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Screening of genotypes against dry root rot of mungbean (*Vigna radiata* L.) R. Wilczek

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Abstract

Mungbean dry root rot incited by *Macrophomina phaseolina* (Tassi) Goid is prime importance in decreased crop production. Mungbean cultivation has recently faced considerable challenges from dry root rot, which can result in production losses by lowering field plant numbers at both the seedling and adult stages. In addition to lowering crop yields, pathogen damage lessens their ability to fix nitrogen, which raises pathogen concentrations in the soil. The greatest approach to managing the mungbean DRR is the host plant resistance since it is both cost-effective and environmentally beneficial. In order to identify sources of genetic resistance to dry root rot incited by *Macrophomina phaseolina,* Forty seven genotypes of mungbean were tested through artificial soil inoculation in poly house at Regional Agricultural Research Station, Warangal, Telangana during the year 2023. Among 47 mungbean genotypes, six genotypes *viz*., MGG-529, MG-549, WGG-42, MG-505, Pusa 9072 and WGG-25 showed a resistant response to dry root rot; fifteen genotypes were found to be moderately resistant; 18 genotypes were shown to be susceptible, and 8 genotypes are highly susceptible under poly house conditions. These lines can also be used as a source of resistance in breeding programmes to create dry root rot-resistant cultivars.

Keywords: Mungbean, dry root rot, resistant, host plant resistance, soil-borne

1. Introduction

In Asia, the mungbean, is a major source of protein. According to Nair *et al.* (2012) [21], it is also a significant pulse crop commercially. Mungbean, often known as "Golden Bean," is a very adaptable crop that is used for grazing, green manure, and seeds. According to Mallaiah and Rao (2018) [19], the states of Rajasthan, Maharashtra, Madhya Pradesh, Orissa, Andhra Pradesh, Tamil Nadu, Telangana, and Uttar Pradesh are among the top producers of mungbean in the world. Mungbean was grown on 0.7 lakh hectares in Telangana in 2020–2021, producing 38.05 thousand tonnes with an average yield of 507 kg ha^{-1}. (2021 INDIASTAT). The production of mungbean is influenced by a variety of biotic and abiotic factors. The main biotic constraints on mungbean productivity are diseases caused by fungi, bacteria, and viruses (Batzer *et al*., 2022) [3]. Major causes of yield loss, which can range from 40–60% in green gram, include these fungal diseases.

The primary factor affecting crop productivity among all fungal diseases is dry root rot caused by *Macrophomina phaseolina* (Tassi) (Raguchander *et al*., 1993) [26]. It is serious illness that has a significant economic impact on several crops. According to Sinclair (1982) [32], *M. phaseolina* is thought to be the source of anthracnose in more than 500 plant species (Tetali *et al*., 2015) [34].

There are two asexual forms of fungi that help them survive better (Dingra and Sinclair, 1978) [5]. As the main source of inoculum for new regions, infected seeds are crucial (Sandhu and Singh, 1998) [29]. It is a soil-borne fungus that reproduces periodically during the harvest season and survives mostly as sclerotia, which act as a major inoculum.

Fungi affect all parts of plants *viz.*, roots, stems, leaves, pods and seeds. In Mungbean, it significantly reduces field plant populations at both the seedling and adult stages, which results in production losses (Khan *et al.*, 2016; Shahid *et al.*, 2016) [13, 30]. Additionally, according to Fuhlbohm *et al.* (2013) [6], the illness results in significant losses in the premium sprout market sector. According to Nair *et al.* (2019) [22], dry root rot results in a 10–44% yield loss in the production of mungbean in India and a 33-44% yield loss owing to Rhizoctonia root rot. In addition to decreasing crop yields, pathogen damage lessens their ability to fix nitrogen in the soil, which raises disease concentrations there (Khaledi *et al*., 2015) [10].

Pathogens cause biological stresses that infect plant growth, resulting in reduced root growth and reduced water and mineral uptake.

