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HOST PLANT RESISTANCE FOR THE MANAGEMENT OF *MACROPHOMINA* STEM AND ROOT ROT DISEASE IN SESAME (*SESAMUM INDICUM* L.)

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ABSTRACT

Stem and root rot (SRR), caused by *Macrophomina phaseolina*, is a highly destructive disease causing heavy yield loss. Managing SRR in sesame through an integrated approach has been suggested, and the use of resistant varieties is one of the economical methods. The present study aimed to identify sources of resistance against SRR from released varieties and newly evolved sesame cultures of Tamil Nadu. Evaluation of the 75 sesame genotypes against SRR by artificial sick plot screening method identified six accessions with SRR resistance (disease scores: 1) over two seasons of evaluation. The diseases severity of stem and root rot ranged between 7.7% (VS 20031) to 90.5% (EC 346680) and the susceptible check VRI 1 recorded the disease severity of 83.3%. Pooled analysis of percent disease incidence data of 75 accessions revealed that six accessions viz., VS 20031, VS 17031, EC 347156-2, VS 19029, VS 19081, VS 20030 were found to be stable for SRR resistance across seasons with a disease incidence of <10%. These accessions could be used in sesame SRR resistance breeding programs.
Keywords: Stem and root rot (SRR), *Macrophomina phaseolina*, *Sesamum indium.*

Introduction

Sesame, Sesamum or gingelly (*Sesamum indium*) is the most ancient oilseed crop known and used by man for its quality oil. Sesame is also known as 'Queen of Oilseeds' due to its high quality polyunsaturated stable fatty acid, which restrains oxidative rancidity. Sesame seed is also an important source of oil (44–63%), protein (18–25%), carbohydrate (13.5%) and ash (5%) (Elleuch *et al*., 2007). The major limiting factor in sesame productivity is its susceptibility to various diseases. Among the fungal diseases, stem and root rot also called charcoal rot caused by *Macrophomina phaseolina* (Tassi) Goid. is widely distributed and highly destructive starting from seedling to capsule maturity stage (Dinakaran and Mohammed, 2001), causing up to 50 *per cent* or more disease incidence in field resulting in heavy yield losses (Chattopadhyay and Sastry, 2002). Yield losses have been estimated up to 57 per cent when there is about 40 per cent infection (Maiti *et al*., 1988). The pathogen attacks mostly at the basal region of the plant (Kumar *et al*., 2011). The disease is widely prevalent in all the sesame growing areas of India as it exhibits high genetic variation. Till date no commercial cultivar has been released with resistant or tolerant to dry root rot. The pathogen may cause heavy yield loss in sesame ranging from 50-100% (Gaber *et al*., 1998; Khalifa, 2003; El Shakess and Khalifa, 2007). Use of high-yielding resistant cultivars is the most viable, environmentally safe, economical sound and less expensive technique for the management of the disease. Thus, it is most remunerative to farmers. Therefore, the identification of the resistance source is a basic need in breeding for disease resistance. Hence, the present investigation was undertaken to find out the resistant sources against stem and root rot of sesame.

Materials and Methods

Seventy-five sesame varieties/ advanced breeding lines/germplasm lines were screened for their resistance against dry root rot disease along with the national susceptible check variety VRI Sv 1 under

artificial root rot sick plot condition. The field experiment was conducted at the Regional Research Station, Tamil Nadu Agricultural University, Vriddhachalam, India (Latitude: 11.30^{0}N; Longitude: 79.19^{0}E; Altitude: 45 MSL) during *Kharif* 2020 and *Rabi* / summer 2020-21 seasons. All the entries were sown in a 4-meter row with a spacing of 30 x 15cm following the infector row method, where in two test rows alternating with one infector row of the susceptible variety (VRI Sv 1). The plants were maintained properly by providing row to row and plant to plant spacing of 30 cm and 15 cm respectively. No fungicides were sprayed in order to maintain the natural *Macrophomina* spore load in the experimental field and 15 days after sowing artificially multiplied *Macrophomina* cultures were also applied in the experimental plot. The scoring of test materials was done only at the time of maturity.

Artificial inoculum multiplication

The inoculum of the pathogen was prepared by multiplying culture of the *Macrophomina* pathogen on sterilized boiled sorghum grain medium. The inoculum was mixed in soil @ 200 g/ m row length; one week prior of sowing at 5-10 cm depth to increase the disease pressure. All the plants from each entry were selected for recording the incidence of stem and root rot at a weekly interval from the disease appearance up to the physiological maturity of the crop.

