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ASSESSMENT OF GENOTYPES AGAINST DRY ROOT ROT OF BLACKGRAM (*VIGNA MUNGO* L.)

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ABSTRACT

M. phaseolina (Tassi) Goid is one of the most important fungal diseases of Blackgram. It inflicts serious economic loss to the crop and was reported to result in a loss of 28.6 per cent in black gram yield. It is an important disease of broad range of crops particularly in regions with warm and dry weather conditions. *M. phaseolina* is a soil and seed-borne pathogenic fungus that causes charcoal rot, various rots and blights in more than 500 crop species. *M. phaseolina* is a polyphagic necrotroph and remains viable in the soil for several years, making disease management challenging. One of the most economical methods for managing dry root rot in blackgram is through an integrated approach that uses resistant varieties. To identify the resistant sources of blackgram against *M. phaseolina*, forty genotypes were screened through artificial inoculation of the test pathogen under *in vitro* (Paper towel method) and pot culture studies at Seed Research and Technology Centre (SRTC), Rajendranagar, Hyderabad. Among 40 genotypes, four (MBG 1220, MBG 1237, MBG-1265, MBG-1110) were classified as Resistant (R), showing minimal disease incidence, twelve genotypes were classified as moderately resistant, nine were moderately susceptible, ten were susceptible and five were highly susceptible. These results underscore the potential of resistant and moderately resistant genotypes for use in breeding programs aimed at enhancing disease resistance.

Keywords **:** Blackgram, dry root rot, resistant, susceptible, integrated approach, soil-borne.

Introduction

The cultivation of blackgram is continuously challenged by many diseases during seed germination to seed production and maturity. Over many fungal pathogens, few viral, bacterial and nematode species are known to attack black gram resulting into substantial yield losses (Agarwal, 2011). Most of the fungal diseases such as *Macrophomina* leaf blights, anthracnose and root rot causing are seed borne in black gram that results in both quantitative and qualitative losses. In blackgram protein content is reduced due to *M. phaseolina* infection in seed. Among the various diseases that infect blackgram, dry root rot caused by *M. phaseolina* is a relatively emerging threat in South Asia (Iqbal *et al.,* 2010), including India (Latha *et al.,* 2017) causes yield loss ranging from 25-48 percent. Seed borne inoculum was responsible for causing the seed rot, seedling mortality (Agrawal, 1993) and reduction in yield, which was attributed to reduced number of pods/plant and 100 grains seed weight (Hiremath and Shambulingappa,1981).

In urdbean, dry root rot reported 40% incidence in Indian climatic conditions (Indira & Gayatri, 2003) with 29% yield loss (Kulkarni *et al.,* 2019). The seed borne propagules of pathogen infect seeds of urdbean and mungbean and causes significant loss in seed germination and viability (Kaur and sahu 2009; Sarita *et al*., 2014).

Managing dry root rot in blackgram caused by *M. phaseolina* is challenging due to the pathogen's wide

host range and its ability to persist in soil through resting structures. Chemical control using fungicides is often costly and poses risks to the environment. Therefore, utilizing the innate resistance present in blackgram genotypes is considered an effective, eco-friendly and economical approach for disease management. The current study aimed to identify mungbean genotypes that exhibit resistance to charcoal rot, which can be used in breeding programs to develop resistant cultivars.

Materials and Methods

The experiment was conducted during the year 2024-25 under *in vitro* and pot culture at Department of Seed Science and Technology, Seed Research and Technology Centre (SRTC), PJTAU, Rajendranagar, Hyderabad.

The pathogenic strain of *M. phaseolina* was isolated from seeds of mungbean. A pure culture was established using single hyphal tip method and maintained on Potato dextrose agar (PDA) medium. For mass multiplication, the fungus was cultured on sorghum grains. These grains were initially half-boiled, air-dried overnight and then transferred into 500 ml Erlenmeyer flasks, each filled to one-fourth of its volume. The flasks were sterilized at 121°C under 15 lbs pressure for 15 minutes. Subsequently, 5 mm mycelial discs of *M. phaseolina* were inoculated into the sterilized sorghum grain medium and incubated at 28 ± 2°C for 15–20 days, with daily shaking to ensure uniform growth. After multiplication on sorghum grains, *M. phaseolina* inoculum were placed in each pot at 50g/kg of soil before 15 days of sowing (Choudhary *et al.,* 2011). Sowing of blackgram genotypes was done in Pots containing sick soil. 15 seeds were sown in each pot and each genotype was maintained in three replications. Observations on percent seed germination, percent seedling mortality, percent seed rot and percent disease incidence were taken at 30 days after sowing.

For screening under paper towel method, the pathogen was mass-multiplied using potato dextrose broth (PDB). For this 2.4 g of potato dextrose granules was added to 100 ml of sterile water in a conical flask, plugged with cotton, covered with aluminum foil and autoclaved at 121 °C for 15–20 minutes. After cooling, 2–3 bits of the pathogen culture were aseptically transferred into the broth under a laminar airflow chamber using a cork borer and needle. The inoculum was developed from a 14-day-old culture grown in 250 ml conical flasks containing potato dextrose broth (pH 5.6), maintained at 30°C under a 12-hour light/dark cycle in a BOD incubator. To prepare the fungal suspension, the developed mycelial mat was blended and tween 20 was added. 0.1 gm of suspension was taken and treated to 10gm of seed, then kept aside for 1hr. After 1 hour the seeds of all genotypes were kept for germination each with three replications for both treated(pathogen) and untreated (Healthy seed). The paper towel roles were kept in germinator to maintain optimum conditions. On the 8th day of germination observations on percent seed germination, percent seed rot, percent seed infection, seedling vigour Index I & II were recorded. The genotypes were categorized based on *Macrophomina* root rot disease rating scale (0 – 9) given by Nene *et al.* (1981) and Pandey et al. (2020) as mentioned below.

Table 1: *Macrophomina* root rot disease rating scale (0 – 9) given by Nene *et al.* (1981) and Pandey et al. (2020).

