disease could now be easily found in India as well and its impact to yield loss is important to be observed. Sheath rot disease was once considered as a minor disease, but in recent years it has become one of a major constraint in almost all the rice-growing countries, particularly in Asia.

Sheath rot disease was first reported as *Acrocylindrium oryzae* Sawada in 1922. Later, the name was changed to *Sarocladium oryzae* (Sawada) W. Gams & D. Hawksw., 1975. Climate change, cropping patterns, presence of insects and introduction of new cultivars are among several causes of the increase in this disease [1]. Rice sheath rot has become a highly destructive rice disease with a high variability in yield loss levels varying from 20 to 85 per cent [2].

The pathogen majorly affects the boot leaf stage which is the economic part of rice plant. The brown lesion has dimensions ranging from 0.5-1×0.2-0.5 cm, whereas, the uninfected sheath looks green [3]. The sheath rot disease spots are linear with irregular margins and in succeeding stage, the brown spots coalesce and take over the whole sheath. Pathogens that infect leaf sheath prevent the young panicles from emerging out of the leaf sheath (Plate 2A and 2B) and solidify or partly appear but produce empty, partly filled and turn brown. Pathogen produces phytotoxins *viz.,* Cerulenin and helvoic acid [4] which are responsible for the production of characteristic greyish brown lesion on flag leaf sheath and discolouration of grains, glume discolouration and also seed discolouration. It also causes poor grain filling and reduction in seed germination.

So in order to control this disease chemical methods alone are currently ineffective in managing. Furthermore, using fungicides to treat diseases has a number of negative side effects, including environmental contamination, pathogen resistance and residual toxicity [5-7]. Thus, crop management techniques, such as the identification of resistance sources from varieties, germplasm, landraces, and wild genetic resources and further deploying them in breeding programs, can successfully help in managing the sheath rot disease.

2. MATERIALS AND METHODS

An experiment of screening of NSN-1(National Screening Nursery-1) cultures of riceagainst sheath rot disease was conducted at Zonal Agricultural Research Station (ZARS), V. C. Farm, Mandya located in Southern Dry Zone (zone 6) of Karnataka having latitude of 12° 31' 25.43'' N and longitude of 76° 53' 40.86'' E during *Kharif*, 2023. Screening was done to record the prevalence and severity of sheath rot disease in three hundred and thirty eightNSN-1 rice cultures. Each line was maintained in 1m length row with 20 x 15 cm spacing. A susceptible check HR-12 was planted after every 10 lines and along the four sides of the field to serve as a source for the disease (infector row technique). The recommended package of practices werefollowed to maintain the crop. The per cent disease intensity was calculated at 5 days interval. The per cent disease intensity was calculated by using the formula [8]:

$$\text{PDI} = \frac{\text{Sum of the individual rating}}{\text{Total number of plants observed} \times \text{Maximum disease grade}} \times 100$$

2.1 Area under Disease Progress Curve (AUDPC)

The "Area Under Disease Progress Curve" was calculated by using the formula suggested by Johnson and Wilcoxson [9].

$$\text{AUDPC} = \sum_{i=1}^{n-1}[\{(X_i + X_{(i+1)})\,)/2\} \times (t_{(i+1)} - t_i)]$$

X_i = disease index expressed as a proportion at the ith observation.
t_i = time (days after transplanting) at the ith observation

Based on the observations recorded, computed for area under disease progress curve (AUDPC) and rate of progress. Based on mean disease severity and AUDPC, all genotypes were categorized into different reactions. The scoring (0-9 scale) was done as per the standard evaluation system for rice given by IRRI (2018)

Tables 1 and 2. The scale adopted for categorising the rice genotypes against sheath rot is as follows (Plate 1).