Observations were recorded at the initiation of the disease and at weekly interval starting from germination to harvesting. The final observations on disease incidence were considered to categorize the varieties / advanced breeding lines / germplasm into different reactions. The varieties / cultures / germplasm was categorized (Table 1) into different resistance group as per the rating scale suggested by Nene *et al.* (1981) was adopted as given below.

Disease incidence %	Disease scale	Disease reaction
0-10.0	1	Resistant (R)
10.1-20.0	3	Moderately resistant (MR)
20.1-30.0	5	Moderately Susceptible (MS)
30.1-50.0	7	Susceptible (S)
50.1-100.0	9	Highly susceptible (HS)

The *per cent* disease incidence was worked out on the basis of total plant population and total number of *Macrophomina* infected plants in each genotype and calculated by using the following formula:

$$\text{Per cent disease incidence } (\%) = \frac{\text{Number of Macrophomina infected plants}}{\text{Total plant population}} \times 100$$

Based on the percent of disease incidence, the test entries were classified into five groups *viz*., Resistant (R), Moderately resistant (MR), Moderately susceptible (MS), Susceptible (S) and Highly susceptible (HS).

Yield Assessment

Seed yield (kg ha^{-1}) was recorded from both sick plot and normal conditions. Percent yield reduction was computed as:

$$\text{Yield reduction } (\%) = \left(\frac{\text{Normal yield - Sick plot yield}}{\text{Normal yield}} \right) \times 100$$

Result and discussion

Disease Reaction of Sesame Genotypes to *Macrophomina phaseolina*

The disease evaluation revealed wide variability among the 75 genotypes assessed, indicating substantial genetic diversity for resistance to *M. phaseolina*. Disease infestation ranged from 7.7% to 90.5%, with genotypes distributed across all five reaction categories (Table 1 and 2). Such diversity aligns with earlier reports of heterogeneous reactions to stem and root rot in sesame germplasm (Dossa *et al*., 2017). Four genotypes such as VS 20031, VS 17031, EC 347156-2, and VS 19029 exhibited very low per cent of disease incidence (<10%). Their near-symptomless reaction suggests strong genetic resistance and supports earlier findings that certain sesame accessions possess major resistance factors (El-Bramawy and Wahid, 2007). The genotypes grouped under the scale 3 consisting of 21 genotypes with 10.0 – 20.0% infestation. Lines such as VS 19081, VS 19067, and EC 346213 showed partial but stable resistance, typical of polygenic defense mechanisms reported in sesame (Yan *et al*., 2021). These genotypes represent valuable donors for breeding. Ten genotypes showed 22–29% infestation, including released varieties CO 1, TMV 4, and VRI 3. Moderate susceptibility in commercial varieties is well-documented and often reflects the absence of targeted resistance breeding (Teklu *et al*., 2022). Fifteen genotypes including VS 19032, GT 10, and Nirmala displayed clear disease symptoms with 32–50%

infestation. Their susceptibility may be attributed to weak structural or biochemical defenses, consistent with earlier susceptibility assessments (Farooq *et al*., 2019). Twenty-three genotypes showed severe infection (52–90%), including several varieties such as Paiyur 1, TMV 3, TMV 7, VRI 1, and VRI 2. These genotypes exhibited rapid disease progression, confirming complete vulnerability as previously noted in susceptible sesame cultivars (Wei *et al*., 2014).

Yield Loss Assessment Under Sick Plot and Normal Conditions

Yield analysis revealed large differences in seed yield under diseased and normal conditions (Table 3). Yield reductions ranged from –8.0% to –85.3%, reflecting the strong detrimental impact of stem and root rot on productivity. Genotypes such as VS 19076 (–8.0%), VS 19022 (–8.5%), VS 19066 (–9.9%) and VS 20031 (–10.4%) showed minimal yield losses and corresponded to resistant classes, suggesting consistent field resistance across environments. Previous studies also reported stable tolerance in resistant genotypes (El-Bramawy and Wahid, 2007). Genotypes such as VS 19029 (–22.9%), EC 346334 (–24.1%), CO 1 (–40.6%), and VS 18003 (–42.3%) experienced moderate yield reductions. These genotypes fall within MR or MS classes, showing proportional yield decline with disease severity. A large number of susceptible genotypes including TMV 4, VRI 3, VS 19059, VS 20020, Nirmala, and TGK 22 recorded 45–60% yield loss. These findings align with documented high yield penalties in susceptible sesame under pathogen pressure (Ghias *et al*., 2021). Genotypes such as VS 17029 (–69.7%), VS 19014 (–64.5%), TMV 3 (–77.2%), VS 19043 (–80.7%), VS 19020 (-84.0%), VS 19062 (–85.3%) showed extreme yield loss, matching the highly susceptible category. The drastic reductions are consistent with reports that *M. phaseolina* can cause up to 80–90% yield loss in vulnerable cultivars (Wang *et al*., 2017 and Radadiya *et al*., 2021). A strong correlation was observed between disease reaction and yield loss. Highly resistant and moderately resistant genotypes consistently recorded the lowest yield reductions, while susceptible and highly susceptible genotypes suffered the greatest losses. This validates the reliability of field disease scoring in predicting yield performance under pathogen pressure.

