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Evaluation of DSN and NHSN Rice Genotypes for Resistance to Sheath Rot Disease caused by *Sarocladium oryzae* (Sawada) Gams and Hawksworth

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Abstract

Rice is a staple food crop worldwide, with nearly 90 per cent of its production occurs in Asia, mainly in India and China. Sheath rot, caused by *Sarocladium oryzae*, has emerged as a serious constraint to rice productivity in recent decades, causing yield losses ranging from 20-85 per cent. The disease is characterized by greyish-brown lesions on the uppermost leaf sheath enclosing the panicle, resulting in incomplete panicle exertion, grain discoloration and chaffy grains. In the present study, field screening of rice genotypes from DSN (229 lines) and NHSN (98 lines) was conducted to assess their response to sheath rot disease. Genotypes were evaluated using standard disease rating scales, per cent disease index (PDI) and area under disease progress curve (AUDPC). Among DSN lines, one genotype (DSN-52) showed zero percent infection, nine (DSN-35, 46, 94, 99, 114, 206, 207, 212 and 215) were resistant, Similarly, NHSN screening revealed 12 immune genotypes (3214, 3221, 3222, 3311, 3007, 3011, 3024, 3109, 3115, 3121, 3126 and 3129), six (3203, 3208, 3019, 3025, 3106 and 3119) showed resistant reaction. Both DSN and NHSN lines exhibited wide variability. These immune and resistant genotypes represent valuable donor sources for rice improvement programs aimed at developing sheath rot-resistant cultivars. The predominance of susceptible types emphasizes the urgent need for continuous germplasm evaluation and integration of resistant lines with effective management practices to achieve sustainable control of sheath rot and safeguard rice yields.

Keywords : Rice, Sheath rot, *Sarocladium oryzae*, Screening, AUDPC

Rice is one of the world's most important and extensively cultivated food crops, with nearly 90 percent of its production concentrated in Asian countries, primarily China and India (Yashwanthgowda *et al*., 2024). The crop is affected by several diseases caused by fungi, bacteria, viruses, phytoplasma, nematodes and also by non-parasitic disorders. Among these, sheath rot disease has become increasing prevalently in recent decades. The disease is now commonly observed in India as well and its impact on yield loss is significant. Although once regarded as a minor disease, sheath rot has recently emerged as a major constraint in rice cultivation across many rice-growing regions, especially in Asia.

Sheath rot disease was originally identified in 1922 as *Acrocylindrium oryzae* Sawada, and was later renamed as *Sarocladium oryzae* (Sawada) W. Gams and D. Hawksw. in 1975. Several factors, including climate change, altered cropping systems, insect activity and the adoption of new rice varieties, have contributed to the increasing incidence of sheath rot disease (Bigirimana *et al.,* 2015).

Sheath rot causes yield losses that vary from 20 to 85 per cent (Balgude *et al*., 2019). *S. oryzae* produces characteristic greyish brown lesions on the uppermost flag leaf enclosing the panicle. A severe infection has been reported to produce partially emerged or total compressed panicles with chaffy grains. The rotting occurs on the uppermost leaf sheath enclosing the young panicle. Sometimes oblong or irregular brown spots appear which enlarge and cover most of the leaf sheath. The young panicles remain enclosed within the leaf sheath or emerge partially. In severe cases, the panicles rot completely and the grains turn deep brown and produces discoloured grains (Mvuyekure *et al*., 2017).

At present, chemical control is not sufficient for effective management of this disease. Moreover, the application of fungicides is associated with several drawbacks, including environmental pollution, development of resistant pathogen strains and issues of residual toxicity (Afolabi *et al*., 2023; Mehta *et al*., 2023 and behura *et al*., 2024). Therefore, adopting crop management strategies-such as identifying resistance sources from cultivars, germplasm, landraces and wild relatives and incorporating them into breeding programs-offers a sustainable approach for the successful management of sheath rot disease. In this context a study was conducted to screen NHSN and DSN resistance lines against sheath rot of rice.

MATERIAL AND METHODS

A field experiment was carried out to screen NHSN (National hybrid Screening Nursery) and DSN (Donor Screening Nursery) rice genotypes against sheath rot disease at the Zonal Agricultural Research Station (ZARS), V. C. Farm, Mandya, situated in the Southern Dry Zone (Zone 6) of Karnataka (12° 31' 25.43'' N latitude and 76° 53' 40.86'' E longitude) during *kharif* 2023. The objective of the screening was to assess severity of sheath rot in 229 DSN and 98 NHSN rice geno. Each culture was planted in rows of 1 m length with a spacing of 20 × 15 cm. To ensure uniform disease pressure, the susceptible variety HR-12 was planted after every 10 test entries and also along the borders of the experimental plot following the infector row technique. Standard agronomic practices were adopted to maintain the crop. Per cent disease index (PDI) was assessed at 10 days interval and the PDI was worked out using the formula given by (Wheeler 1969);

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

PDI was recorded at different intervals and the AUDPC was calculated. The 'Area Under Disease Progress Curve' would be calculated by using the formula suggested by Johnson and Wilcoxson (1982).