In advanced stages, plants wilt and finally die (Khan *et al*., 2017; Shahid *et al*., 2017) [14, 31]. Leaf yellowing was a typical indication of the illness. The affected stems and leaves seem straw-colored, brittle, and dry. When plants with Macrophomina infections are plucked from the ground and the main root and basal stem are inspected, root rot symptoms are evident. In the latter stages, sclerotioid bodies may be seen on the afflicted tissues (Gahlot *et al*., 2022; Kumar *et al*., 2019) [7, 16]. For up to 3 years, the pathogen can survive as a sclerotia in crop wastes or soil (Su *et al*., 2001) [33]. It is challenging for Mungbean producers to control the illness because of this pathogen's sclerotial characteristics (Kumari *et al*., 2012) [18].

Due to its polyphagous nature and ability to survive in the soil through its resting structures, management of *Macrophomina phaseolina*-caused dry root rot is more difficult. Due to the fact that fungicides are expensive and harmful to our ecology. As a result, using the host plant's natural resistance as a breeding tool to create resistant mungbean types is one of the best strategies to combat dry rot root of green gram. This method is economical and environmentally benign. The purpose of this study was to identify resistant sources of dry root in mungbean genotypes.

2. Materials and Methods

The study was conducted during the year 2023 in Poly house at Regional Agricultural Research Station, Warangal.

The pathogenic strain of *Macrophomina phaseolina* was isolated from diseased stems of mungbean, pure culture was done by single hyphal tip method, and cultures were maintained on Potato dextrose agar media, was multiplied on the sorghum grains. The grains were first half-boiled in water, dried Over Night and filled in 500 ml Erlenmeyer conical flasks to 1/4th of their capacity and sterilized at 15 lbs pressure at 121 ºC for 15 minutes. Thereafter, this *M. phaseolina* discs of 5 mm was inoculated in to the sterilized sorghum grains containing flasks and incubated at 28+2 ºC for 15-20 days. The flasks were shaken every day. After multiplication on sorghum grain, *M. phaseolina* inoculum were placed in each pot at 50g/kg of soil (spore load 10^{-4}) before 15 days of sowing (Choudhary *et al.*, 2011) [4].

Sowing of mungbean genotypes was done in Pots containing sick soil. 50 seeds were sown in each pot and each genotype was maintained in three replications. Observations were recorded at 15, 30, 45 and 60 days after sowing to record percent disease incidence in each genotype and each replication.

PDI was calculated as follows

% incidence = [(No. of Infected plants)/ (Total no. of plants)] × 100

The data so obtained on percent disease incidence was analysed and the percent disease reaction of the genotypes was recorded on the basis of their mean percent disease incidence as per the scale (AICRP on MULLaRP 2020). Data was analysed through Online Statistical Analysis Tools (O.P. Sheoran).

3. Results and Discussion

3.1 Screening of genotypes of Mungbean against *M. phaseolina*

The data from Table 2 is evident that all genotypes differed in their response to dry root rot disease at different growth stages. Among Forty seven Mungbean genotypes evaluated against *Macrophomina phaseolina* under poly house conditions, the incidence of dry root rot was recorded using a rating scale from AICRP on MULLaRP scale, 2020. Based on the disease reaction, Mungbean genotypes was grouped into, highly resistant (HR), Resistant (R), Moderately resistant (MR), Susceptible (S) and Highly susceptible. (HS) (Table 2). Among the 47 genotypes evaluated none of the genotypes recorded as highly resistant and six genotypes namely MGG-505, MGG-529, MGG-549, WGG-25, WGG-42 and Pusa 9072 showed disease incidence with 8.6, 9.2, 9.9, 9.8, 9.9 and 9.9% respectively. At 15 DAS 17 entries namely MGG-295, MGG-347, MGG-385, MGG-474, MGG-514, MGG-527, MGG-531, MGG-540, MGG-551, WGG-2, WGG-18, WGG-20, WGG-33 TARM 1, RMP-22-3, RMP-22-7 and Pusa BM-11 showed MR reaction with 10.1 to 20.0 range of % disease incidence. Among these 17 MR genotypes, few genotypes *viz.*, MGG-531, MGG-347, MGG-514 and WGG-2 has showed Moderately resistant reaction up to 30 days after sowing. Then after these are progressed to Susceptible to the dry root rot disease at 45 and 60 days after sowing.