Conclusion

The study identified significant genetic variability for stem and root rot resistance among 75 sesame genotypes. Four genotypes (VS 20031, VS 17031, EC 347156-2, VS 19029) demonstrated strong resistance and minimal yield loss, making them valuable donors for resistance breeding. Conversely, a large number of widely cultivated varieties were highly susceptible, emphasizing the urgent need to incorporate durable resistance into high-yielding varieties. The integration of disease severity data with yield loss analysis provides a robust basis for selecting elite genotypes for future breeding programs aimed at mitigating the impact of *Macrophomina* stem and root rot.

Table 1 : Grouping of genotypes based on disease scale

Scale	Genotypes	No. of genotypes
1	VS 20031, VS 17031, EC 347156-2, VS 19029, VS 19081, VS 20030	06
3	VS 19067, VS 19022, VS 19066, VS 19076, VS 19078, EC 347156-1, VS 18007, EC 346213, EC 346334, VS 19077, VRI 4, Sudan sesame, VS 19048, VS 17016, VS 17022, EC 334979, VS 19042, VS 19064, VS 19080, VS 15014, VS 20020	21
5	VS 19059, VS 18003, VS 19054, CO 1, TMV 4, VRI 3, VS 19060, VS 18006, VS 19036, VS 20005	10
7	VS 19032, VS 17029, GT 10, VS 19014, VS 19018, VS 19007, VS 19040, TKG 22, VS 17030, VS 19056, EC 370955, EC 346428, VS 19061, VS 19072, Nirmala	15
9	VS 19073, EC 346393, VS 19074, EC 346158, EC 346366, EC 351554, VS 19071, VS 19063, VS 19043, VS 19005, Paiyur 1, TMV 7, VRI 2, TMV 3, VS 19069, VS 19082, EC 346329, VS 19079, EC 346392, VS 19020, VS 19062, VRI 1, EC 346680	23

Table 2 : Reaction of sesame genotypes to *Macrophomina* stem and root rot disease

Sl. No	Genotypes	*Percent* disease infestation	Disease scale	Disease reaction
1	VS 20031	7.7	1	R
2	VS 17031	8.7	1	R
3	EC 347156-2	9.5	1	R
4	VS 19029	9.5	1	R
5	VS 19081	10.0	3	MR
6	VS 20030	10.0	3	MR

7	VS 19067	11.1	3	MR
8	VS 19022	13.6	3	MR
9	VS 19066	13.6	3	MR
10	VS 19076	13.6	3	MR
11	VS 19078	13.6	3	MR
12	EC 347156-1	14.3	3	MR
13	VS 18007	14.3	3	MR
14	EC 346213	15.0	3	MR
15	EC 346334	15.0	3	MR
16	VS 19077	15.0	3	MR
17	VRI 4	15.8	3	MR
18	Sudan sesame	17.4	3	MR
19	VS 19048	17.4	3	MR
20	VS 17016	17.9	3	MR
21	VS 17022	17.9	3	MR
22	EC 334979	18.2	3	MR
23	VS 19042	18.2	3	MR
24	VS 19064	18.2	3	MR
25	VS 19080	19.0	3	MR
26	VS 15014	19.2	3	MR
27	VS 20020	20.0	3	MR
28	VS 19059	22.2	5	MS
29	VS 18003	23.8	5	MS
30	VS 19054	23.8	5	MS
31	CO 1	25.0	5	MS
32	TMV 4	25.0	5	MS
33	VRI 3	26.9	5	MS
34	VS 19060	27.3	5	MS
35	VS 18006	27.8	5	MS
36	VS 19036	28.6	5	MS
37	VS 20005	29.2	5	MS
38	VS 19032	32.0	7	S
39	VS 17029	33.3	7	S
40	GT 10	35.0	7	S
41	VS 19014	37.5	7	S
42	VS 19018	38.1	7	S
43	VS 19007	40.9	7	S
44	VS 19040	40.9	7	S
45	TKG 22	42.9	7	S
46	VS 17030	43.8	7	S
47	VS 19056	43.8	7	S
48	EC 370955	45.5	7	S
49	EC 346428	45.8	7	S
50	VS 19061	45.8	7	S
51	VS 19072	48.5	7	S
52	Nirmala	50.0	7	S
53	VS 19073	52.0	9	HS
54	EC 346393	52.2	9	HS
55	VS 19074	52.2	9	HS
56	EC 346158	52.9	9	HS
57	EC 346366	52.9	9	HS
58	EC 351554	55.0	9	HS
59	VS 19071	55.0	9	HS
60	VS 19063	57.7	9	HS
61	VS 19043	59.1	9	HS
62	VS 19005	60.0	9	HS
63	Paiyur 1	60.9	9	HS