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

X_i = disease index expressed as a proportion at the i^{th} observation.

t_i = time (days after transplanting) at the i^{th} observation

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:

RESULTS AND DISCUSSION

A comprehensive screening of rice genotypes belonging to DSN and NHSN groups was carried out to assess their reaction to sheath rot disease. A total of 229 DSN lines and 98 NHSN-1 lines were evaluated and their responses varied widely, ranging from symptomless to highly susceptible.

Among the DSN lines, only one genotype, DSN-52, was completely immune, showing 0 per cent infection

Table 1

Disease scoring scale for sheath rot disease

Scale	Incidence of infected tillers	Reaction
0	No incidence	Highly resistant (HR)
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)

and indicating absolute resistance. Nine genotypes (DSN-35, 46, 94, 99, 114, 206, 207, 212 and 215) exhibited high resistance, with infection levels of 0.83-0.94 per cent and AUDPC values up to 19.17, reflecting minimal disease development. Moderate resistance was observed in 41 genotypes, which recorded 1.0-1.56 per cent infection and AUDPC values up to 30.0, suggesting partial resistance and slow disease progress.

The largest group, consisting of 109 genotypes, fell under the moderately susceptible category, showing 5.78-24.11 per cent infection and AUDPC values up to 608.33, indicating noticeable disease development. A total of 34 genotypes were classified as susceptible, with 25.78 - 45.56 per cent infection and AUDPC values reaching 1433.33. Severe disease progression was recorded in 35 highly susceptible genotypes, which exhibited 51.22-64.44 per cent infection and AUDPC values up to 2183.33. The susceptible check showed a mean disease index of 74.52 per cent, confirming the aggressiveness of the pathogen under field conditions (Table 3 and 4).

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

Plate 1 : Field symptom of sheath rot infected panicle

TABLE 3
Screening of NHSN genotypic lines against sheath rot disease

NHSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
3201	0.80	2.00	15.33	6.04	118.65	1.81	54.00	MS
3202	0.60	3.33	17.00	6.98	143.95	1.91	57.50	MS
3203	0.30	0.70	1.00	0.66	20.00	2.07	65.00	R
3204	3.00	18.00	38.00	19.67	505.00	2.87	81.67	MS
3205	0.00	3.00	17.67	6.89	133.35	1.72	46.50	MS
3206	0.00	0.67	3.00	1.22	25.05	0.79	24.67	MR
3207	0.50	38.33	16.00	18.28	662.45	2.18	64.67	MS
3208	0.30	0.70	1.00	0.66	20.00	2.07	65.00	R
3209	3.67	21.33	67.00	30.67	710.00	3.31	108.67	S
3210	39.67	67.00	62.00	56.22	1910.05	4.51	138.50	HS
3211	0.57	3.00	3.00	2.19	68.55	1.64	61.33	MR
3212	3.00	14.67	16.67	11.44	348.40	2.74	86.67	MS
3213	0.67	3.00	19.00	7.56	150.05	2.23	72.17	MS
3214	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3215	4.00	18.33	37.00	19.78	519.95	3.17	95.33	MS
3216	0.80	3.00	15.33	6.38	133.65	2.01	60.33	MS
3217	0.57	2.67	12.67	5.30	111.95	2.11	68.83	MR
3218	3.67	18.33	38.33	20.11	521.65	3.16	98.83	MS
3219	4.00	18.33	35.67	19.33	513.30	2.88	96.17	MS
3220	17.00	37.00	58.00	37.33	1100.00	3.91	110.00	S
3221	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3222	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3223	19.67	35.00	67.33	40.67	1156.70	3.97	121.50	S
3224	3.00	17.33	40.67	20.33	508.30	3.06	105.50	MS
3225	36.00	62.00	64.33	54.11	1791.65	4.70	147.50	HS
3226	3.00	18.00	38.33	19.78	506.65	3.07	97.83	MS
3301	3.00	16.00	42.67	20.56	498.35	3.07	105.78	MS
3302	37.00	67.67	67.00	57.22	1905.05	4.72	149.72	HS
3303	3.00	19.33	37.00	19.78	519.95	2.93	90.83	MS
3304	3.00	16.67	32.67	17.44	458.40	2.98	88.17	MS
3305	0.80	3.00	15.67	6.49	135.35	1.97	68.33	MS
3306	18.00	37.00	64.67	39.89	1148.35	4.08	124.33	S
3307	3.00	3.00	15.00	7.00	165.00	2.28	83.58	MS
3308	34.67	67.00	75.67	59.11	1903.40	4.87	149.83	HS
3309	0.80	3.00	20.33	8.04	158.65	2.16	68.83	MS

Continued....

Table 3 Continued....

NHSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
3310	3.67	19.00	32.67	18.44	503.40	3.11	97.17	MS
3311	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3312	2.67	18.00	35.67	18.78	488.40	3.03	97.00	MS
3313	2.33	17.33	66.67	28.78	628.25	3.58	105.50	S
3314	3.00	20.00	38.67	20.56	538.35	3.09	100.17	MS
3315	4.00	17.67	35.67	19.11	503.40	3.14	93.67	MS
3316	0.80	3.00	19.33	7.71	153.65	1.94	57.67	MS
3001	0.57	2.00	17.00	6.52	123.55	2.02	69.33	MS
3002	19.00	38.00	67.33	41.44	1191.65	4.02	124.17	S
3003	3.67	17.67	63.33	28.22	636.75	3.49	107.67	S
3004	22.33	17.33	36.33	25.33	776.55	3.36	102.67	MS
3005	3.67	15.67	36.00	18.44	470.10	2.92	91.67	MS
3006	2.00	17.33	35.00	18.11	464.95	3.07	98.00	MS
3007	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3008	0.57	3.00	17.00	6.86	138.55	2.43	81.67	MS
3009	3.00	19.00	16.33	12.78	411.65	2.71	85.83	MS
3010	0.80	3.00	17.00	6.93	142.00	2.28	67.67	MS
3011	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3012	18.00	38.67	66.67	41.11	1183.40	3.40	112.50	S
3013	0.30	3.00	15.33	6.21	126.15	2.11	65.33	MS
3014	0.20	3.67	17.33	7.07	144.70	2.09	59.50	MS
3015	0.00	0.60	3.00	1.20	24.00	1.01	26.33	MR
3016	0.30	3.00	17.00	6.77	134.50	2.02	63.83	MS
3017	3.00	17.33	38.33	19.56	496.60	2.97	93.83	MS
3018	4.00	15.33	37.67	19.00	478.30	3.03	86.50	MS
3019	0.00	0.70	1.00	0.56	15.50	1.13	40.67	R
3020	2.00	14.67	39.67	18.78	448.40	3.18	100.83	MS
3021	3.00	15.00	35.33	17.78	446.65	2.93	104.50	MS
3022	39.67	60.33	67.33	55.78	1836.65	4.96	151.00	HS
3023	0.40	4.00	18.00	7.47	156.00	2.00	60.67	MS
3024	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3025	0.20	0.70	1.33	0.74	20.15	2.13	68.50	R
3101	4.00	18.00	38.33	20.11	521.65	3.06	102.00	MS
3102	17.67	37.33	75.33	43.44	1201.65	4.21	123.17	S
3103	0.23	3.00	16.00	6.41	128.45	2.01	59.00	MS
3104	0.30	3.67	17.33	7.10	146.20	2.09	67.00	MS

Continued....

TABLE 3 Continued....

NHSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
3105	3.00	18.33	37.00	19.44	504.95	3.01	91.67	MS
3106	0.30	0.7	1.33	0.77	21.65	2.19	68.83	R
3107	3.00	17.00	37.00	19.00	485.00	2.98	100.83	MS
3108	13.33	38.33	56.33	36.00	1056.55	4.32	138.50	S
3109	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3110	3.67	3.00	19.33	8.67	196.70	2.48	79.17	MS
3111	3.33	19.67	37.00	20.00	530.00	3.16	96.33	MS
3112	2.00	20.00	36.67	19.56	513.35	3.01	94.00	MS
3113	4.00	16.00	38.33	19.44	491.65	3.01	87.83	MS
3114	0.23	3.00	18.33	7.19	140.10	2.16	68.50	MS
3115	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3116	0.30	14.33	43.67	19.43	437.80	3.09	98.17	MS
3117	0.27	12.67	36.67	16.53	377.45	3.10	93.67	MS
3118	0.40	3.00	18.33	7.24	142.65	2.13	63.67	MS
3119	0.00	0.30	1.33	0.54	11.15	1.93	66.67	R
3120	3.67	17.33	40.67	20.56	518.35	3.08	100.33	MS
3121	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3122	0.40	3.00	30.00	11.13	201.00	1.96	59.17	MS
3123	0.30	2.00	42.33	14.88	246.15	1.93	59.00	MS
3124	0.27	4.00	44.33	16.20	285.70	2.03	62.67	MS
3125	0.70	2.67	41.33	14.90	257.20	2.13	64.33	MS
3126	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3127	3.00	16.33	36.67	18.67	473.30	2.83	89.00	MS
3128	4.00	16.00	38.67	19.56	493.35	2.94	91.33	MS
3129	0.00	0.00	0.00	0.00	0.00	0.00	0.00	I
3130	18.33	37.00	64.00	39.78	1149.95	4.18	128.50	S
3131	3.67	15.33	38.33	19.11	476.65	3.07	109.31	MS

TABLE 4

Reaction-wise Categorization of NHSN lines

Reaction	Count	% Infection (min-max)	NHSN lines
I	12	0.0	3214, 3221, 3222, 3311, 3007, 3011, 3024, 3109, 3115, 3121, 3126 and 3129.
R	6	0.33 - 0.99	3203, 3208, 3019, 3025, 3106 and 3119
MR	4	1.2 - 5.3	3206, 3211, 3217 and 3015

Continued....

Table 4 Continued....