Score	Description	Inferred Reaction type
1	No Infection	Immune
>1 to ≤3	A few small lesions covered roots (5% of the root tissue affected)	Resistant
>3 to ≤5	Clear and small lesions on the roots, new roots free from infection	Moderately resistant
>5 to ≤6	Root lesions are moderate; new roots are free from infection	Moderately susceptible
>6 to ≤8	Many lesions are found on roots, new roots unaffected	Susceptible
>8 to 9	Roots with severe infection and discoloration	Highly susceptible

$$\text{Seed Germination (\%)} = \frac{\text{Number of seeds germinated}}{\text{Total number of seeds evaluated}} \text{ X } 100$$

$$\text{Seed Rot (\%)} = \frac{\text{Number of rotted seeds}}{\text{Total number of seeds evaluated}} \text{ X } 100$$

$$\text{Seed infection (\%)} = \frac{\text{Number of seeds infected by } \textit{Macrophomina} \text{ sp.}}{\text{Total number of seeds assessed/ evaluated}} \text{ X } 100$$

$$\text{Seedling mortality(\%)} = \frac{\text{Number of seedlings dead}}{\text{Total number of planted seedlings}} \text{ X } 100$$

$$\text{Percent Disease Incidence (PDI)} = \frac{\text{Number of infected plants}}{\text{Total number of plants assessed}} \text{ X } 100$$

Seedling vigour index (SVI-I and SVI-II)

Seedling vigour index I and II were calculated as suggested by Abdul Baki and Anderson (1973) SVI-I = Germination (%) x Seedling length (cm)

SVI-II = Germination (%) x Seedling dry weight (mg)

Results and Discussion

Screening of genotypes against *M. phaseolina* under *invitro* using Paper towel method

M. phaseolina is a major fungal pathogen causing seed and seedling diseases like charcoal rot, especially in legumes and cereals. It impairs seed germination, increases seed rot and reduces early seedling vigor, leading to poor crop establishment. Due to limited resistance in many cultivars, identifying resistant genotypes is crucial. This study aimed to evaluate the resistance or susceptibility nature of 40 blackgram genotypes under both inoculated and control conditions.

The response of genotypes to dry root rot disease is recorded and presented in Tables 2 and the data indicated that all genotypes showed difference in their response to dry root rot disease compared to untreated control. Among 40 blackgram genotypes evaluated against *M. phaseolina* using paper towel method, the incidence of dry root rot was recorded by following a rating scale based on modified scales developed by Nene *et al.* (1981) and Pandey *et al.* (2020). Of the 40 blackgram genotypes screened against *M. phaseolina,* 28 genotypes have showed germination per cent above Indian Minimum Seed Certification Standards (>75%). The germination percentage recorded by the pathogen treated seed of different genotypes ranged from 53.00 per cent to 89.00 per cent, with highest germination 89.00 per cent recorded in MBG-1220 which is on par with the genotype MBG-1237 with 87.00 per cent while, the lowest of 53.00 per cent was observed in genotype MBG-1134. However, the pathogen treated seed of the genotypes MBG-1247 (71%), MBG- 1259 (73%), MBG-1274 (67%), MBG-1133 (67%), MBG-1158 (60%), MBG-1134 (53%), MBG-1167 (69%), MBG-1169 (74%), MBG-1194 (73%), MBG-1080 (72%), LBG-904 (74%) and MBG-1206 (73%) have recorded minimum percent germination below the standards of IMSCS. It was observed that there was a reduction in germination per cent in treated seed of different genotypes over the untreated control. Among the genotypes, MBG-1220 showed 8.24 per cent minimum per cent reduction in germination while maximum per cent reduction in germination was observed in the genotype, MBG-1158. The Seedling Vigour Index-I among the pathogen treated seed genotypes ranged from 1179 (MBG-1158) to 2400 (MBG-1216). The control seed recorded an overall highest SVI-I mean (2157) compared to treated seed (1730). This indicated that *Macrophomina* infection significantly affected seedling vigour, leading to a marked reduction across most of the genotypes under study. The highest SVI-I (2352) was observed in the genotype, MBG-1237 followed by MBG-1184, TBG-104 and MBG-1110 with 2192, 2166 and 2136 respectively. However, none of the treatments showed on par performance with MBG 1237. The lowest SVI-I 914 was observed in the genotype, MBG-1158 followed by MBG-1134 (967) which is on par with MBG 1158 under treated conditions. However, genotypes MBG-1237 (2.97%), TBG-104 (2.73%), MBG-1220 (7.10%), IPU-2-43 (9.95%) and MBG-1265 (12.37%) have reported lower per cent reduction in SVI I over control, highlighting their stable seedling performance even under pathogen stress. In contrast, maximum percent reduction in SVI-I was observed in the genotype, MBG-1158 (36.70%) followed by MBG-1134 (39.41%), MBG-1123 (30.47%), MBG-1242 (25.55%) and MBG-1274 (30.37%). Seedling Vigour Index-II (SVI-II) among the genotypes ranged from 1196 (MBG-1134) to 2172 (MBG-1237), with the control seeds showed a higher mean value of 2015 compared to 1624 in treated seeds. This decline under *Macrophomina* infected conditions indicated significant impact on seedling vigour across the tested genotypes. The highest SVI-II of 2067 in pathogen treated condition was observed in the genotype, MBG-1237 followed by IBT-BG-15 (2014), MBG-1220 (2004), MBG-1110 (2004) and MBG-1184 (1902) and the minimum SVI-II of 931 was recorded in the genotype, MBG-1134. The results of the study stated that higher seedling vigour under pathogen-stress conditions can be attributed to disease tolerance. Therefore, the genotypes such as MBG-1237, MBG-1110 and MBG-1220 were found to be resistant to *Macrophomina* infection with minimum percent reduction in seedling vigour and potential for use in resistance breeding. The seed rot percentage among the genotypes ranged from 3.67 per cent (MBG-1220) to 18 per cent (MBG-1134), with an overall mean of 11.36 per cent under treated conditions and 3.54 per cent under control conditions. The results indicated that control seeds exhibited significantly lower seed rot compared to seeds inoculated with *M. phaseolina*. Of the treated seed of various genotypes, the lowest 5.33 percent seed rot was recorded by the seeds of the genotypes MBG-1220 and MBG-1110, followed by MBG-1238 (6.67 %) indicating their superior tolerance to seed rot, but none of the genotypes were on par with best genotypes (MBG-1220 and MBG-1110). How ever, under untreated control conditions the genotypes

MBG-1237 showed lowest seed rot of 1.33 per cent, followed by MBG-1220 (2%), MBG-1244 (2%) and MBG-1080 (2%). Highest seed rot was observed in MBG-1134 (29.33%) indicating high susceptibility to infection by *Macrophomina*. The results stated increased seedling mortality under *Macrophomina* infection compared to untreated control, confirming the susceptibility of many genotypes to the pathogen. Under treated conditions, among the genotypes, minimum 5.33 per cent seedling mortality was recorded in MBG-1237 followed by 6.00 percent in MBG-1220. It was noticed in the study that the genotypes MBG-1265, MBG-1184 and MBG-1110 have recorded similar per cent seedling mortality of 6.67 percent and were on par with the genotype MBG-1237, indicating their inherent ability to suppress seedling mortality under disease pressure. However maximum percent seedling mortality under treated conditions was observed in MBG-1158 with 19.33% followed by MBG-1167 (18.67%), MBG-1247 (18.67%), MBG-1134 (17.33%) and MBG-1133 (16.67%) indicating a high degree of susceptibility to *Macrophomina* infection. Screening for resistant and moderately resistant genotypes is crucial for effective disease management. Identifying such genotypes enables the development of resistant cultivars, reducing dependence on chemical control and enhancing sustainable crop production. This approach helps maintain seed quality, ensures better yield stability and supports long-term disease resistance breeding programs. The present findings are in agreement with Iqbal *et al.* (2003), who evaluated 71 urd bean genotypes using the paper towel method and identified six highly resistant, seven resistant, and ten moderately resistant genotypes against *Macrophomina phaseolina*. Similarly, Choudhary *et al.* (2011) reported three mungbean lines resistant to dry root rot among 25 germplasm accessions. These resistant lines also showed superior performance in agronomic traits such as root and shoot growth, biomass, nodulation, and pod number. Pandey *et al.* (2020) identified the line IPM99-125 as resistant among 43 mungbean genotypes evaluated under both paper towel and sick pot assays.