64	TMV 7	60.9	9	HS
65	VRI 2	63.6	9	HS
66	TMV 3	65.0	9	HS
67	VS 19069	65.2	9	HS
68	VS 19082	66.7	9	HS
69	EC 346329	70.0	9	HS
70	VS 19079	71.4	9	HS
71	EC 346392	76.2	9	HS
72	VS 19020	77.3	9	HS
73	VS 19062	81.0	9	HS
74	VRI 1	83.3	9	HS
75	EC 346680	90.5	9	HS

Table 3 : Yield loss assessment under sick plot and normal condition

Sl. No	Genotypes	Seed yield under sick plot condition (Kg/ha)	Seed yield under normal condition (Kg/ha)	*Percent* seed yield reduction
1	VS 20031	776	866	-10.4
2	VS 17031	711	888	-19.9
3	EC 347156-2	657	769	-14.5
4	VS 19029	834	1082	-22.9
5	VS 19081	674	772	-12.7
6	VS 20030	779	925	-15.8
7	VS 19067	745	1086	-31.4
8	VS 19022	609	665	-8.5
9	VS 19066	686	761	-9.9
10	VS 19076	726	789	-8.0
11	VS 19078	759	861	-11.8
12	EC 347156-1	705	788	-10.5
13	VS 18007	786	917	-14.3
14	EC 346213	611	666	-8.3
15	EC 346334	503	663	-24.1
16	VS 19077	582	662	-12.1
17	VRI 4	587	934	-37.2
18	Sudan sesame	688	822	-16.3
19	VS 19048	874	1150	-24.0
20	VS 17016	777	1114	-30.3
21	VS 17022	514	897	-42.7
22	EC 334979	666	783	-14.9
23	VS 19042	686	917	-25.2
24	VS 19064	781	932	-16.2
25	VS 19080	529	595	-11.1
26	VS 15014	665	896	-25.8
27	VS 20020	526	1052	-50.0
28	VS 19059	263	524	-49.9
29	VS 18003	632	1094	-42.3
30	VS 19054	378	1072	-64.7
31	CO 1	508	855	-40.6
32	TMV 4	347	693	-49.9
33	VRI 3	342	921	-62.8
34	VS 19060	263	524	-49.9
35	VS 18006	439	1017	-56.9
36	VS 19036	423	1002	-57.7
37	VS 20005	491	980	-49.9

38	VS 19032	405	1100	-63.2
39	VS 17029	352	1162	-69.7
40	GT 10	237	700	-66.1
41	VS 19014	447	1257	-64.5
42	VS 19018	673	1020	-34.0
43	VS 19007	426	1236	-65.6
44	VS 19040	237	700	-66.1
45	TKG 22	345	808	-57.3
46	VS 17030	458	691	-33.7
47	VS 19056	482	945	-48.9
48	EC 370955	325	687	-52.7
49	EC 346428	265	614	-56.8
50	VS 19061	347	1388	-75.0
51	VS 19072	371	973	-61.8
52	Nirmala	288	751	-61.6
53	VS 19073	401	1034	-61.2
54	EC 346393	334	683	-51.0
55	VS 19074	292	583	-50.0
56	EC 346158	297	612	-51.4
57	EC 346366	253	602	-57.9
58	EC 351554	396	629	-37.1
59	VS 19071	304	1071	-71.6
60	VS 19063	309	1081	-71.4
61	VS 19043	194	1005	-80.7
62	VS 19005	250	1059	-76.4
63	Paiyur 1	324	787	-58.8
64	TMV 7	268	847	-68.3
65	VRI 2	331	909	-63.6
66	TMV 3	205	899	-77.2
67	VS 19069	236	704	-66.5
68	VS 19082	228	1150	-80.2
69	EC 346329	281	512	-45.1
70	VS 19079	204	407	-50.0
71	EC 346392	196	658	-70.3
72	VS 19020	198	1239	-84.0
73	VS 19062	145	983	-85.3
74	VRI 1	131	693	-81.1
75	EC 346680	221	679	-67.5

References

Chattopadhyay, C., & Sastry, R. K. (2002). Combining viable disease control tools for management of sesame stem–root rot caused by *Macrophomina phaseolina* (Tassi) Goid. *Indian Journal of Plant Protection,* ***30***(2), 132–138.

