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SCREENING OF MUNGBEAN [*VIGNA RADIATA* (L.) WILCZEK] GENOTYPES UNDER FIELD CONDITION FOR RESISTANCE AGAINST MUNGBEAN YELLOW MOSAIC VIRUS (MYMV)

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Abstract

One among the vicious diseases of mungbean, Mungbean yellow mosaic virus (MYMV) disease is recognised as the major threat in India for more than five decades. From the virus family Geminiviridae of genus begomovirus, a group of geminiviruses cause yellow mosaic virus disease. They are typically transmitted by whitefly (*Bemisia tabaci*) in a continual mode. The best method to control this disease is by breeding for resistant or tolerant genotypes. The present study meant to identify stable MYMV resistant lines through screening under natural condition during kharif 2019.Eighty one genotypes of mungbean were screened against MYMV at Bhuvanagiri in cuddalore district. By visual scoring of symptoms in the field under natural conditions, the resistance levels were evaluated. The per cent disease incidence (PDI) of MYMV among 81 mungbean genotypes were monitored up to ninth week after sowing and it varied from 5.04 to 82.88%. The germplasms were grouped in to resistant and susceptible depending upon severity of infection. The differential reaction of mungbean genotypes to MYMV was observed and none of the genotype was found to be highly resistant. Seven genotypes *i.e.* IC76361, IC119020-1, PLM490, IC75200, IC119020-2, CO7, CO8 were found as resistant. Fifteen genotypes were moderately resistant and ten were moderately susceptible. Remaining twenty seven accessions were classified as susceptible and twenty two as highly susceptible accessions. The results revealed that most of the genotypes were classified under susceptible to highly susceptible. The resistant accessions obtained could be used in future breeding programmes to develop green gram cultivars resistant to MYMV or could be used directly as varieties to manage MYMV disease infection after adoption to various agro-climatic regions.

Key words: MYMV, Mungbean, Resistant, PDI, Field Screening.

Introduction

Mungbean (*Vigna radiata* L. Wilczek) belongs to fabaceae, is a vital crop cultivated throughout Asia. It is relatively tolerant to drought and can be harvested within 60 to 75 days. This legume crop is well suited for large number of cropping systems and constitutes a main source of cereal based diets for worldwide. Asia alone credits for 90% of world's mungbean production. Mungbean contains carbohydrate (51%), protein (24%_26%), minerals (4%) and vitamins (3%). Beside this it has the property of helping the symbiotic root rhizobia to fix atmospheric nitrogen which helps add on soil fertility.

The susceptibility of the crop towards insects, weeds and diseases caused by fungus, virus or bacteria tends to low yield. Viruses are the focal group of plant pathogens affecting the production of the crop. They cause severe diseases and economic losses in mungbean by plummeting seed yield and quality (Kang *et al.,* 2005). Mungbean yellow mosaic disease (YMD) can reduce seed yield up to 100% under severe conditions (Nene, 1973) or even kill a plant infected at primary vegetative stage. Geminivirus (genus Begomovirus, family Geminiviridae), which has bipartite genomes (DNA A and DNA B) causes the yellow mosaic disease in plants. These viruses are transmitted by the vector whitefly (*Bemisia tabaci*) which can infect mungbean at all growth stages. The best notable symptoms are present on the foliage as small yellow specks along the veinlets and spreads over the lamina followed by necrosis. The symptoms consist of shortening of internodes, severe stunting of plants with

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no yield or few flowers and pods become thin and curl upwards producing small, immature and shrivelled seeds.

Many disease management strategies have been developed or implemented for MYMV disease by vector control through application of synthetic and non-synthetic insecticides but so far, this is neither sustainable nor economically viable. The development of resistance in vectors, environmental pollution are some potential hazards accompanied with random use of pesticides.

Table 1: Mungbean genotypes used in the experiment.

G No.	Genotype Name	G. No.	Genotype Name	G No.	Genotype Name
G1	PLM634	G28	IC282110	G55	CO 7
G2	PLM776	G29	IC314919	G56	VRM 1
G3	IC76417	G30	IC282095	G57	ADT-3
G4	IC76381	G31	IC148401	G58	CO 6
G5	PLM350-1	G32	IC565301	G59	VBN 3
G6	IC76361	G33	IC148403	G60	CO 8
G7	IC76322	G34	IC75200	G61	AKM 1502
G8	IC76441	G35	IC148423	G62	AKM 4
G9	PLM188	G36	IC148419	G63	AKM 8803
G10	IC76477	G37	IC149428	G64	KAMBAM
G11	IC39563	G38	IC314291	G65	PUSA VISHAL
G12	PLM746	G39	EC398952	G66	TAP 7
G13	1C76491	G40	EC398413	G67	MAYILA DUDURAI
G14	PLM232	G41	EC398893	G68	VIRUDHU NAGAR
G15	PLM420	G42	EC398881	G69	IPM99 125
G16	PLM858	G43	EC398953	G70	K 17 2
G17	PLM506	G44	EC396419	G71	K 17 3
G18	PLM350-2	G45	IC119020-2	G72	KM 2
G19	IC119020-1	G46	VBN 1	G73	ADT 2
G20	PLM614	G47	AKM0503	G74	VAIBHAV
G21	IC121233	G48	POM 262	G75	CO 4
G22	PLM475	G49	CO 9016	G76	VBN 2
G23	IC314804	G50	UTKARSH	G77	VRMGg-1
G24	IC398746	G51	AKM 1507	G78	K 17 1
G25	IC102913	G52	TARM 2	G79	KM 1
G26	IC546476	G53	K 851	G80	ML 5
G27	PLM490	G54	NIRMAL465	G81	PAIYUR

Table 2: Scale used for MYMV reaction by Bashir *et al.,* (2005).