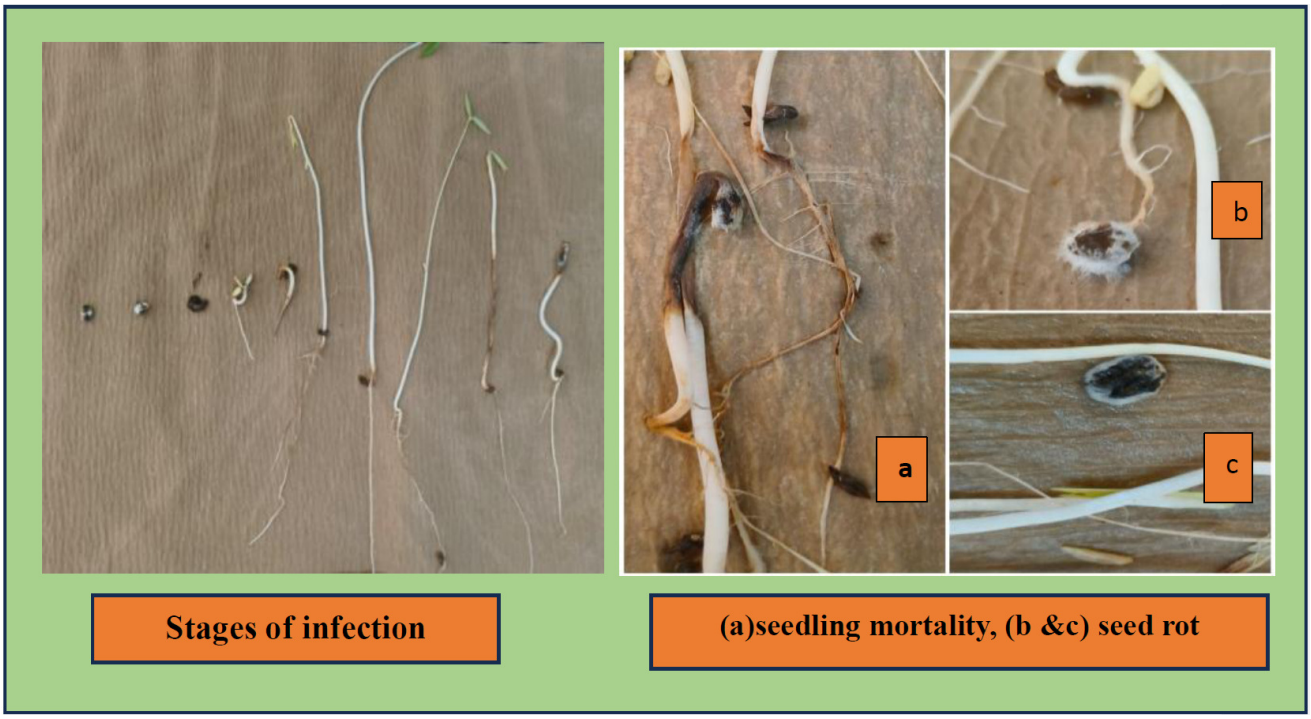

Plate 1 : Image showing symptoms of *Macrophomina* infection

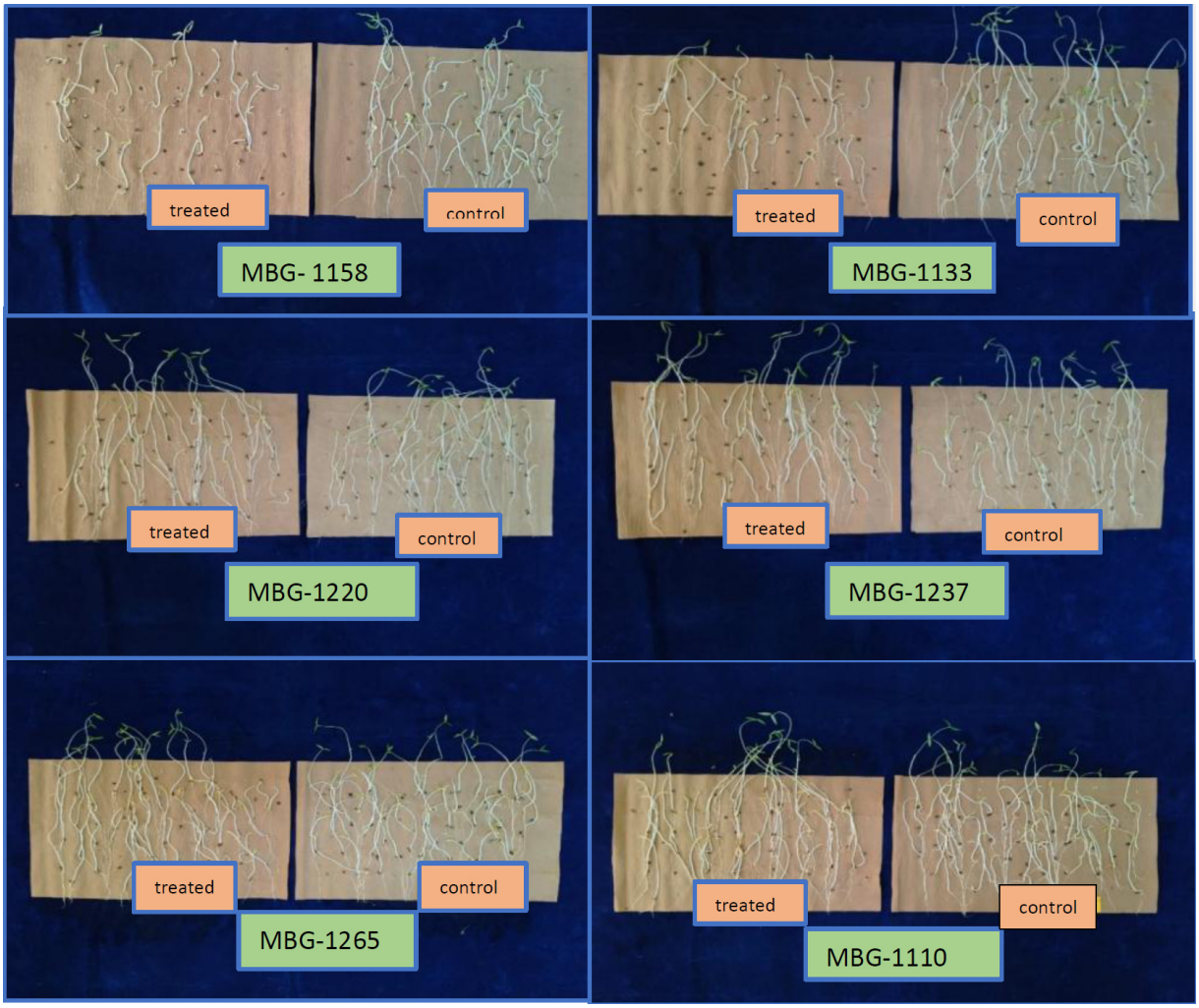

Plate 2 : Effect of *Macrophomina* on seed germination in different genotypes of blackgram.