2.2 Comparison of Infection RATE Deduced by Using Logistic Model

The epidemiological concept infection rate is a better measure of resistance was calculated from the data generated in the field. The infection rate expressed as the logistic function "r" was computed by using the formula given by Vanderplank for "r" [10].

$$r = \frac{(\text{logit Y2} - \text{logit Y1})}{(t2 - t1)}$$

Where,

r= logistic infection rate
Y_1 =Initial proportion of disease at time t_1
Y_2 =Proportion of disease at time t_2

Table 1. Disease scoring scale for sheath rot disease

Scale	Incidence of infected tillers	Reaction
0	No incidence	Immune (I)
1	< 1 %	Resistant (R)
3	1-5 %	Moderately resistant (MR)
5	6-25%	Moderately susceptible (MS)
7	26-50%	Susceptible (S)
9	51-100%	Highly susceptible (HS)

Table 2. Description (0-9 scale) of disease scoring scale for sheath rot disease

Scale	Description
0	Healthy plants free from the sheath rot
1	Small brown lesions on the leaf sheath, normal panicle emergence and grain setting normal
3	Lesions tend to enlarge, coalesce and cover about half of the leaf sheath, glumes are discoloured, grain filling is normal
5	Lesions tend to cover the entire sheath, glumes discoloured, incomplete exertion of the panicle with stray sterile spikelets
7	Panicle struggles to emerge with 25-50 per cent of the spikelets sterile, severe glume discoloration, entire sheath rots
9	Panicle emergence from sheath, sheath rots while enclosing the panicle

3. RESULTS AND DISCUSSION

Out of three hundred and thirty eight NSN-1 rice cultures were screened against sheath rot, reaction was varied considerably. The AUDPC (area under disease progress curve) was calculated and reactions were presented in Table 3. Out of 338, seven NSN-1 cultures were found immune with no

disease(*viz.,* NSN-1-4612, NSN-1-4628, NSN-1-4502, NSN-1-4304, NSN-1-5310, NSN-1-4138 and Rasi). One NSN-1-5815 line showed resistance reaction with less than one per cent disease, one hundred and onecultures showed medium resistant reaction with disease percentage 1-5 per cent. One hundred and thirteen NSN-1 lines were found moderately susceptible with disease infection ranges from 6-25 per cent, sixty five genotypic lines showed susceptible reaction with 26-50 per cent disease infection and fifty lines showed highly susceptible reaction with more than 50 per cent disease infection and one line was not germinated.

The lesion length on the panicle was also measured it ranges upto 5.3cm length in highly susceptible cultivars like NSN-1-4907, NSN-1-5206, NSN-1-5211, NSN-1-3502, NSN-1-3806, NSN-1-6008, NSN-1-6009*etc.,* Based on lesion length AUDPC was calculated which ranges upto 84.444 in highly susceptible genotypes.

Among different 338 NSN-1 lines based on percent infection AUDPC was calculated which ranged upto 827.5 in NSN-1-4907 line. Highest AUDPC value of 819.17 and 806.67 was recorded in NSN-1-4109 and NSN-1-4312genotypic lines respectively. Lowest AUDPC value of 3.5 and 17.5 was recorded in NSN-1-5815 and NSN-1-5811 respectively. Infection rate "r" was calculated, it was 0 in case immune lines and ranges from 0.0186 to 0.441 in resistant and highly susceptible lines respectively.

The present results were in agreement with findings of Saha et al. [11] screened total 149 entries of NSN-1 during the *Kharif* 2000 at Bankura and Chinsurah, West Bengal, India and found that one entry at Bankura and 6 entries at Chinsurah showed resistance, however 21 and 56 entries were found moderately resistant to the disease at Bankura and Chinsurah locations, respectively.An investigation was conducted by Fetene et al. [12] to identify resistant sources among rice germplasm. Eighty germplasms along four checks were evaluated in field trials for two years at two locations arranged in an augmented design. Results indicated that three immune germplasms (SCRID014-1-1-1-1, SCRID037-4-2-2-5-2 and YUNLU N0.33) were found to be suitable for resistant variety development. The remaining germplasms were found to exhibit different levels of reactions, of which 27 resistant, 35 moderately resistant, 13 moderately susceptible and two susceptible, with PSI ranging between 1.48-56.17 per cent.