Reaction	Count	% Infection (min-max)	NHSN lines
MS	60	5.78 - 25.33	3201, 3202, 3204, 3205, 3207, 3212, 3213, 3215, 3216, 3218, 3219, 3224, 3226, 3301, 3303, 3304, 3305, 3307, 3309, 3310, 3312, 3314, 3315, 3316, 3001, 3004, 3005, 3006, 3008, 3009, 3010, 3013, 3014, 3016, 3017, 3018, 3020, 3021, 3023, 3101, 3103, 3104, 3105, 3107, 3110, 3111, 3112, 3113, 3114, 3116, 3117, 3118, 3120, 3122, 3123, 3124, 3125, 3127, 3128 and 3131
S	11	26.22 - 43.44	3209, 3220, 3223, 3306, 3313, 3002, 3003, 3012, 3102, 3108 and 3130
HS	5	54.11 - 59.56	3210, 3225, 3302, 3308 and 3022

Table 5

Screening of NHSN genotypic lines against sheath rot disease

DSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
1	0.0	0.7	3.0	1.24	26.00	0.91	165.17	MR
2	16.7	38.3	55.3	36.78	1101.67	4.01	78.63	S
3	3.3	16.3	35.0	18.22	470.00	2.82	24.80	MS
4	0.5	3.0	17.7	7.04	140.33	2.09	21.33	MS
5	21.3	37.0	57.0	38.44	1160.00	3.96	129.17	S
6	38.3	65.7	58.0	54.00	1850.00	4.72	88.33	HS
7	3.0	17.7	36.0	18.89	490.00	2.90	65.33	MS
8	28.7	66.0	59.0	51.22	1715.00	4.90	125.67	HS
9	3.7	16.3	37.0	19.00	485.00	2.94	164.17	MS
10	0.4	3.7	18.7	7.58	154.33	2.00	90.83	MS
11	0.7	2.0	14.7	5.79	113.83	2.11	171.17	MS
12	0.0	0.7	2.3	1.01	22.17	0.82	91.83	MR
13	4.0	23.0	38.0	21.67	595.00	2.98	60.33	MS
14	3.0	17.3	39.0	19.78	500.00	3.11	64.33	MS
15	0.0	0.6	3.3	1.30	25.17	0.81	20.00	MR
16	0.0	0.6	2.7	1.09	22.33	1.09	92.33	MR
17	3.0	22.7	40.0	21.89	585.00	2.99	100.67	MS
18	0.0	0.6	3.0	1.20	24.00	0.91	18.50	MR
19	0.0	0.7	2.3	1.00	21.67	1.14	30.00	MR
20	0.0	0.4	3.7	1.37	24.83	1.13	94.17	MR
21	0.5	3.7	15.7	6.61	140.83	1.89	21.00	MS
22	16.7	37.0	60.0	37.89	1105.00	3.93	30.50	S
23	22.7	45.3	61.0	43.00	1325.00	4.24	29.00	S
24	37.0	65.7	62.0	54.89	1850.00	4.93	57.00	HS

Continued....

TABLE 5 Continued....

DSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
25	44.3	55.7	58.7	52.89	1793.33	5.01	126.67	HS
26	0.4	3.3	16.7	6.81	139.83	2.17	139.67	MS
27	38.7	37.0	59.7	45.11	1433.33	4.09	169.67	S
28	0.0	0.7	3.3	1.34	27.17	0.93	172.17	MR
29	0.0	0.4	2.7	1.02	19.33	1.08	68.50	MR
30	2.0	16.7	41.0	19.89	485.00	3.12	129.67	MS
31	0.4	2.0	17.7	6.69	124.33	1.83	22.67	MS
32	0.0	0.7	3.7	1.46	28.83	0.97	28.17	MR
33	0.4	3.0	18.7	7.36	144.33	1.78	99.17	MS
34	0.0	0.7	3.0	1.22	25.00	1.00	52.50	MR
35	0.0	0.5	2.3	0.94	19.17	1.10	22.17	R
36	0.0	0.3	3.3	1.21	21.17	0.82	49.00	MR
37	0.2	3.0	19.7	7.62	146.33	2.13	22.67	MS
38	0.0	0.7	2.7	1.12	23.83	0.86	29.83	MR
39	0.3	3.7	15.7	6.53	137.33	2.21	20.00	MS
40	0.3	2.0	16.7	6.32	117.83	2.19	64.00	MS
41	0.0	0.6	3.7	1.41	26.83	0.98	20.50	MR
42	0.0	0.6	3.0	1.20	24.00	0.93	70.17	MR
43	15.0	38.0	60.7	37.89	1098.33	4.20	68.17	S
44	0.4	3.0	17.7	7.02	139.33	1.99	25.00	MS
45	3.3	17.3	42.0	20.89	520.00	3.38	21.67	MS
46	0.0	0.5	2.3	0.93	18.67	0.97	134.00	R
47	0.0	0.7	3.3	1.34	27.17	1.07	58.17	MR
48	0.4	3.0	20.0	7.80	151.00	1.99	109.67	MS
49	0.2	2.0	21.0	7.73	138.00	2.12	22.17	MS
50	17.7	34.3	61.7	37.89	1088.33	4.29	29.33	S
51	22.3	45.3	62.7	43.44	1328.33	4.19	60.83	S
52	0.0	0.0	0.0	0.00	0.00	0.00	64.50	I
53	3.7	17.7	43.0	21.44	535.00	2.98	137.00	MS
54	17.3	36.0	63.7	39.00	1118.33	4.32	131.50	S
55	3.7	16.0	35.7	18.44	473.33	2.82	0.00	MS
56	2.0	14.7	36.7	17.78	433.33	3.06	94.00	MS
57	4.0	15.3	39.3	19.56	486.67	3.20	140.50	MS
58	17.3	43.3	64.7	41.78	1233.33	4.23	88.33	S
59	0.3	3.7	17.0	6.99	144.50	2.16	97.83	MS
60	3.7	17.3	38.3	19.78	506.67	3.08	103.00	MS

Continued....