Table 2: Effect of *M. phaseolina* on seed quality under *in vitro* (paper towel method)

S.No	Genotype	Germination (%)			SVI I			SVI II		
		Treated	Control	Mean	Treated	Control	Mean	Treated	Control	Mean
1	MBG-1220	89	97	93	2015	2169	2092	2004	2198	2101
2	MBG-1237	87	98	93	2352	2424	2388	2067	2278	2172
3	MBG-1238	83	91	87	1952	2085	2018	1599	1918	1759
4	MBG-1240	82	93	87	1675	1964	1820	1695	1949	1822
5	MBG-1241	81	94	88	1891	2078	1985	1545	1880	1712
6	MBG-1242	75	95	85	1235	1659	1447	1381	1881	1631
7	MBG-1244	77	96	86	1717	2267	1992	1481	1985	1733
8	MBG-1245	83	95	89	1907	2157	2032	1764	2065	1915
9	MBG-1247	71	93	82	1570	2118	1844	1389	1915	1652
10	MBG-1251	76	94	85	1521	2027	1774	1622	1974	1798
11	MBG-1254	80	95	87	2143	2165	2154	1707	2019	1863
12	MBG-1259	73	90	82	1358	1730	1544	1369	1890	1630
13	MBG-1262	82	95	88	1807	2154	1981	1695	2051	1873
14	MBG-1265	83	95	89	1650	1883	1766	1650	1969	1810
15	MBG-1272	80	95	88	1700	2096	1898	1653	2098	1876
16	MBG-1274	67	93	80	1316	1890	1603	1325	2053	1689
17	MBG-1290	79	95	87	1990	2425	2208	1782	2209	1996
18	MBG-1123	74	94	84	1104	1588	1346	1233	1724	1479
19	MBG-1133	67	90	78	1627	2380	2004	1557	1704	1630

20	MBG-1158	60	91	76	914	1444	1179	1018	1705	1361
21	MBG-1134	53	83	68	967	1596	1282	931	1461	1196
22	MBG-1164	75	87	81	1658	2067	1862	1733	2023	1878
23	MBG-1167	69	92	80	1394	2183	1788	1445	2055	1750
24	MBG-1169	74	92	83	1896	2374	2135	1726	2147	1936
25	MBG-1184	83	94	88	2192	2389	2290	1902	2166	2034
26	MBG-1194	73	93	83	1431	2294	1862	1496	2131	1814
27	MBG-1216	79	95	87	2120	2680	2400	1706	2287	1997
28	IBT-BG-15	77	95	86	2020	2662	2341	2014	2146	2080
29	MBG- 1080	72	85	79	1948	2402	2175	1464	1905	1684
30	MBG- 1110	85	95	90	2136	2411	2274	2004	2083	2043
31	LBG- 752	75	92	83	1500	2435	1967	1496	2085	1791
32	LBG-787	81	93	87	1699	2018	1859	1625	2115	1870
33	LBG-904	74	92	83	1587	2159	1873	1575	2115	1845
34	MBG-1206	73	93	83	1792	2364	2078	1735	2131	1933
35	IPU-2-43	75	95	85	2025	2249	2137	1889	2051	1970
36	PU- 31	84	93	89	1931	2335	2133	1850	1991	1921
37	MBG-1070	78	96	87	2069	2648	2359	1766	2175	1970
38	MBG- 207	75	92	84	1492	1943	1718	1558	1994	1776
39	TBG-104	81	92	86	2166	2227	2196	1774	2085	1929
40	GBG- 45	81	95	88	1720	2141	1931	1721	1988	1855
Means		77	93		1730	2157		1624	2015	
FACTORS		**A**	**B**	**AXB**	**A**	**B**	**AXB**	**A**	**B**	**AXB**
CD@5%		2.86	0.64	4.06	73.61	16.46	104.1	102.6	22.94	145.1
SE(m)		1.02	0.22	1.44	26.33	5.88	37.24	36.7	8.20	51.9
CV		2.96			3.32			4.94		

Table 3: Effect of *M. phaseolina* on seed rot (%) seed infection % under *in vitro* (paper towel method)

S. No	Genotype	Seed Rot (%)			Seed Infection (%)			DS	DR
		Treated	Control	Mean	Treated	Control	Mean		
1	MBG-1220	5.33	2.00	3.67	6.00	1.33	3.66	>1 to ≤3	R
2	MBG-1237	7.33	1.33	4.33	5.33	0.66	2.99	>1 to ≤3	R
3	MBG-1238	6.67	3.66	5.17	10.67	2.33	6.50	>3 to ≤5	MR
4	MBG-1240	7.33	2.33	4.83	10.67	3.33	7.00	>3 to ≤5	MR
5	MBG-1241	8.00	3.33	5.67	10.67	1.33	6.00	>3 to ≤5	MR
6	MBG-1242	8.67	3.33	6.00	16.00	2.00	9.00	>5 to ≤6	MS
7	MBG-1244	6.67	2.00	4.34	16.67	2.00	9.33	>5 to ≤6	MS
8	MBG-1245	8.67	2.66	5.66	12.00	2.00	7.00	>3 to ≤5	MR
9	MBG-1247	10.67	3.33	7.00	18.67	4.00	11.33	>6 to ≤8	S
10	MBG-1251	14.67	4.00	9.34	9.33	2.00	5.66	>5 to ≤6	MS
11	MBG-1254	10.00	3.33	6.67	10.00	2.00	6.00	>3 to ≤5	MR
12	MBG-1259	12.67	3.66	8.17	14.00	3.33	8.66	>6 to ≤8	S
13	MBG-1262	8.67	2.66	5.67	9.33	2.66	5.99	>3 to ≤5	MR
14	MBG-1265	10.00	2.66	6.33	6.67	2.00	4.33	>1 to ≤3	R
15	MBG-1272	10.67	3.33	7.00	9.33	1.33	5.33	>3 to ≤5	MR
16	MBG-1274	18.67	4.00	11.34	14.00	2.66	8.33	>8 to 9	HS
17	MBG-1290	10.00	2.66	6.33	11.33	2.66	6.99	>5 to ≤6	MS
18	MBG-1123	12.00	3.33	7.67	14.00	2.66	8.33	>6 to ≤8	S
19	MBG-1133	16.67	3.66	10.17	16.67	4.00	10.33	>8 to 9	HS
20	MBG-1158	20.67	3.66	12.17	19.33	3.33	11.33	>8 to 9	HS
21	MBG-1134	29.33	6.66	18.00	17.33	5.66	11.49	>8 to 9	HS
22	MBG-1164	8.00	6.66	7.33	16.67	4.66	10.66	>5 to ≤6	MS
23	MBG-1167	12.67	4.00	8.34	18.67	4.00	11.33	>8 to 9	HS
24	MBG-1169	15.33	4.66	10.00	10.67	3.33	7.00	>6 to ≤8	S
25	MBG-1184	10.67	2.66	6.67	6.67	3.33	5.00	>3 to ≤5	MR
26	MBG-1194	12.00	4.00	8.00	15.33	3.33	9.33	>6 to ≤8	S
27	MBG-1216	8.00	3.33	5.67	13.33	1.33	7.33	>5 to ≤6	MS