Plate 1. Scoring of sheath rot by using 0-9 scale

Table 3. Screening of NSN-1 genotypes against sheath rot of rice

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
1	4601	2.00	22.50	0.110	2.2	8.33	MR
2	4602	1.91	22.00	0.110	2.1	22.22	MR
3	4603	26.56	302.50	0.256	4.1	37.78	S
4	4604	2.22	25.00	0.161	2.1	5.28	MR
5	4605	2.13	24.50	0.110	2.1	15.00	MR
6	4606	2.67	30.00	0.161	2.0	11.11	MR
7	4607	14.61	165.00	0.314	3.2	21.67	MS
8	4608	2.44	27.50	0.161	1.9	11.67	MR
9	4609	13.33	150.00	0.304	3.3	8.33	MS
10	4610	2.44	27.50	0.161	1.9	7.78	MR
11	4611	2.83	32.50	0.161	2.0	16.39	MR
12	4612	0.00	0.00	0.000	0.0	0.00	I
13	4613	11.72	132.50	0.294	2.9	26.11	MS
14	4614	15.47	174.50	0.314	3.4	25.00	MS
15	4615	2.71	31.50	0.161	2.0	21.11	MR
16	4616	2.67	30.00	0.161	2.4	6.11	MR
17	4617	26.56	302.50	0.256	4.0	40.28	S
18	4618	27.29	307.67	0.371	4.3	38.06	S
19	4619	55.47	624.50	0.442	5.4	32.78	HS
20	4620	12.00	135.00	0.294	3.1	6.11	MS
21	4621	2.67	30.00	0.161	2.0	8.89	MR
22	4622	11.98	135.50	0.294	3.2	24.72	MS
23	4623	11.78	132.50	0.294	3.1	10.28	MS
24	4624	2.44	27.50	0.161	2.1	8.61	MR
25	4625	15.98	180.50	0.322	3.2	22.50	MS
26	4626	14.00	157.50	0.304	2.9	18.06	MS
27	4627	31.22	355.00	0.275	4.2	47.22	S
28	4628	0.00	0.00	0.000	0.0	0.00	I
29	4629	10.18	115.17	0.271	4.0	30.00	MS
30	4630	29.00	330.00	0.266	4.1	46.11	S
31	4501	2.44	27.50	0.161	2.2	6.11	MR

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
32	4502	0.00	0.00	0.000	0.0	0.00	I
33	4503	2.00	22.50	0.110	2.2	5.28	MR
34	4504	14.19	160.33	0.304	2.9	28.89	MS
35	4505	2.44	27.50	0.161	2.1	6.11	MR
36	4506	10.14	114.67	0.271	3.3	11.94	MS
37	4507	2.67	30.00	0.161	2.1	6.39	MR
38	4508	23.80	268.67	0.361	4.2	26.67	MS
39	4509	30.49	344.00	0.385	4.0	20.28	S
40	4510	2.44	27.50	0.161	2.1	7.50	MR
41	4511	2.67	30.00	0.161	2.0	10.00	MR
42	4512	1.78	20.00	0.110	1.9	11.11	MR
43	4513	2.93	34.00	0.161	1.9	15.00	MR
44	4514	11.28	127.50	0.283	3.2	28.89	MS
45	4515	11.88	134.00	0.294	3.5	23.89	MS
46	4516	2.60	29.83	0.161	2.0	18.89	MR
47	4517	2.67	30.00	0.161	2.0	5.83	MR
48	4518	2.83	32.50	0.161	2.4	11.94	MR
49	4520	25.89	295.83	0.200	4.1	46.39	S
50	4901	56.00	652.50	0.137	4.8	57.22	HS
51	4902	26.58	299.50	0.371	4.1	28.89	S
52	4903	2.44	27.50	0.161	1.8	6.67	MR
53	4904	29.00	330.00	0.266	4.2	46.94	S
54	4905	16.71	189.00	0.322	2.7	31.39	MS
55	4906	30.83	347.50	0.385	4.0	26.39	S
56	4907	69.33	827.50	0.432	5.3	84.44	HS
57	4908	56.44	661.67	0.118	4.6	62.22	HS
58	4909	52.33	592.50	0.325	4.4	46.39	HS
59	4910	64.00	765.00	0.076	4.7	76.67	HS
60	4911	56.22	655.00	0.140	4.7	79.44	HS
61	4912	13.24	149.50	0.304	3.1	30.00	MS
62	4913	2.00	22.50	0.110	1.9	6.67	MR
63	4914	11.28	127.50	0.283	3.2	26.11	MS
64	4915	50.22	570.00	0.271	5.7	54.72	S