Twenty of the genotypes were recorded as susceptible against dry root rot with range of % disease incidence from 23.2 to 49.8 and nine genotypes WGG-21, WGG-29, IC-436528, RMP-22-6, CO-6 WGG-3, WGG-27, WGG-34 and IC-436526 were reported as highly susceptible reaction with range of % disease incidence from 74.27 to 86.70% genotypes for the dry root rot disease of mungbean.

Among 47 genotypes six genotypes showed resistant reaction, seventeen genotypes, had shown moderately resistant reaction namely MGG-295, MGG-347, MGG-385, MGG-474, MGG-514, MGG-527, MGG-531, MGG-540, MGG-551, WGG-2, WGG-18, WGG-20, WGG-33 TARM 1, RMP-22-3, RMP-22-7, Pusa BM-11 with the range of 11.1 to 19.5% and other twenty genotypes *viz.*, MGG- 453, MGG-512, MGG-519, MGG-544, WGG-6, WGG-19, WGG-21, WGG-29, WGG-38, IC-436526, VBN (Gg) 2, VBN-4, VGG 17-106, Pusa BM 12, RMP-22-4, RMP-22-6, IPM 1603-3, COGG 16-10, TMB 127 and CO-6 showed Susceptible reaction with 23.1 to 49.0% disease incidence and remaining four genotypes WGG-3, WGG-27, WGG-34 and IC- 436528 showed Susceptible reaction initially up to 30 days after sowing of the crop but, later on disease incidence increased gradually from Susceptible to Highly susceptible at pod filling stage and maturity stage. At 60 Days after Sowing the same six genotypes namely MGG-505, MGG-529, MGG-549, WGG-25, WGG-42 and Pusa 9072 showed resistant reaction, thirteen genotypes *viz.*, MGG-295, MGG-385, MGG-474, MGG-540, MGG-527, MGG-551, TARM 1, RMP-22-3, RMP-22-7, Pusa BM-11, WGG-18, WGG-20 and WGG-33 recorded as moderately resistant reaction, whereas the 19 genotypes MGG-347, MGG- 453, MGG-512, MGG-514, MGG-519, MGG-531, MGG-544, WGG-2, WGG-6, WGG-19, WGG-38, VBN (Gg) 2, VBN-4, VGG 17-106, Pusa BM 12, RMP-22-4, IPM 1603-3, COGG 16-10 and TMB 127 showed susceptible reaction and remaining nine genotypes namely WGG-3, WGG-21, WGG-27, WGG-29, WGG-34, IC-436526, IC- 436528, RMP-22-6 and CO 6 recorded as highly susceptible reaction against dry root rot.

In majority of the crops, including black gram (*Vigna mungo*) and several other grain legumes, complete resistance to *M. phaseolina* has not yet been recorded (Sajeena *et al.* 2004, Rao 2008) [28, 27]. Dry root rot incidence varied from 8.6 to 86.7%. The genotypes "WGG-34" and "MGG-549" had the highest and lowest rates of disease incidence, respectively, throughout the research. Finally MGG-529, MGG-549, WGG-42, MGG-505, Pusa 9072 and WGG-25 are the six genotypes which were identified as resistant and these genotypes can be used for crop improvement programmes after further testing.

Screening of different crops against *M. phaseolina* has been investigated Mirza *et al*. 1982 [20] (sunflower), Pande *et al.* 2004 [23] (chickpea) Abawi and Pastor-Corrales, 1990 (cowpea). Similarly, Choudhary *et al.* (2011) [4] tested twenty-five of mungbean genotypes to determine the source of resistance to DRR in the field. They concluded that three genotypes *viz.*, MSJ-118, KM 4-44 and KM 4-59 were recorded as resistant to dry root rot in mungbean.