28	IBT-BG-15	14.00	3.33	8.67	9.33	2.00	5.66	>5 to ≤6	MS
29	MBG- 1080	15.33	6.66	11.00	12.67	5.66	9.16	>6 to ≤8	S
30	MBG- 1110	5.33	3.33	4.33	6.67	2.00	4.33	>1 to ≤3	R
31	LBG- 752	14.00	4.00	9.00	11.33	4.66	7.99	>6 to ≤8	S
32	LBG-787	10.67	4.00	7.34	8.00	2.66	5.33	>3 to ≤5	MR
33	LBG-904	12.67	4.66	8.67	13.33	3.33	8.33	>6 to ≤8	S
34	MBG-1206	10.67	4.00	7.34	16.00	3.33	9.66	>6 to ≤8	S
35	IPU-2-43	12.00	3.33	7.67	13.33	2.00	7.66	>6 to ≤8	S
36	PU- 31	7.33	4.00	5.67	8.67	2.66	5.66	>3 to ≤5	MR
37	MBG-1070	12.67	2.00	7.34	9.33	2.00	5.66	>5 to ≤6	MS
38	MBG- 207	10.67	3.33	7.00	14.00	3.33	8.66	>5 to ≤6	MS
39	TBG-104	8.67	3.66	6.17	10.00	3.33	6.66	>3 to ≤5	MR
40	GBG- 45	10.67	2.66	6.67	8.67	2.66	5.66	>3 to ≤5	MR
Means		11.36	3.54		12.01	2.82			
FACTORS		**A**	**B**	**AXB**	**A**	**B**	**AXB**		
CD@5%		0.60	0.13	0.85	2.08	0.46	2.94		
SE(m)		0.21	0.04	0.30	0.74	0.16	1.05		
CV		6.95			6.98				

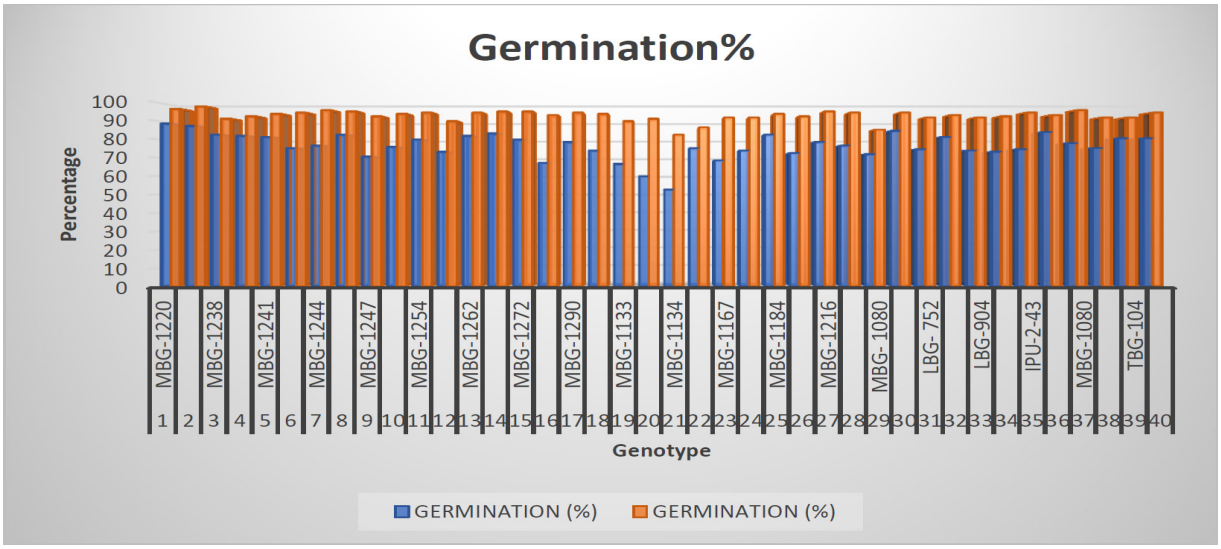

Fig 1: Graph representing Germination (%) of Treated and untreated seeds under Paper towel method.

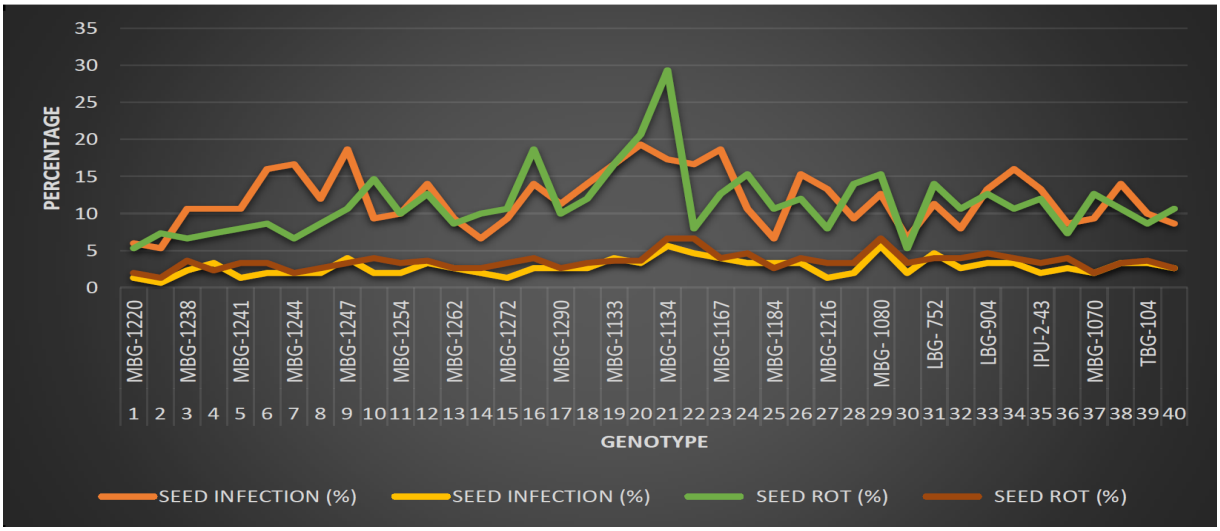

Fig 2: Graph representing seed rot (%) and seed infection (%) of Treated and untreated seeds using Paper towel method.