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
65	4916	27.44	312.50	0.261	4.1	41.94	S
66	4917	27.67	315.83	0.210	3.8	41.39	S
67	4918	29.86	336.17	0.381	3.8	35.28	S
68	4919	16.13	182.00	0.322	3.1	30.83	MS
69	4920	26.56	302.50	0.256	4.0	44.72	S
70	4921	22.33	255.83	0.189	3.9	41.67	MS
71	4922	26.67	305.00	0.205	4.3	41.11	S
72	4001	12.17	137.50	0.294	3.1	26.94	MS
73	4002	15.56	175.00	0.322	3.3	17.78	MS
74	4003	12.83	145.00	0.294	4.0	25.83	MS
75	4004	27.31	308.00	0.371	4.3	35.00	S
76	4005	31.22	355.00	0.275	4.3	45.83	S
77	4006	2.00	22.50	0.110	2.1	7.78	MR
78	4007	26.56	302.50	0.256	4.3	42.50	S
79	4008	27.78	317.50	0.210	4.3	42.22	S
80	4009	10.39	117.50	0.283	4.0	29.44	MS
81	4010	29.44	335.83	0.215	4.3	48.61	S
82	4011	29.72	335.00	0.381	4.2	24.17	S
83	4012	11.16	126.50	0.283	3.0	25.56	MS
84	4013	2.00	22.50	0.110	1.8	7.78	MR
85	4014	2.81	32.17	0.161	1.6	29.44	MR
86	4015	2.58	29.50	0.161	1.6	21.11	MR
87	4016	12.67	142.50	0.294	2.8	13.33	MS
88	4017	16.17	182.50	0.322	3.2	25.83	MS
89	4018	10.44	118.33	0.283	2.8	26.39	MS
90	3701	2.44	27.50	0.161	1.6	6.11	MR
91	3702	27.38	309.00	0.371	4.3	25.56	S
92	3703	62.33	750.00	0.065	5.2	80.83	HS
93	3704	10.83	122.50	0.283	3.0	25.83	MS
94	3705	26.33	300.00	0.256	4.1	45.28	S
95	3706	15.98	180.50	0.322	3.3	30.56	MS
96	3707	2.22	25.00	0.161	2.0	7.50	MR
97	3708	10.83	122.50	0.283	3.0	20.83	MS

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
98	3709	1.78	20.00	0.110	2.0	9.44	MR
99	3710	57.22	668.33	0.130	5.2	60.28	HS
100	3711	11.50	130.00	0.283	3.0	36.11	MS
101	3712	2.67	30.00	0.161	2.4	8.89	MR
102	3713	14.17	160.00	0.304	3.0	26.94	MS
103	3714	15.58	176.17	0.314	2.8	26.11	MS
104	3715	2.71	31.50	0.161	2.3	12.22	MR
105	3716	2.00	22.50	0.110	2.3	6.67	MR
106	4801	2.67	30.00	0.161	2.2	6.11	MR
107	4802	51.78	606.67	0.119	4.9	60.28	HS
108	4803	57.89	655.00	0.337	5.4	54.44	HS
109	4804	53.22	603.33	0.276	5.2	43.89	HS
110	4805	14.67	165.83	0.314	2.9	20.00	MS
111	4806	27.22	310.83	0.205	3.9	43.33	S
112	4807	32.22	367.50	0.224	4.4	38.61	S
113	4808	27.56	310.83	0.371	3.7	27.50	S
114	4809	25.60	289.00	0.366	3.2	30.00	S
115	3401	2.00	22.50	0.110	2.3	7.78	MR
116	3402	2.44	27.50	0.161	2.1	9.72	MR
117	3403	12.82	144.83	0.294	2.9	25.00	MR
118	3404	2.44	27.50	0.161	2.0	7.78	MR
119	3405	2.83	32.50	0.161	1.9	29.44	MR
120	3406	10.17	115.00	0.271	2.9	25.00	MS
121	3407	24.33	277.50	0.246	4.3	42.78	MS
122	3408	2.44	27.50	0.161	2.2	6.67	MR
123	3409	10.18	115.17	0.271	2.8	28.89	MS
124	3410	31.22	355.00	0.275	4.3	45.83	S
125	3411	2.13	24.50	0.110	1.9	27.22	MR
126	3412	2.67	30.00	0.161	1.9	8.06	MR
127	5501	2.67	30.00	0.161	2.0	10.56	MR
128	5502	28.56	325.00	0.266	4.3	46.39	S
129	5503	30.39	342.50	0.385	4.1	29.72	S
130	5504	58.33	680.83	0.132	5.2	62.78	HS