The results are in conformity with earlier work of Haseeb *et al.* (2013) [8] they tested twenty seven mungbean genotypes against *M. phaseolina* in the field under artificial inoculation. They concluded that out of twenty seven genotypes, single genotype was also not recorded with complete resistance, whereas genotypes *viz.*, Azari 2006, NM 2006 and AUM-9 was found to be resistant.

Akhtar and Shoaib (2018) [2] screened 26 genotypes, and reported that 2 genotypes (MNUYT-317 and NM-2011) were highly resistant, and other 10 genotypes were recorded as moderately resistant.

Pandey *et al.* (2020) [24] evaluated 43 mungbean genotypes against an *M. phaseolina* isolation of mungbean using the rolled paper towel technique. Resistant genotypes with low disease scores were further tested for resistance using the sick pot technique. IPM99-125 regularly outperformed the other genotypes in terms of plant survival.

Kumar *et al*. (2021) [17] examined 25 germplasm lines against *Macrophomina phaseolina* and determined that four green gram germplasm lines, namely IPM-02-03, G-2, MH-2-15, and MUM-2, displayed a resistant reaction to dry root rot. The genotype RMG-26 was recorded as susceptible variety.

Pandey *et al.* (2021) [25] used the paper towel technique to test 296 mungbean mini-core accessions against the isolate MP1. They found 29 accessions with DRR resistance (disease scores: 3), and 18 of them with consistent resistance in the repeated trial. During the glasshouse screening of 18 resistant accessions, nine accessions were found to have DRR resistance in repeated sick pot trials with a 10% disease incidence. Based on their *in vitro* DRR responses, a subset of 30 accessions from the mini-core collection were chosen. In 2018 and 2019, these accessions were tested for DRR resistance in the field in Yezin, Myanmar. Ten of the 30 accessions were positive for DRR resistance with a 10% disease incidence in both years of testing.

Most workers gathered germplasm against *Macrophomina phaseolina* and discovered resistant or somewhat resistant germplasm during selection. Similarly in this study also we found resistant and moderately resistant genotypes against *Macrophomina phaseolina*, which may be employed in crop development programmes after additional testing, and these findings are supported by prior studies.

After testing with a different genotypes against *M. phaseolina* strains, resistant germplasm can be employed in crop enhancement programmes. The genotype IPM99-125 has increased plant survival and might be used in green gram breeding programmes to develop DRR-resistant genotypes (Pandey *et al*., 2020) [24].

Table 1: Disease rating scale of Dry root rot – AICRP on MULLaRP scale, 2020

% infected plants	Reaction
0	Free
0.1-5	Highly resistant
5.1-10	Resistant (R)
10.1-20	Moderately resistant (MR)
20.1-50	Susceptible (S)
Above 50%	Highly susceptible (HS)

Table 2: Phenotypic reaction of Mungbean genotypes against dry root rot caused by *Macrophomina phaseolina*