Seve -rity	% Infection	Infection Category	Reaction Group
0	All plants free of	Highly	
	virus symptoms	resistant	HR
1	1-10% infection	Resistant	R
2	11-20% infection	Moderately resistant	MR
3	21-30% infection	Moderately susceptible	MS
4	30-50% infection	Susceptible	S
5	More than 50%	Highly susceptible	HS

Hence, the only feasible, effective, economical, environment friendly and sustainable solution to alleviate Yellow Mosaic Disease incidence in areas is to develop and use resistant varieties to both virus and its vector in legume cultivation. Screening of mungbean germplasm should be done in order to obtain the resistance lines. In mungbean genotypes, resistance against MYMV has been screened prior by different workers using the scale based on disease severity (Ahmad, 1975, Murtza *et al*., 1983; Ghafoor *et al*., 1992; Bashir and Zubair 2002, Bashir 2005, Bashir *et al*., 2006, Khattak *et al*., 2008). Studies were conducted to identify markers which are linked to the resistance of black gram and mungbean from some resistant germplasm (Basak *et al.,* 2004; Selvi *et al.,*

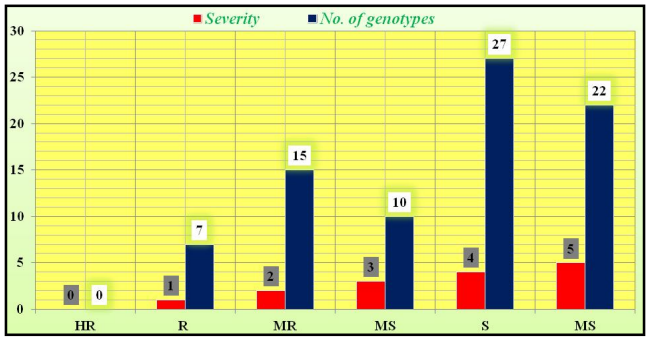

Fig. 1: Categorization of mungbean genotypes in different disease reaction against MYMV.

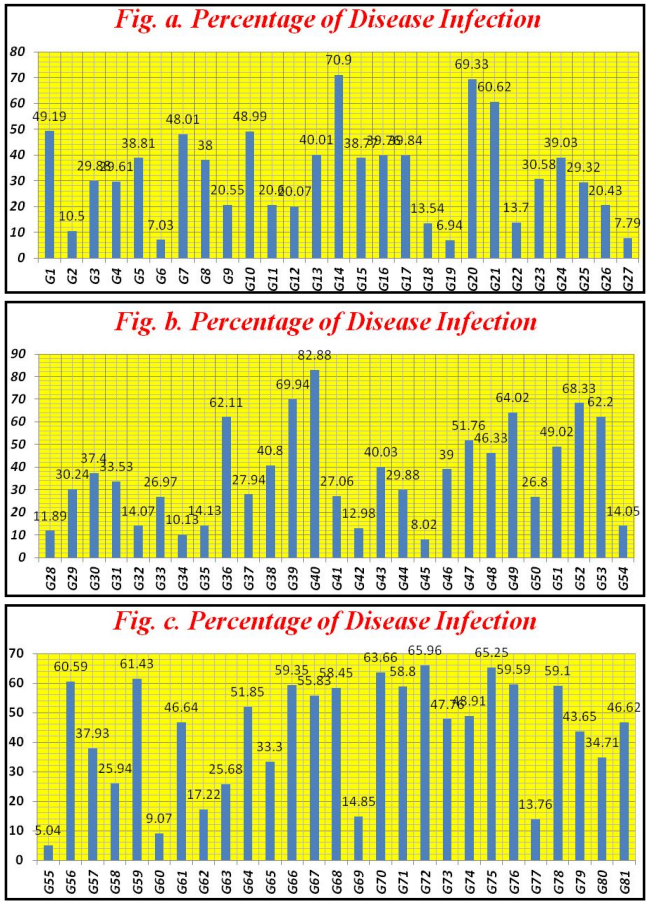

Table 2: Distribution of mungbean genotypes in various infection categories.