SI. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
131	5505	2.44	27.50	0.161	2.0	6.11	MR
132	5506	24.17	272.50	0.361	3.0	28.61	MS
133	5507	27.00	307.50	0.256	2.8	33.61	S
134	5508	27.67	315.83	0.210	4.1	40.56	S
135	5201	2.17	25.00	0.110	1.7	17.78	MR
136	5202	2.60	29.83	0.161	2.1	21.11	MR
137	5203	2.67	30.00	0.161	2.1	9.72	MR
138	5204	63.22	735.83	0.140	5.4	72.50	HS
139	5205	2.44	27.50	0.161	1.7	7.50	MR
140	5206	65.11	780.00	0.071	5.4	76.39	HS
141	5207	12.23	138.50	0.294	3.3	27.78	MS
142	5208	12.04	136.50	0.294	3.3	24.72	MS
143	5209	2.00	22.50	0.110	2.0	6.11	MR
144	5210	27.00	307.50	0.256	3.9	45.00	S
145	5211	62.00	725.00	0.128	5.2	63.89	HS
146	5212	8.83	100.00	0.256	3.3	25.56	MS
147	3501	2.44	27.50	0.161	1.9	5.00	MR
148	3502	64.67	776.67	0.066	5.0	83.61	HS
149	3503	2.44	27.50	0.161	2.1	5.28	MR
150	3504	11.71	132.33	0.294	3.3	30.00	MS
151	3505	2.44	27.50	0.161	1.8	6.94	MR
152	3506	2.67	30.00	0.161	1.7	9.72	MR
153	3507	2.67	30.00	0.161	2.3	7.50	MR
154	3508	2.61	30.00	0.161	2.2	18.89	MR
155	3509	13.22	152.50	0.185	3.2	34.44	MS
156	3510	22.71	256.50	0.356	3.8	24.44	MS
157	3511	2.00	22.50	0.110	2.1	5.83	MR
158	3512	12.17	137.50	0.294	3.6	22.22	MS
159	3514	2.00	22.50	0.110	2.0	5.28	MR
160	3515	1.79	21.00	0.110	1.8	26.67	MR
161	3516	56.89	665.83	0.127	5.2	63.89	HS
162	3517	12.87	145.50	0.294	3.2	23.61	MS
163	3518	14.41	162.83	0.314	3.4	26.94	MS