S. No	Variety	PDI at 15 DAS	Host Reaction	PDI at 30DAS	Host Reaction	PDI at 45DAS	Host Reaction	PDI at 60DAS	Host Reaction
1	MGG-295	10.6 (18.9)	MR	15.0 (22.6)	MR	18.3 (25.1)	MR	19.7 (26.2)	MR
2	MGG-347	16.8 (24.2)	MR	19.4 (26.1)	MR	30.9 (33.7)	S	46.1 (42.7)	S
3	MGG-385	10.3 (18.7)	MR	11.1 (19.4)	MR	16.1 (23.5)	MR	18.9 (25.6)	MR
4	MGG 453	22.4 (28.1)	S	31.6 (34.1)	S	37.57(37.7)	S	49.5 (44.7)	S
5	MGG 474	10.3 (18.7)	MR	13.4 (21.4)	MR	17.5 (24.7)	MR	19.9 (26.4)	MR
6	MGG-505	5.9(14.0)	R	6.5 (14.7)	R	7.5 (15.8)	R	8.5 (16.9)	R
7	MGG-512	20.2 (26.7)	S	25.6 (30.3)	S	27.4 (31.4)	S	35.8 (36.0)	S
8	MGG-514	14.9 (22.7)	MR	19.1 (25.9)	MR	37.7 (37.8)	S	49.7 (44.8)	S
9	MGG-519	21.4 (27.4)	S	28.8 (32.4)	S	40.1 (39.2)	S	48.1 (43.9)	S
10	MGG-527	10.3 (18.7)	MR	13.6 (21.6)	MR	16.6 (24.0)	MR	19.7 (26.3)	MR
11	MGG-529	5.2 (13.2)	R	6.5 (14.8)	R	8.1 (16.5)	R	9.1 (17.5)	R
12	MGG-531	10.2 (18.6)	MR	13.0 (21.1)	MR	20.1 (26.5)	S	23.1 (28.7)	S
13	MGG-540	10.1 (18.5)	MR	12.2 (20.4)	MR	15.6 (23.3)	MR	19.2 (25.9)	MR
14	MGG-544	21.5 (27.6)	S	24.5 (29.6)	S	26.3 (30.8)	S	27.8 (31.8)	S
15	MGG-549	5.1 (13.1)	R	6.4 (14.6)	R	8.9 (17.3)	R	9.9 (18.3)	R
16	MGG-551	10.1 (18.6)	MR	12.6 (20.7)	MR	15.7 (23.3)	MR	20.0 (26.5)	MR
17	WGG-2	13.2 (21.2)	MR	16.3 (23.8)	MR	21.1 (27.3)	S	24.1 (29.4)	S
18	WGG-3	50.9 (45.4)	HS	55.6 (48.2)	HS	62.2 (52.0)	HS	74.2 (59.5)	HS
19	WGG-6	20.5 (26.4)	S	25.5 (30.1)	S	35.4 (36.2)	S	45.0 (42.0)	S
20	WGG-18	12.1 (20.3)	MR	13.9 (21.8)	MR	18.1 (25.1)	MR	19.8 (26.4)	MR