Screening of genotypes against *M. phaseolina* under pot culture

The response of genotypes to dry root rot disease under pot culture is recorded and presented in table (4 and 5). The data indicated that all the genotypes showed difference in their response to dry root rot disease. The percent germination recorded by the genotypes under treated and control conditions. It stated that the per cent germination decreased across the genotypes in the seed infected with *Macrophomina* over control under pot culture. Where in the per cent germination ranged from 27% (MBG-1158) to 79% (MBG-1237) in treated seeds, while untreated seeds recorded a maximum per cent germination ranging from 69% (MBG-207) to 95% (LBG-787) with an overall mean germination of 55% and 86% for treated control seeds respectively. Among the pathogen treated seeds, the genotypes MBG-1237, MBG-1220, MBG-1110 and MBG- 1265 have recorded per cent germination above IMSCS. Of the genotypes evaluated, MBG-1237 showed maximum per cent seed germination of 79.00 per cent followed by MBG-1110 (77%), MBG-1220 and MBG 1265 (75%); and minimum per cent seed germination by the genotype MBG-1158 and MBG- 1134 with 27.00 and 29.00 per cent respectively. Whereas in untreated control out of 40 genotypes except for the three genotypes, MBG-207 (69%), MBG-1158 (71%) and MBG-1134 (71%) have recorded germination per cent above IMSCS with> 75%. However, the maximum germination per cent was recorded by the genotype LBG-787 with 95.00 per cent. Sodji *et al.* (2025) also reported that a high plant stand ranging from 63.33–76.67% in cowpea genotypes (IT84S-2049, IT10K-837-1, IT11K-61-82, SARI-3-11-100) indicated resistance to charcoal rot.

Seedling mortality among the genotypes under pot culture conditions varied widely, where the treated seedlings showed mortality ranging from 11.11 per cent to 35.55 per cent, while the control seedlings exhibited mortality from nil to 14.44 per cent. However, it was noticed that *Macrophomina* inoculated seed showed maximum seedling mortality across the genotypes over control. The mean seedling mortality was 17.77 and 5.33 per cent in treated and control seedlings respectively. Among the genotypes, MBG-1158 (35.55%) recorded maximum seedling mortality followed by, MBG-1274 and MBG-1167 with per cent 28.88 in treated conditions indicating high susceptibility of these genotypes to *Macrophomina* infection during early seedling stages. While, the genotypes such as MBG-1184 and MBG-1110 which have exhibited the same and lowest seedling mortality (11.11%) were found on par with the genotypes, MBG-1237, MBG 1241, MBG 1254, PU-31, TBG 104 and GBG 45 which showed similar per cent seedling mortality of 13.33 per cent. The genotypes MBG-1237, MBG-1241 and PU-31 showed on par seedling mortality with MBG-1184 and MBG-1110 under treated conditions. The per cent seed rot among the genotypes under pot culture conditions ranged from nil to 24.44 per cent in treated seeds, nil to 6.66 per cent in control seeds. The overall mean seed rot was 6.32 per cent and 2.8 per cent in treated and control seeds respectively (Table 4.6). Among the treated seed, the genotype MBG-1237 exhibited the nil seed rot (0.00%) followed by lowest seed rot of 2.22% by the genotypes MBG-1220, MBG-1238, MBG-1241, MBG 1242, MBG 1254, MBG 1259, MBG-1265, MBG 1274, MBG 1169 and PU-31 and were on par with MBG-1237 while the genotype MBG-1134 has recorded the highest seed rot of 24.44%, followed by MBG-1194 with 22.22 per cent seed rot. However, no seed rot was observed in several genotypes such as MBG-1237, MBG-1241, MBG-1254, MBG-1259, PU-31 and GBG-45 in control conditions. The mean seed rot percentage in treated seeds was significantly higher than in control, demonstrating the effect of *Macrophomina* infection on seed health. The per cent disease incidence under treated conditions, among the genotypes ranged from 6.66 per cent (MBG-1110) to 20.55 per cent (MBG-1158), with a mean PDI of 20.22 per cent while the control conditions seed showed significantly lower disease incidence with a mean of 2.83 per cent, indicating the impact of *M. phaseolina* on disease expression across the genotypes. Among the genotypes, the lowest per cent disease incidence under treated conditions was recorded in MBG-1110 (6.66%) followed by MBG-1220, MBG-1265 with 13.33% PDI, whereas the highest disease incidence was observed in the genotypes MBG-1158 and LBG-904 with PDI 31.11 per cent followed by MBG-207 (28.88%), MBG-1133, MBG-1167 (26.66%), stating high susceptibility to the pathogen. How ever the PDI recorded by the genotypes MBG-1237, MBG-1240, MBG- 1241, PU-31 was on par with the genotypes MBG-1220 and MBG-1265 under treated conditions. The results align with findings from Haseeb *et al.* (2013), Farooq *et al.* (2019), Mishra *et al.* (2021) and Avanija *et al.* (2023).

Table 4: Data recorded by screening of blackgram genotypes against *M. phaseolina* under pot culture.