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
164	3519	25.67	292.50	0.251	3.8	46.11	S
165	3520	12.86	145.33	0.294	2.9	21.39	MS
166	3521	31.44	358.33	0.224	4.1	43.33	S
167	3522	31.78	362.50	0.224	4.1	38.61	S
168	3523	12.93	146.50	0.294	3.2	27.50	MS
169	3524	10.00	112.50	0.271	3.2	15.28	MS
170	4101	9.78	110.00	0.271	3.1	16.67	MS
171	4102	9.79	111.00	0.271	3.1	22.22	MS
172	4103	9.82	111.50	0.271	3.3	27.22	MS
173	4104	14.83	167.50	0.314	2.9	26.11	MS
174	4105	62.67	753.33	0.065	5.2	81.11	HS
175	4106	14.21	160.67	0.304	3.3	23.33	MS
176	4107	23.60	266.50	0.356	4.3	21.94	MS
177	4108	12.36	139.50	0.294	3.3	23.61	MS
178	4109	68.56	819.17	0.441	5.3	78.61	HS
179	4110	61.89	723.33	0.128	5.3	57.78	HS
180	4111	62.56	753.33	0.060	5.3	77.78	HS
181	4112	58.33	705.00	0.057	5.3	77.78	HS
182	4113	24.82	279.83	0.361	3.0	28.33	MS
183	4114	10.89	123.33	0.283	3.3	25.56	MS
184	4115	25.67	292.50	0.251	4.0	46.11	S
185	4116	10.20	115.50	0.271	3.0	23.89	MS
186	4117	9.99	113.17	0.271	3.2	23.33	MS
187	4118	49.67	579.17	0.137	5.3	60.00	S
188	4120	12.27	139.00	0.294	3.0	26.11	MS
189	4121	54.56	638.33	0.125	5.3	63.33	HS
190	4122	56.78	664.17	0.127	5.3	58.61	HS
191	4123	2.00	22.50	0.110	1.9	8.61	MR
192	4124	10.17	115.00	0.271	3.0	25.56	MS
193	4125	44.33	502.50	0.308	5.3	43.61	S
194	4126	10.67	120.00	0.283	3.2	18.33	MS
195	4127	2.19	25.33	0.110	2.2	18.89	MR
196	4128	2.93	34.00	0.161	2.3	21.39	MR

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
197	4129	27.22	310.00	0.261	4.0	42.50	S
198	4130	10.22	115.00	0.283	3.0	16.39	MS
199	4131	2.68	31.00	0.161	1.9	17.50	MR
200	4132	2.00	23.33	0.110	2.0	14.72	MR
201	4133	2.44	27.50	0.161	2.0	8.06	MR
202	4134	2.44	27.50	0.161	2.4	9.17	MR
203	4135	26.69	301.17	0.371	3.9	23.33	S
204	4301	2.00	22.50	0.110	2.2	7.78	MR
205	4302	12.27	139.00	0.294	3.1	27.50	MS
206	4303	58.67	707.50	0.057	4.6	78.06	HS
207	4304	0.00	0.00	0.000	0.0	0.00	I
208	4305	10.88	123.17	0.283	2.9	28.06	MS
209	4306	11.60	131.50	0.283	3.3	28.06	MS
210	4307	14.89	167.50	0.314	3.0	19.44	MS
211	4308	2.44	27.50	0.161	2.0	8.33	MR
212	3801	51.33	600.00	0.129	4.1	60.28	HS
213	3802	62.78	754.17	0.065	5.3	82.78	HS
214	3803	9.89	115.00	0.161	3.0	45.00	MS
215	3804	2.13	24.50	0.110	2.2	28.06	MR
216	3805	2.13	24.50	0.110	2.2	23.89	MR
217	3806	46.33	525.00	0.314	5.2	45.56	S
218	3807	37.33	467.50	0.019	4.3	84.44	S
219	3808	2.00	22.50	0.110	2.0	8.61	MR
220	3809	57.11	686.67	0.062	5.3	79.17	HS
221	3811	2.64	30.50	0.161	2.1	25.28	MR
222	3812	10.23	116.00	0.271	3.4	21.67	MS
223	3813	10.93	124.00	0.283	2.9	24.17	MS
224	3814	27.67	315.83	0.210	3.9	44.72	S
225	3815	13.72	155.00	0.304	3.3	25.00	MS
226	3816	11.12	126.00	0.283	3.3	21.67	MS
227	3817	15.78	178.33	0.322	2.9	28.61	MS
228	3818	2.93	34.00	0.161	2.1	22.22	MR
229	3819	12.00	135.00	0.294	3.2	18.06	MS