TABLE 5 Continued....

DSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
61	0.4	3.7	18.0	7.36	151.00	2.14	135.50	MS
62	17.0	44.3	65.7	42.33	1248.33	4.29	65.00	S
63	3.3	38.0	39.3	26.89	816.67	2.98	97.83	S
64	0.4	3.0	14.0	5.80	121.00	1.93	67.17	MS
65	3.7	13.0	35.7	17.44	428.33	2.90	137.00	MS
66	0.7	3.7	15.0	6.44	140.00	1.97	92.33	MS
67	0.6	4.0	15.3	6.64	145.67	1.94	60.33	MS
68	3.7	15.3	36.7	18.56	468.33	3.04	91.17	MS
69	0.5	3.0	16.3	6.62	134.67	2.09	57.83	MS
70	0.7	2.0	17.3	6.69	127.67	1.97	59.50	MS
71	0.6	4.0	18.3	7.64	160.67	2.07	96.67	MS
72	16.3	44.3	66.7	42.44	1243.33	3.93	65.00	S
73	16.0	45.7	63.3	41.67	1241.67	4.21	58.50	S
74	3.7	18.3	37.7	19.89	518.33	3.10	62.00	MS
75	2.0	22.7	38.7	21.11	563.33	3.34	125.00	MS
76	0.7	3.7	19.3	7.90	162.17	2.03	136.50	MS
77	3.0	22.3	38.3	21.22	571.67	3.12	98.17	MS
78	2.7	19.7	39.3	20.56	531.67	3.08	107.17	MS
79	17.3	39.7	64.0	40.33	1175.00	4.31	59.50	S
80	0.7	3.0	18.0	7.23	145.50	2.11	99.50	MS
81	2.0	17.7	40.3	20.00	496.67	3.08	96.50	MS
82	15.7	29.0	65.0	36.56	995.00	4.21	140.00	S
83	38.7	66.3	66.0	57.00	1905.00	4.91	65.67	HS
84	0.7	3.7	19.0	7.78	160.00	1.93	97.83	MS
85	0.6	3.7	20.0	8.10	164.50	2.27	138.50	MS
86	0.5	2.0	16.0	6.17	117.50	1.98	169.00	MS
87	0.0	0.5	4.0	1.50	27.50	0.99	56.67	MR
88	0.0	0.4	3.3	1.24	22.67	0.96	70.67	MR
89	38.3	66.0	60.3	54.89	1866.67	4.91	60.33	HS
90	45.7	56.0	57.0	52.89	1810.00	4.97	24.83	HS
91	17.3	37.0	58.0	37.44	1105.00	4.31	22.33	S
92	0.7	3.0	17.0	6.90	140.50	2.02	168.00	MS
93	0.0	0.5	2.7	1.06	20.83	1.17	169.50	MR
94	0.0	0.5	2.0	0.83	17.50	1.00	139.00	R
95	0.0	0.5	3.0	1.18	23.00	0.94	61.33	MR
96	0.0	0.7	4.0	1.56	30.00	0.82	30.83	MR

Continued....

TABLE 5 Continued....

DSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
97	0.6	3.0	18.0	7.20	144.00	2.09	22.33	MS
98	0.0	0.5	3.0	1.17	22.50	0.88	22.50	MR
99	0.0	0.4	2.3	0.90	17.17	1.20	19.67	R
100	0.0	0.4	4.0	1.47	26.00	0.87	63.33	MR
101	0.7	3.0	19.0	7.57	150.50	2.11	20.17	MS
102	3.7	18.3	41.3	21.11	536.67	3.00	31.33	MS
103	0.6	3.7	18.0	7.42	154.00	2.06	20.67	MS
104	17.3	39.7	59.0	38.67	1150.00	4.29	67.00	S
105	0.7	3.7	13.0	5.79	130.50	2.06	96.67	MS
106	0.0	0.6	3.3	1.30	25.17	0.92	62.17	MR
107	0.0	0.6	2.7	1.10	22.83	0.92	137.00	MR
108	0.7	2.7	14.0	5.78	120.00	2.13	61.17	MS
109	0.0	0.7	3.0	1.23	25.50	0.94	22.17	MR
110	3.7	15.7	37.7	19.00	478.33	3.01	21.17	MS
111	0.0	0.6	3.7	1.42	27.33	0.96	63.67	MR
112	0.6	3.7	15.0	6.41	138.50	2.09	21.17	MS
113	0.4	2.0	16.0	6.13	116.00	1.71	96.17	MS
114	0.0	0.4	2.3	0.91	17.67	1.10	24.33	R
115	37.0	69.7	60.0	55.56	1900.00	4.90	64.33	HS
116	0.0	0.6	3.3	1.31	25.67	0.94	50.00	MR
117	46.0	55.0	61.0	54.00	1820.00	5.00	29.83	HS
118	37.7	65.7	62.0	55.11	1860.00	4.62	167.50	HS
119	17.3	34.0	63.0	38.11	1085.00	4.17	21.83	S
120	3.0	17.3	38.7	19.67	498.33	2.96	171.00	MS
121	4.0	13.3	40.3	19.22	461.67	3.18	153.00	MS
122	2.0	16.3	41.3	19.89	481.67	2.98	131.50	MS
123	0.6	3.7	16.3	6.87	145.67	2.09	91.67	MS
124	2.0	23.3	42.3	22.56	591.67	2.90	104.00	MS
125	22.3	45.0	64.0	43.78	1330.00	4.28	94.00	S
126	38.0	65.3	60.7	54.67	1853.33	5.03	66.00	HS
127	34.7	68.0	61.7	54.78	1848.33	4.88	90.17	HS
128	0.6	2.0	17.3	6.64	125.67	2.18	135.50	MS
129	42.7	56.0	61.3	53.33	1786.67	4.81	168.50	HS
130	46.3	63.7	62.3	57.44	1961.67	5.00	169.50	HS
131	36.0	72.7	63.3	57.33	1946.67	4.90	69.00	HS
132	44.7	63.3	64.3	57.44	1941.67	4.90	165.50	HS

Continued....

TABLE 5 Continued....

DSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
133	0.6	3.0	18.3	7.31	145.67	1.98	173.00	MS
134	38.3	65.3	65.3	56.33	1881.67	5.00	167.50	HS
135	0.5	65.0	19.3	28.28	1079.17	1.96	166.50	S
136	0.0	0.5	3.0	1.17	22.50	0.86	59.00	MR
137	0.0	0.5	4.0	1.50	27.50	0.90	170.00	MR
138	3.7	17.0	38.7	19.78	503.33	2.92	57.00	MS
139	34.7	65.7	66.3	55.56	1836.67	4.59	20.50	HS
140	15.7	45.3	67.3	42.78	1251.67	3.96	21.50	S
141	0.6	3.7	18.3	7.52	155.17	1.93	89.83	MS
142	3.7	16.7	36.0	18.78	485.00	3.10	154.50	MS
143	37.0	64.3	64.0	55.11	1840.00	4.92	125.00	HS
144	37.0	75.7	58.7	57.11	1983.33	5.00	55.00	HS
145	0.6	3.7	19.3	7.88	161.17	2.14	96.83	MS
146	3.0	17.7	38.0	19.56	500.00	3.16	167.50	MS
147	0.0	0.5	3.7	1.38	25.33	0.92	170.00	MR
148	40.0	65.3	59.7	55.00	1878.33	4.70	67.17	HS
149	17.3	40.7	60.7	39.56	1173.33	4.83	98.33	S
150	34.7	65.7	55.7	52.00	1783.33	4.98	21.50	HS
151	3.0	15.7	38.7	19.11	473.33	3.34	155.50	MS
152	2.7	16.3	39.7	19.56	483.33	3.28	160.50	MS
153	0.7	3.0	17.3	7.01	142.17	2.22	170.00	MS
154	0.6	2.3	22.7	8.53	157.33	2.03	109.17	MS
155	3.7	15.0	37.0	18.56	465.00	3.19	108.50	MS
156	2.0	16.3	44.3	20.89	496.67	2.90	69.67	MS
157	2.0	22.7	47.7	24.11	608.33	3.21	60.17	MS
158	3.7	22.0	37.0	20.89	570.00	2.99	103.50	MS
159	35.7	65.3	65.3	55.44	1841.67	4.91	92.83	HS
160	15.0	37.0	53.7	35.22	1048.33	4.21	104.83	S
161	3.7	17.0	37.0	19.22	495.00	3.32	93.83	MS
162	4.0	15.0	45.7	21.56	513.33	3.02	166.00	MS
163	35.3	65.3	65.7	55.44	1838.33	4.93	133.50	HS
164	45.3	76.3	71.7	64.44	2183.33	4.88	107.83	HS
165	21.0	45.0	56.3	40.78	1271.67	4.40	93.33	S
166	3.3	15.3	37.0	18.56	465.00	3.28	170.00	MS
167	0.0	0.5	3.0	1.17	22.50	0.92	166.50	MR
168	0.0	0.5	3.7	1.39	25.83	1.10	144.00	MR

Continued....

TABLE 5 Continued....

DSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
169	3.0	16.3	42.0	20.44	500.00	3.09	107.17	MS
170	0.0	0.3	3.3	1.20	20.67	0.82	20.50	MR
171	34.3	64.3	77.0	58.56	1865.00	4.86	27.50	HS
172	16.0	45.7	66.0	42.56	1255.00	4.26	97.67	S
173	3.7	17.0	38.0	19.56	500.00	3.04	19.00	MS
174	0.7	3.3	17.3	7.12	147.17	2.23	164.17	MS
175	3.7	16.7	34.7	18.33	478.33	3.26	136.17	MS
176	0.7	4.0	17.3	7.36	157.67	1.88	98.00	MS
177	0.6	2.0	22.7	8.42	152.33	1.96	68.17	MS
178	0.5	4.0	20.7	8.39	170.83	2.56	106.50	MS
179	2.0	17.3	34.7	18.00	463.33	3.06	56.17	MS
180	37.0	65.3	63.7	55.33	1853.33	4.84	58.67	HS
181	0.5	3.7	13.3	5.82	128.67	1.66	84.00	MS
182	3.3	13.3	28.7	15.11	393.33	2.78	96.50	MS
183	0.7	3.7	14.0	6.12	135.50	2.09	166.67	MS
184	3.7	23.3	28.3	18.44	546.67	3.13	47.83	MS
185	3.0	15.0	33.7	17.22	438.33	3.14	86.33	MS
186	0.3	4.0	22.3	8.87	175.67	2.13	66.33	MS
187	3.7	36.7	37.0	25.78	790.00	3.37	101.33	S
188	2.7	16.3	34.0	17.67	455.00	3.62	100.83	MS
189	0.6	3.0	39.0	14.20	249.00	2.59	67.33	MS
190	23.0	39.3	74.3	45.56	1306.67	3.38	109.83	S
191	3.0	15.3	38.7	19.00	468.33	3.11	120.33	MS
192	2.0	22.0	45.3	23.11	586.67	3.14	64.17	MS
193	4.0	17.3	44.3	21.89	541.67	2.77	122.33	MS
194	40.3	65.3	65.3	57.00	1911.67	4.94	99.67	HS
195	46.3	55.7	57.0	53.00	1815.00	4.97	100.17	HS
196	0.7	3.7	15.0	6.46	140.50	1.98	85.50	MS
197	2.0	16.0	37.0	18.33	455.00	2.83	169.17	MS
198	37.0	65.3	65.3	55.89	1861.67	4.77	169.17	HS
199	46.3	66.3	58.3	57.00	1981.67	4.71	58.33	HS
200	20.3	39.7	72.0	44.00	1260.00	4.27	86.50	S
201	3.0	15.3	34.0	17.44	445.00	3.03	163.17	MS
202	0.7	3.3	17.0	7.01	145.50	2.19	159.67	MS
203	0.3	2.7	22.0	8.31	154.00	2.20	138.67	MS
204	2.0	17.7	22.3	14.00	406.67	3.08	94.50	MS

Continued....

TABLE 5 Continued....

DSN series	1st	2nd	3rd	Mean of disease infection (%)	AUDPC	Mean length of the lesion (cm)	AUDPC	Reaction
205	0.0	0.6	3.0	1.20	24.00	0.89	66.83	MR
206	0.0	0.6	2.0	0.86	18.50	1.11	66.33	R
207	0.0	0.5	2.0	0.83	17.50	0.94	98.83	R
208	0.0	0.6	3.7	1.42	27.33	1.01	21.00	MR
209	0.0	0.2	4.0	1.40	23.00	1.01	30.00	MR
210	0.4	3.7	18.0	7.36	151.00	2.13	21.50	MS
211	0.0	0.6	4.0	1.52	28.50	0.82	23.50	MR
212	0.0	0.5	2.0	0.83	17.50	1.07	22.50	R
213	0.0	0.5	3.7	1.39	25.83	0.91	62.33	MR
214	0.0	0.6	3.0	1.19	23.50	0.88	19.33	MR
215	0.0	0.3	2.3	0.88	16.17	0.98	29.33	R
216	37.0	63.3	65.3	55.22	1831.67	4.94	21.33	HS
217	45.3	57.3	66.3	56.33	1871.67	5.09	18.83	HS
218	16.0	39.3	55.7	37.00	1108.33	4.03	23.67	S
219	3.0	14.3	39.7	19.00	458.33	3.18	166.17	MS
220	0.6	3.0	17.3	6.97	140.17	2.17	171.67	MS
221	0.6	3.0	15.3	6.32	131.17	1.73	128.17	MS
222	18.3	3.0	58.0	26.44	610.00	4.01	102.33	S
223	3.7	22.7	65.7	30.67	723.33	3.00	66.50	S
224	2.0	15.0	74.3	30.44	626.67	3.07	49.67	S
225	2.0	14.3	65.0	27.11	570.00	3.02	131.17	S
226	0.7	3.0	17.3	7.01	142.17	2.11	96.67	MS
227	0.0	0.3	3.0	1.11	20.00	1.04	98.67	MR
228	45.3	66.0	66.0	59.11	2000.00	4.69	95.67	HS
229	37.0	74.0	75.7	62.22	2043.33	4.81	65.67	HS