21	WGG-19	20.5 (26.9)	S	33.0 (35.0)	S	40.8 (39.7)	S	48.8 (44.3)	S
22	WGG-20	10.3 (18.7)	MR	13.1 (21.2)	MR	15.4 (23.1)	MR	18.4 (25.3)	MR
23	WGG-21	20.2 (26.6)	S	30.5 (33.5)	S	60.2 (51.0)	HS	80.2 (63.6)	HS
24	WGG-25	5.5 (13.5)	R	6.6 (14.9)	R	8.1 (16.5)	R	9.8 (18.2)	R
25	WGG-27	50.8 (45.4)	HS	63.0 (52.5)	HS	72.3 (58.2)	HS	85.0 (67.3)	HS
26	WGG-29	44.4 (41.7)	S	48.9 (44.3)	S	68.1 (55.6)	HS	69.0 (56.1)	HS
27	WGG-33	10.7 (19.0)	MR	11.8 (20.1)	MR	15.4 (23.1)	MR	18.5 (25.5)	MR
28	WGG-34	50.3 (45.1)	HS	60.9 (51.3)	HS	70.8 (57.4)	HS	86.7 (68.6)	HS
29	WGG-38	27.0 (31.2)	S	36.1 (36.9)	S	43.2 (41.0)	S	49.3 (44.5)	S
30	WGG-42	6.3 (14.5)	R	6.8 (15.1)	R	8.8 (17.2)	R	9.9 (18.3)	R
31	IC-436526	51.7 (45.9)	HS	57.8 (49.4)	HS	70.2 (56.8)	HS	79.1 (62.8)	HS
32	IC-436528	21.3 (27.1)	S	29.9 (32.7)	S	54.4 (47.5)	HS	63 (52.561)	HS
33	VBN (Gg) 2	22.1 (28.0)	S	27.2 (31.4)	S	33.4 (35.3)	S	49.2 (44.5)	S
34	VBN-4	20.2 (26.6)	S	23.1 (28.1)	S	36.5 (36.8)	S	47.8 (43.6)	S
35	VGG 17-106	24.3 (29.4)	S	30.6 (33.5)	S	37.1 (37.5)	S	45.8 (42.5)	S
36	Pusa BM-11	12.1 (20.3)	MR	15.2 (22.9)	MR	17.9 (25.0)	MR	19.6 (26.2)	MR
37	Pusa BM 12	22.6 (28.3)	S	28.2 (32.0)	S	38.1 (38.1)	S	46.6 (43.0)	S
38	Pusa 9072	5.1 (13.1)	R	6.8 (15.1)	R	7.5 (15.8)	R	9.9 (18.2)	R
39	RMP-22-3	11.3 (19.5)	MR	14.6 (22.4)	MR	18.1 (25.1)	MR	19.4 (26.1)	MR
40	RMP-22-4	25.4 (30.1)	S	30.1 (33.1)	S	35.3 (36.4)	S	45.9 (42.6)	S
41	RMP-22-6	37.9 (37.9)	S	42.5 (40.6)	S	64.1 (53.2)	HS	68.6 (56.0)	HS
42	RMP-22-7	13.1 (21.1)	MR	14.2 (22.1)	MR	18.0 (25.1)	MR	19.7 (26.3)	MR
43	COGG 16-10	20.9 (27.0)	S	27.6 (31.4)	S	34.8 (36.0)	S	49.1 (44.4)	S
44	IPM 1603-3	25.8 (30.4)	S	31.7 (34.2)	S	40.4 (39.4)	S	49.7 (44.8)	S
45	TMB 127	10.3 (18.7)	MR	12.8 (20.9)	MR	16.4 (23.8)	MR	19.6 (26.3)	MR
46	TARM 1	22.5 (28.3)	S	30.9 (33.7)	S	38.8 (38.5)	S	49.2 (44.5)	S
47	CO 6	20.2 (26.4)	S	27.8 (31.6)	S	51.9 (46.0)	HS	62.5 (52.3)	HS
	C.D.	5.528		6.791		7.273		9.888	
	S.E(m)	1.936		2.378		2.547		3.462	
	S.E(d)	2.738		3.363		3.601		4.897	
	C.V.	10.867		11.831		10.763		13.001	

Table 3: Promising genotypes identified against *Macrophomina phaseolina. causing* dry root rot of Mungbean

Disease reaction	**Disease incidence**	**Genotypes**
Highly resistant	0-5.0	None
Resistant	5.1-10	MGG-529, MGG-549, WGG-42, MGG-505, Pusa 9072, WGG-25
Moderately resistant	10.1-20	MGG-295, MGG-385, MGG-474, MGG-540, MGG-527, MGG-551, TARM 1, RMP-22-3, RMP-22-7, Pusa BM-11, WGG-18, WGG-20, WGG-33
Susceptible	20 .1-50	MGG-347, MGG- 453, MGG-512, MGG-514, MGG-519, MGG-531, MGG-544, WGG-2, WGG-6, WGG-19, WGG-38, VBN (Gg) 2, VBN-4, VGG 17-106, Pusa BM 12, RMP-22-4, IPM 1603-3, COGG 16-10, TMB 127
Highly susceptible	Above 50%	WGG-3, WGG-21, WGG-27, WGG-29, WGG-34, IC-436526, IC- 436528, RMP-22-6, CO 6,

4. Conclusion

Out of 47 genotypes screened, seven genotypes *viz.*, MGG-529, MGG-549, WGG-42, MGG-505, Pusa 9072, WGG-25 and Nineteen genotypes were recorded as moderately resistant against dry root rot disease of *M. phaseolina*. The resistant genotypes identified in the present study can be utilized as potential donors for future resistance breeding programme against dry root rot in Mungbean.

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6. Conflict of interest

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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