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
230	3820	25.44	290.00	0.251	4.1	44.44	MS
231	3821	8.87	100.50	0.256	3.1	27.50	MS
232	5801	56.33	681.67	0.054	5.1	79.17	HS
233	5802	5.89	70.83	0.034	3.1	35.56	MS
234	5803	2.00	22.50	0.110	2.3	9.44	MR
235	5804	8.27	94.00	0.256	3.2	26.67	MS
236	5805	58.33	705.00	0.057	4.6	80.28	HS
237	5806	2.00	22.50	0.110	2.3	10.00	MR
238	5807	2.83	32.50	0.161	2.1	26.67	MR
239	5808	11.82	134.00	0.294	3.1	26.67	MS
240	5809	2.44	27.50	0.161	1.7	8.61	MR
241	5810	2.67	30.00	0.161	1.8	7.78	MR
242	5811	1.56	17.50	0.110	2.0	7.50	MR
243	5812	2.47	28.67	0.161	1.8	15.56	MR
244	5813	25.33	290.00	0.200	4.1	41.39	MS
245	5814	10.67	124.17	0.110	3.1	34.72	MS
246	5815	0.33	3.75	0.000	1.3	0.00	R
247	5816	2.27	26.50	0.110	2.2	21.11	MR
248	5817	2.83	32.50	0.161	2.0	22.78	MR
249	5818	12.88	145.67	0.294	3.1	21.67	MS
250	5819	2.44	27.50	0.161	1.7	8.06	MR
251	5820	25.67	292.50	0.251	4.3	45.28	S
252	5821	31.44	358.33	0.224	4.3	45.00	S
253	6001	11.94	135.00	0.294	3.3	29.72	MS
254	6002	2.00	22.50	0.110	2.2	10.00	MR
255	6003	27.78	317.50	0.210	4.3	43.33	S
256	6004	55.67	673.33	0.051	5.8	69.72	HS
257	6005	12.22	138.33	0.294	3.1	26.94	MS
258	6006	25.22	288.33	0.200	4.3	49.17	MS
259	6007	31.56	360.00	0.224	4.2	44.17	S
260	6008	43.78	498.33	0.256	5.2	37.78	S
261	6009	49.33	558.33	0.319	5.0	43.61	S
262	6010	22.61	255.00	0.356	3.9	24.17	MS

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
263	6011	57.33	691.67	0.057	5.2	75.56	HS
264	6012	57.11	669.17	0.118	5.3	58.06	HS
265	6013	63.78	765.00	0.068	5.5	81.94	HS
266	6014	13.36	151.17	0.304	3.3	27.22	MS
267	6015	15.80	178.67	0.322	3.0	24.72	MS
268	6016	59.44	721.67	0.047	5.2	70.00	HS
269	6017	60.89	741.67	0.038	5.0	79.17	HS
270	5301	55.33	645.00	0.137	5.1	71.94	HS
271	5302	26.00	297.50	0.200	4.3	45.56	S
272	5303	60.44	725.00	0.068	5.0	80.00	HS
273	5304	47.22	535.00	0.316	4.8	53.06	S
274	5305	2.00	22.50	0.110	2.2	7.22	MR
275	5306	11.72	132.50	0.294	3.1	25.28	MS
276	5307	9.33	105.00	0.271	3.0	17.78	MS
277	5308	2.00	22.50	0.110	1.8	5.83	MR
278	5309	12.17	137.50	0.294	3.1	27.22	MS
279	5310	0.00	0.00	0.000	0.0	0.00	I
280	5311	3.22	40.83	0.182	1.9	45.28	MR
281	5312	2.22	25.00	0.161	1.9	8.06	MR
282	5314	25.89	295.83	0.200	4.2	44.17	S
283	5315	29.33	335.00	0.215	4.0	42.50	S
284	4310	9.28	105.00	0.271	3.3	21.39	MS
285	4311	54.11	655.00	0.053	5.2	76.94	HS
286	4312	66.67	806.67	0.052	5.3	79.44	HS
287	4313	9.06	102.50	0.271	3.1	22.50	MS
288	4314	27.67	370.00	0.023	5.2	78.89	S
289	4315	46.56	528.33	0.262	5.3	51.11	S
290	4316	52.22	591.67	0.273	5.3	48.61	HS
291	4317	60.00	690.00	0.188	0.0	58.61	HS
292	4318	13.29	150.17	0.304	3.3	23.89	MS
293	4319	12.17	137.50	0.294	3.1	20.83	MS
294	3526	2.00	22.50	0.110	1.9	5.83	MR
295	3527	12.22	140.83	0.173	3.3	43.06	MS