S. No	Genotype	Germination (%)			Seedling Mortality (%)		
		Treated	Control	Mean	Treated	Control	Mean
1	MBG-1220	75.00	89.00	79.00	15.55	6.66	11.10
2	MBG-1237	79.00	93.00	82.00	13.33	2.22	7.77
3	MBG-1238	64.00	91.00	78.00	15.55	2.22	8.88
4	MBG-1240	60.00	87.00	73.00	20.00	6.66	13.33
5	MBG-1241	64.00	89.00	77.00	13.33	6.66	9.99
6	MBG-1242	58.00	84.00	71.00	17.77	5.55	11.66
7	MBG-1244	62.00	87.00	74.00	15.55	2.22	8.88
8	MBG-1245	56.00	84.00	70.00	17.77	7.77	12.77
9	MBG-1247	58.00	89.00	73.00	15.55	4.44	9.99
10	MBG-1251	56.00	89.00	72.00	17.77	2.22	9.99
11	MBG-1254	64.00	91.00	78.00	13.33	6.66	9.99
12	MBG-1259	62.00	89.00	76.00	20.00	0.00	10.00
13	MBG-1262	47.00	84.00	66.00	22.22	0.00	11.11
14	MBG-1265	75.00	91.00	80.00	15.55	4.44	9.99
15	MBG-1272	51.00	82.00	67.00	17.77	8.88	13.32
16	MBG-1274	44.00	89.00	67.00	28.88	2.22	15.55
17	MBG-1290	60.00	84.00	72.00	15.55	7.77	11.66
18	MBG-1123	47.00	84.00	66.00	17.77	12.22	14.99
19	MBG-1133	44.00	93.00	69.00	24.44	0.00	12.22
20	MBG-1158	27.00	71.00	49.00	35.55	7.77	21.66
21	MBG-1134	29.00	71.00	50.00	22.22	7.77	14.99
22	MBG-1164	56.00	84.00	70.00	20.00	11.11	15.55
23	MBG-1167	36.00	91.00	63.00	28.88	4.44	16.66
24	MBG-1169	60.00	93.00	77.00	15.55	2.22	8.88
25	MBG-1184	67.00	87.00	77.00	11.11	4.44	7.77
26	MBG-1194	38.00	78.00	58.00	15.55	6.66	11.10
27	MBG-1216	51.00	89.00	70.00	15.55	8.88	12.21
28	IBT-BG-15	58.00	91.00	74.00	17.77	0.00	8.88
29	MBG- 1080	49.00	82.00	66.00	17.77	7.77	12.77
30	MBG- 1110	77.00	91.00	81.00	11.11	4.44	7.77
31	LBG- 752	42.00	89.00	66.00	22.22	4.44	13.33
32	LBG-787	56.00	95.00	76.00	17.77	2.22	9.99
33	LBG-904	42.00	78.00	60.00	15.55	7.77	11.66
34	MBG-1206	58.00	78.00	68.00	17.77	14.44	16.10
35	IPU-2-43	58.00	91.00	74.00	17.77	0.00	8.88
36	PU- 31	64.00	87.00	76.00	13.33	2.22	7.77
37	MBG-1070	60.00	87.00	73.00	15.55	8.88	12.21
38	MBG- 207	49.00	69.00	59.00	15.55	11.11	13.33
39	TBG-104	67.00	91.00	79.00	13.33	2.22	7.77
40	GBG- 45	67.00	93.00	80.00	13.33	6.66	9.99
Means		55.43	86.43		17.77	5.35	
FACTORS		**A**	**B**	**AXB**	**A**	**B**	**AXB**
CD@5%		8.02	1.79	11.34	2.45	0.55	3.47
SE(m)		2.87	0.64	4.06	0.87	0.19	1.24
CV		6.8			10.44		

Table 5: Data recorded by screening of blackgram genotypes against *M. phaseolina* under pot culture.

S. No	Genotype	SEED ROT (%)			PDI			DR
		Treated	Control	Mean	Treated	Control	Mean	
1	MBG-1220	2.22	2.22	2.22	13.33	0.00	6.65	MR
2	MBG-1237	0.00	0.00	0.00	15.55	0.00	7.75	MR
3	MBG-1238	2.22	2.22	2.22	17.77	2.22	9.95	MR
4	MBG-1240	4.44	2.22	3.33	15.55	0.00	7.77	MR
5	MBG-1241	2.22	0.00	1.11	15.55	2.22	8.85	MR

6	MBG-1242	2.22	2.22	2.22	22.22	7.77	14.95	MS
7	MBG-1244	4.44	2.22	3.33	17.77	2.22	9.99	MR
8	MBG-1245	4.44	2.22	3.33	22.22	0.00	11.11	MS
9	MBG-1247	6.66	2.22	4.44	17.77	4.44	11.10	MR
10	MBG-1251	8.88	4.44	6.66	17.77	2.22	9.95	MR
11	MBG-1254	2.22	0.00	1.11	20.00	2.22	11.11	MR
12	MBG-1259	2.22	0.00	1.11	15.55	3.33	9.44	MR
13	MBG-1262	8.88	4.44	6.66	22.22	7.77	14.95	MS
14	MBG-1265	2.22	2.22	2.22	13.33	0.00	6.65	MR
15	MBG-1272	6.66	3.33	4.99	24.44	3.33	13.85	MS
16	MBG-1274	2.22	2.22	2.22	24.44	6.66	15.55	MS
17	MBG-1290	4.44	2.22	3.33	20.00	0.00	10.00	MR
18	MBG-1123	11.11	2.22	6.66	24.44	0.00	12.22	MS
19	MBG-1133	4.44	2.22	3.33	26.66	0.00	13.33	MS
20	MBG-1158	6.66	2.22	4.44	31.11	10.00	20.55	S
21	MBG-1134	24.44	6.66	15.55	24.44	6.66	15.55	MS
22	MBG-1164	4.44	2.22	3.33	20.00	2.22	11.11	MR
23	MBG-1167	8.88	2.22	5.55	26.66	2.22	14.44	MS
24	MBG-1169	2.22	2.22	2.22	22.22	2.22	12.22	MS
25	MBG-1184	6.66	2.22	4.44	15.55	0.00	7.75	MR
26	MBG-1194	22.22	7.77	14.95	24.44	6.66	15.55	MS
27	MBG-1216	8.88	2.22	5.55	24.44	0.00	12.22	MS
28	IBT-BG-15	4.44	2.22	3.33	20.00	6.66	13.33	MR
29	MBG-1080	11.11	6.66	8.88	22.22	3.33	12.75	MR
30	MBG-1110	13.33	4.44	8.88	6.66	0.00	3.33	R
31	LBG- 752	11.11	6.66	8.88	24.44	0.00	12.22	MS
32	LBG-787	4.44	2.22	3.33	22.22	0.00	11.11	MS
33	LBG-904	11.11	6.66	8.88	31.11	0.00	15.55	S
34	MBG-1206	6.66	3.33	4.95	17.77	4.44	11.10	MR
35	IPU-2-43	8.88	4.44	6.66	15.55	4.44	9.99	MR
36	PU- 31	2.22	0.00	1.11	15.55	5.55	10.55	MR
37	MBG-1070	6.66	4.44	5.55	17.77	0.00	8.88	MR
38	MBG- 207	6.66	6.66	6.66	28.88	10.00	19.44	MS
39	TBG-104	4.44	2.22	3.33	15.55	2.22	8.88	MR
40	GBG- 45	15.55	0.00	7.75	15.55	0.00	7.77	MR
Means		6.32	2.8		20.22	2.83		
FACTORS		**A**	**B**	**AXB**	**A**	**B**	**AXB**	
CD@5%		2.30	0.42	2.69	3.73	0.83	5.27	
SE(m)		0.68	0.15	0.96	1.33	0.29	1.88	
CV		10.42			11.22			