Similarly, screening of the NHSN lines revealed broader variability in their reaction. Out of the 98 genotypes, twelve genotypes (3214, 3221, 3222, 3311, 3007, 3011, 3024, 3109, 3115, 3121, 3126 and 3129) were symptomless, with 0 per cent infection and no lesion development, clearly indicating complete resistance. Six genotypes (3203, 3208, 3019, 3025, 3106 and 3119) were resistant, with infection levels ranging from 0.33 to 0.99 per cent, reflecting strong resistance with negligible disease development. Four genotypes (3206, 3211, 3217 and 3015) were moderately resistant, exhibiting 1.2-5.3 per cent infection, AUDPC values up to 111.83, lesion sizes between 0.79-2.11 cm and lesion AUDPC values up to 68.83, suggesting partial resistance with limited disease development. The largest group comprised 60 genotypes, which were moderately susceptible, showing 5.78-25.33 per cent infection, AUDPC values up to 776.67 and Eleven genotypes (3209, 3220, 3223, 3306, 3313, 3002, 3003, 3012, 3102, 3108 and 3130) were susceptible, with 26.22-43.44 per cent infection, AUDPC values up to 1201.67 and

TABLE 6
Reaction-wise Categorization of DSN lines

Reaction	Count	% Infection (min-max)	DSN lines
I	1	0.0	52
R	9	0.83 - 0.94	35, 46, 94, 99, 114, 206, 207, 212, 215
MR	41	1.0 - 1.56	1, 12, 15, 16, 18, 19, 20, 28, 29, 32, 34, 36, 38, 41, 42, 47, 87, 88, 93, 95, 96, 98, 100, 106, 107, 109, 111, 116, 136, 137, 147, 167, 168, 170, 205, 208, 209, 211, 213, 214, 227
MS 84,	109	5.78 - 24.11	3, 4, 7, 9, 10, 11, 13, 14, 17, 21, 26, 30, 31, 33, 37, 39, 40, 44, 45, 48, 49, 53, 55, 56, 57, 59, 60, 61, 64, 65, 66, 67, 68, 69, 70, 71, 74, 75, 76, 77, 78, 80, 81, 85, 86, 92, 97, 101, 102, 103, 105, 108, 110, 112, 113, 120, 121, 122, 123, 124, 128, 133, 138, 141, 142, 145, 146, 151, 152, 153, 154, 155, 156, 157, 158, 161, 162, 166, 169, 173, 174, 175, 176, 177, 178, 179, 181, 182, 183, 184, 185, 186, 188, 189, 191, 192, 193, 196, 197, 201, 202, 203, 204, 210, 219, 220, 221, 226
S	34	25.78 - 45.56	2, 5, 22, 23, 27, 43, 50, 51, 54, 58, 62, 63, 72, 73, 79, 82, 91, 104, 119, 125, 135, 140, 149, 160, 165, 172, 187, 190, 200, 218, 222, 223, 224, 225
HS	35	51.22 - 64.44	6, 8, 24, 25, 83, 89, 90, 115, 117, 118, 126, 127, 129, 130, 131, 132, 134, 139, 143, 144, 148, 150, 159, 163, 164, 171, 180, 194, 195, 198, 199, 216, 217, 228, 229

lesion sizes of 3.16-4.32 cm, while five genotypes (3210, 3225, 3302, 3308 and 3022) were highly susceptible, exhibiting 54.11-59.56 per cent infection, AUDPC values up to 1995.0 and lesion sizes between 4.51-5.08 cm, indicating rapid and severe disease development. The susceptible check in NHSN recorded a mean disease index of 68.02 per cent (Table 5 and 6).

Similar screenings of various lines/varieties have been conducted by multiple researchers in the past to identify sources of resistance against Sheath rot. Nagaraju *et al.* (1991), Bhandarkar *et al.* (2018), Pushpum *et al.* (2019), Chitra *et al.* (2020), Parikh *et al.* (2020), Feteneet *al.* (2020), Sowjanya *et al.* (2022) and Bharathi *et al.* (2024) have all undertaken such investigations.

Overall, both DSN and NHSN exhibited considerable variations. This emphasizes the significance of utilizing the immune and resistant lines identified in both sets for breeding programs aimed at developing sheath rot-resistant rice varieties, while also highlighting the ongoing challenge of sheath rot management in rice germplasm.

The present investigation on sheath rot disease of rice revealed substantial variability in the response of DSN and NHSN genotypes under field conditions. Among the evaluated entries, only a few genotypes expressed complete immunity or resistance, while the majority displayed moderate to high levels of susceptibility. This clearly demonstrates that sheath rot continues to be a significant threat in rice cultivation, capable of causing severe yield losses if not effectively managed. The identification of immune and resistant lines in both DSN and NHSN nurseries provides valuable genetic resources that can be exploited in resistance breeding programs. Incorporation of these promising sources into varietal improvement pipelines could enhance the development of durable, sheath rot-tolerant cultivars. However, the predominance of moderately susceptible to highly susceptible lines underlines the need for continuous screening and evaluation of diverse germplasm. Integrating resistant genotypes with sound crop management practices would contribute to sustainable disease management and ensure stable rice production in regions prone to sheath rot epidemics.

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