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
296	3528	26.78	305.83	0.205	3.8	39.72	S
297	3529	2.00	22.50	0.110	2.0	15.83	MR
298	4320	2.67	30.00	0.161	2.0	7.78	MR
299	4321	3.11	35.00	0.161	1.9	6.67	MR
300	4322	2.90	33.50	0.161	2.0	20.00	MR
301	4323	61.67	740.00	0.071	5.7	80.00	HS
302	4137	46.56	528.33	0.262	4.9	42.50	S
303	4138	0.00	0.00	0.000	0.0	0.00	I
304	4139	12.27	139.00	0.294	3.1	22.50	MS
305	4140	16.17	182.50	0.322	3.3	23.89	MS
306	4141	2.00	22.50	0.110	2.2	10.83	MR
307	4142	52.11	611.67	0.119	5.2	57.22	HS
308	4143	43.22	490.00	0.308	5.2	52.78	S
309	4144	12.26	138.83	0.294	3.1	21.94	MS
310	3823	9.12	103.50	0.271	2.7	23.89	MS
311	3824	14.67	165.00	0.314	3.3	13.61	MS
312	3825	51.89	588.33	0.273	5.2	46.39	HS
313	3826	2.00	22.50	0.110	2.2	7.50	MR
314	3827	2.44	27.50	0.161	2.1	4.72	MR
315	3828	2.87	33.00	0.161	2.2	20.00	MR
316	3829	63.33	760.00	0.068	4.6	77.22	HS
317	3830	54.89	665.00	0.051	5.3	76.39	HS
318	3831	25.67	292.50	0.251	4.2	40.83	S
319	3832	66.00	791.67	0.068	5.3	76.67	HS
320	3833	2.00	22.50	0.110	2.2	7.50	MR
321	3834	12.93	146.50	0.294	3.2	26.67	MS
322	3835	30.56	347.50	0.271	4.2	44.17	S
323	3836	10.90	123.50	0.283	3.1	21.94	MS
324	3837	14.71	166.50	0.314	3.3	21.11	MS
325	3838	2.00	22.50	0.110	2.2	8.06	MR
326	3839	55.89	684.17	0.034	5.0	76.39	HS
327	HR-12	22.78	260.00	0.240	4.3	39.44	MS
328	TN1	26.78	305.83	0.205	4.0	45.28	S

Sl. No.	NSN-1 series	Mean of disease infection (%)	AUDPC	r value	Mean length of the lesion	AUDPC	Reaction
329	Vikramarya	9.76	110.50	0.271	3.3	29.17	MS
330	Nidhi	10.49	119.00	0.283	3.1	23.89	MS
331	IR-50	24.91	281.17	0.361	4.3	26.11	MS
332	IR-64	28.00	315.00	0.376	4.0	14.44	S
333	Co-39	48.78	570.83	0.123	4.6	56.11	S
334	Swarnadhan	49.67	562.50	0.319	5.3	37.78	S
335	Ajaya	62.44	759.17	0.041	5.3	79.44	HS
336	RP-Bio-226	2.00	22.50	0.110	2.3	7.78	MR
337	Rasi	0.00	0.00	0.0	0.0	0.00	I
338	Tetep	UG	UG	UG	UG	UG	UG
SEM±1	-	6.39	-	-	0.21	-	-
C.D@ 5%	-	17.75	-	-	0.59	-	-

Plate 2. A) Complete chaffiness due to sheath rot infection

Plate 2. B) Partial emergence of panicle due to sheath rot infection

4. CONCLUSION

Our study provides valuable insights into the host plant resistance to sheath rot caused by *Sarocladium oryzae* in paddy. Through the evaluation of NSN-1 genotypic lines, we have identified promising lines exhibiting different levels of resistance, seven NSN-1 cultures were found immune. Oneline showed resistance reaction with less than one per cent disease, one resistant and one hundred one lines were moderately resistant to this devastating disease. These findings contribute to the ongoing efforts to develop resistant rice varieties, ultimately aiding in the sustainable management of sheath rot and ensuring the productivity and resilience of paddy cultivation. Further research and field trials will be crucial for validating these results and advancing the development of resistant rice cultivars.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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