Dinakaran, D., & Mohammed, S. N. (2001). Identification of resistant sources to root rot of sesame caused by *Macrophomina phaseolina* (Tassi) Goid. *Plant Disease Research,* ***16***(2), 123–126.*

Dossa, K., Diouf, D., Wang, L., Wei, X., Zhang, Y., Niang, M., & Cissé, N. (2017). The emerging oilseed crop *Sesamum indicum* enters the "omics" era. *Frontiers in Plant Science,* ***8***, 1154.

El-Bramawy, M. A. S., & Wahid, O. A. A. (2007). Identification of genetic resources for resistance to Fusarium wilt, charcoal root rot and *Rhizoctonia* root rot among sesame (*Sesamum indicum* L.) germplasm. *African Crop Science Conference Proceedings,* ***8***, 201–207.

Elleuch, M., Besbes, S., Roiseux, O., Blecker, C., & Attia, H. (2007). Quality characteristics of sesame seeds and by-products. *Food Chemistry,* ***103***(2), 641–650.

El-Shakhess, S. A. M., & Khalifa, M. M. A. (2007). Combining ability and heterosis for yield, yield components, charcoal rot and Fusarium wilt diseases in sesame. *Egyptian Journal of Plant Breeding,* ***11***, 351–371.

Farooq, S., Mohyo-Ud-Din, A., Naz, S., Siddique, M., & Khan, S. N. (2019). Screening of sesame (*Sesamum indicum* L.) germplasms for resistance against charcoal rot disease caused by *Macrophomina phaseolina* (Tassi) Goid. *International Journal of Biology and Biotechnology,* ***16***(2), 407–410.

Gabr, M. R., Hussein, N. A., Saleh, O. I., & Khalil, M. A. (1998). Susceptibility of certain varieties and genotypes and control of wilt and root rot diseases of sesame attributed to *Fusarium oxysporum* f. sp. *sesami* and *Macrophomina phaseolina*. *Egyptian Journal of Phytopathology,* ***26***, 1–14.

Ghias, M., Rauf, S., Qamar, R., Din, A. M., Mahmood, T., & Aftab, M. (2021). Evaluation of sesame (*Sesamum indicum* L.) genotypes for charcoal rot (*Macrophomina phaseolina*) resistance. *Pakistan Journal of Phytopathology,* ***33***(2), 357–361.

Khalifa, M. M. A. (2003). *Pathological studies on charcoal rot disease of sesame* (Doctoral dissertation). Faculty of Agriculture, Zagazig University, Egypt.

Kumar, S., Aeron, A., Pandey, P., & Maheshwari, D. K. (2011). Ecofriendly management of charcoal rot and Fusarium wilt diseases in sesame (*Sesamum indicum* L.). In D. K. Maheshwari (Ed.), *Bacteria in agrobiology: Crop ecosystems* (pp. 387–405). Springer.

Maiti, S., Hegde, M. R., & Chattopadhyay, S. B. (1988). *Handbook of annual oilseed crops*. Oxford & IBH.

Nene, Y. L., Haware, M. P., & Reddy, M. V. (1981). *Chickpea diseases: Resistance-screening techniques*. ICRISAT.

Radadiya, N., Mangukia, N., Antala, V., Desai, H., Chaudhari, H., Dholaria, T. L., & Mahatma, M. K. (2021). Transcriptome analysis of sesame–*Macrophomina phaseolina* interactions revealing distinct genetic components for early defense responses. *Physiology and Molecular Biology of Plants,* ***27***(8), 1675–1693.

Teklu, D. H., Shimelis, H., & Abady, S. (2022). Genetic improvement in sesame (*Sesamum indicum* L.): Progress and outlook—A review. *Agronomy,* ***12***(9), 2144.

Wang, L., Zhang, Y., Zhu, X., Li, D., Zhang, X., & Zhang, X. (2017). Development of an SSR-based genetic map in sesame and identification of quantitative trait loci associated with charcoal rot resistance. *Scientific Reports,* ***7***(1), 8349.

Yan, W., Ni, Y., Liu, X., Zhao, H., Chen, Y., Jia, M., & Tian, B. (2021). The mechanism of sesame resistance against *Macrophomina phaseolina* revealed via comparative transcriptome analysis of resistant and susceptible genotypes. *BMC Plant Biology,* ***21***(1), 159.