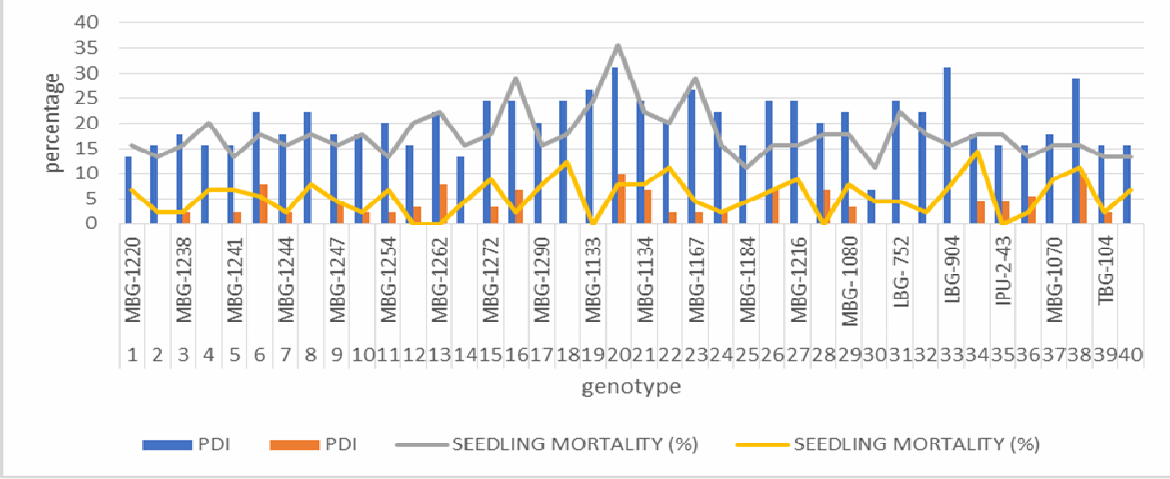

Fig 3: Graph representing Seedling mortality (SM%), Percent disease incidence (PDI) of genotypes screened under pot culture.

In the present study based on modified rating scale (1-9) given by Nene *et al* (1981) and Pandey *et al* (2020), the blackgram genotypes with reference through disease reaction and germination percent recorded through paper towel method were grouped into different categories (Table 4) such as Immune (I), Resistant (R), Moderately Resistant (MR), Moderately Susceptible (MS), Susceptible (S) and Highly Susceptible (HS). Among 40 genotypes evaluated, none of the genotypes recorded a disease score of 1.0 and hence none were classified as immune. However, four genotypes MBG-1220, MBG-1237, MBG-1265 and MBG-1110 recorded the minimum disease incidence with only 5% of the root tissue affected and scored between >1 to ≤3 and thus classified as resistant (R). Twelve genotypes, MBG-1238, MBG-1240, MBG-1241, MBG-1245, MBG-1254, MBG-1262, MBG-1272, MBG-1184, LBG-787, PU-31, TBG-104 and GBG-45 with clear small lesions on roots and new roots remained unaffected, were classified as moderately resistant (MR) with disease scores ranging between >3 to ≤ 5. Nine genotypes which are found to be moderately susceptible (MS) with disease scores between > 5 to ≤ 6 were MBG-1242, MBG-1244, MBG-1251, MBG-1290, MBG-1164, MBG-1216, IBT-BG-15, MBG-1070 and MBG-207. These genotypes exhibited moderate root lesions, although new roots remained largely unaffected. Ten genotypes MBG-1247, MBG-1259, MBG-1123, MBG-1169, MBG-1194, MBG-1080, LBG-752, LBG-904, MBG-1206 and IPU-2-43 with scores ranging from >6 to ≤8 were included under susceptible (S) group. These genotypes exhibited greater number of lesions on roots with clear signs of infection. Finally, five genotypes MBG-1274, MBG-1133, MBG-1158, MBG-1134 and MBG-1167 recorded disease scores between >8 and up to 9 with severe root infection symptoms and pronounced root discoloration were categorized as highly susceptible and were considered unsuitable for cultivation in disease prone environments. However, such entries are also valuable in targeted pathological studies or as susceptible checks in breeding programs.

Based on PDI range, the test genotypes were ranked as Highly Resistant (No disease), Resistant (Disease incidence ≤ 10%), Moderately Resistant (Disease incidence 10.1 to 20%), Moderately Susceptible (Disease incidence 20.1 to 30%), Susceptible (Disease incidence 30.1 to 50%) and Highly Susceptible (Disease incidence >50%) Elmerich *et al.* (2022).

In pot culture studies, based on the PDI values recorded by various genotypes, the test genotypes were categorized as Highly resistant, Resistant, Moderately resistant, Moderately susceptible, Susceptible and Highly susceptible. Of the 40 genotypes, 22 genotypes MBG-1220, MBG-1237, MBG-1238, MBG-1240, MBG-1241, MBG-1244, MBG-1247,MBG-1251, MBG-1254, MBG-1259, MBG-1265, MBG-1290, MBG-1164, MBG-1184, IBT-BG-15, MBG-1080, MBG-1206, IPU-2-43, PU-31, MBG-1070, TBG-104 and GBG-45 were found to be Moderately resistant, 15 genotypes, MBG-1242, MBG-1245, MBG-1262, MBG-1272, MBG-1274, MBG-1123, MBG-1133, MBG-1134, MBG-1167, MBG-1169, MBG-1194, MBG-1184, LBG-752, LBG-787 and MBG-207 were Moderately susceptible, two genotypes LBG-904 and MBG-1158 were susceptible and the genotype MBG-1110 was found resistant to the disease incidence.

Plate 3: Image represents screening of genotypes under Pot culture

Table 4: Classification of Blackgram Genotypes Based on Disease Reaction to *M. phaseolina*

Disease Reaction	Disease Score	Genotype(s)
Resistant (R)	>1 to ≤3	MBG-1220, MBG-1237, MBG-1265, MBG-1110
Moderately Resistant (MR)	>3 to ≤5	MBG-1238, MBG-1240, MBG-1241, MBG-1245, MBG-1254, MBG-1262, MBG-1272, MBG-1184, LBG-787, GBG-45, PU-31, TBG-104
Moderately Susceptible (MS)	>5 to ≤6	MBG-1242, MBG-1244, MBG-1251, MBG-1290, MBG-1164, MBG-1216, IBT-BG-15, MBG-1070, MBG-207
Susceptible (S)	>6 to ≤8	MBG-1247, MBG-1259, MBG-1123, MBG-1169, MBG-1194, MBG-1080, LBG-752, LBG-904, MBG-1206, IPU-2-43
Highly Susceptible (HS)	>8 to 9	MBG-1274, MBG-1133, MBG-1158, MBG-1134, MBG-1167

Conclusion

This study successfully screened 40 blackgram genotypes for resistance to *M. phaseolina* using paper towel and pot culture methods. Significant variation was observed among genotypes in terms of germination, seed rot, infection and seedling vigor under pathogen stress. No genotype was completely immune but some of them showed strong resistance.

MBG-1237, MBG-1220, MBG-1265 and MBG-1110 consistently performed well in both methods. These genotypes exhibited high germination, low disease incidence and minimal vigor loss. They are ideal candidates for cultivation in disease-prone areas.

Moderately resistant genotypes also showed good potential under moderate disease pressure whereas susceptible genotypes like MBG-1134 and MBG-1158 showed poor performance but are useful for disease studies. Overall, the study confirms the reliability of both screening methods. The identified resistant genotypes offer valuable resources for breeding durable disease-resistant blackgram varieties.

Disclaimer (Artificial Intelligence)

Author(s) hereby declares that no generative AI technologies such as Large Language Models (Chat GPT, COPILOT, etc) and text-to-image generators have been used by them during writing or editing manuscripts.

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Competing Interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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