Severity	Infection Category	genotypes	No. of genotypes
0	HR	-	0
1	R	G6,G19,G27,G34,G45,G5, G60	7
2	MR	G2,G9,G11,G12,G18,G22,G26,G28, G32,G35,G42,G54,G62,G69,G77	15
3	MS	G3,G4,G25,G33,G37,G41,G44,G50,G58,G63	10
4	S	G1,G5,G7,G8,G10,G13,G15,G16,G17,G23, G24,G29,G30,G31,G38,G43,G46,G48,G51, G57,G61,G65,G73,G74,G79,G80,G81	27
5	HS	G14,G20,G21,G36,G39,G40,G47,G49,G52, G53,G56,G59,G64,G66,G67,G68,G70, 71,G72,G75,G76,G78	22

2006; Souframanien and Gopalakrishna, 2006; Tuba Anjum *et al.,* 2010; Prasanthi *et al.,* 2013) but these studies relied upon screening procedures either natural disease pressures or are exclusively based on laboratory screening. In the absence of a uniform robust screening technique, no reliable results could be obtained (Akhtar and Khan, 2002). Hence, the present study was envisaged to screen the mungbean germplasms and identify the resistant MYMV genotypes through field screening under natural conditions in order to identify resistant genotypes which could beneficial in the improvement of breeding process.

Table 3: PDI at maturity of MYMV on mungbean genotypes.

Genotypes	PDI	MYMV	Genotypes	PDI	MYMV	Genotypes	PDI	MYMV
G1	49.19	S	G28	11.89	MR	G55	5.04	R
G2	10.5	MR	G29	30.24	S	G56	60.59	HS
G3	29.88	MS	G30	37.4	S	G57	37.93	S
G4	29.61	MS	G31	33.53	S	G58	25.94	MS
G5	38.81	S	G32	14.07	MR	G59	61.43	HS
G6	7.03	R	G33	26.97	MS	G60	9.07	R
G7	48.01	S	G34	10.13	R	G61	46.64	S
G8	38	S	G35	14.13	MR	G62	17.22	MR
G9	20.55	MR	G36	62.11	HS	G63	25.68	MS
G10	48.99	S	G37	27.94	MS	G64	51.85	HS
G11	20.6	MR	G38	40.8	S	G65	33.3	S
G12	20.07	MR	G39	69.94	HS	G66	59.35	HS
G13	40.01	S	G40	82.88	HS	G67	55.83	HS
G14	70.9	HS	G41	27.06	MS	G68	58.45	HS
G15	38.77	S	G42	12.98	MR	G69	14.85	MR
G16	39.76	S	G43	40.03	S	G70	63.66	HS
G17	39.84	S	G44	29.88	MS	G71	58.8	HS
G18	13.54	MR	G45	8.02	R	G72	65.96	HS
G19	6.94	R	G46	39	S	G73	47.76	S
G20	69.33	HS	G47	51.76	HS	G74	48.91	S
G21	60.62	HS	G48	46.33	S	G75	65.25	HS
G22	13.7	MR	G49	64.02	HS	G76	59.59	HS
G23	30.58	S	G50	26.8	MS	G77	13.76	MR
G24	39.03	S	G51	49.02	S	G78	59.1	HS
G25	29.32	MS	G52	68.33	HS	G79	43.65	S
G26	20.43	MR	G53	62.2	HS	G80	34.71	S
G27	7.79	R	G54	14.05	MR	G81	46.62	S

Materials and Methods

Experimental materials

Field screening for MYMV disease was carried out at bhuvanagiri, cuddalore district of Tamil Nadu during kharif-2019 using infector row technique. Eighty one genotypes were collected in which forty five of them were cultures obtained from NBPGR, New Delhi and the remaining were local varieties from National Pulses Research Centre, Vamban table 1 The genotypes were sown in single row with a length of 4 meters and a spacing of 30×10 cm in three replications. One row of infector line was raised with paiyur-1 after every five test entries.

Disease screening methodology

Susceptible check was raised all around the experimental plot in order to attract white fly and enhance infection of MYMV under field conditions. All the recommended cultural practices except insecticide sprays were followed to maintain the experimental field. Insecticide sprays were not given to encourage the white fly population for the disease to spread. The crop was regularly monitored for the presence of whitefly and development of MYMV. In the subsequent 6 weeks the infection and disease severity of MYMV will be developed. The disease was scored on 0-5 arbitrary scale, as recommended by Bashir *et al.,* (2005) which is described in table 2. The disease scoring was recorded from initial flowering to harvesting by weekly intervals.

Percentage of disease infection

The percentage of disease infection was calculated by counting the number of diseased plants to the total number of plants using the formula given below.

Percentage of disease infection (PDI) =

$$\frac{Number\ of\ \text{inf}ected\ plants\ in\ a\ row}{Total\ number\ of\ plants} \times 100$$

The genotypes were later grouped into different categories based on the disease score from highly resistant to highly susceptible according to Bashir *et al.* (2005). The genotypes were categorized using 0-5 arbitrary scale as Highly Resistant (HR), Resistant (R),

Moderately resistant (MR), Moderately susceptible (MS), Susceptible (S) and Highly Susceptible (HS) based on disease severity.

Results and Discussion

MYMV disease can severely reduce the yield of various legume crops. The presence of massive vector population in the field, favourable environmental conditions and the greater susceptibility of genotypes to MYMV are the reasons for disease development. The screening of mungbean genotypes towards MYMV in field condition depends on the above situations. Variation in genotype response towards MYMV represents the difference in their genetic makeup. Earlier it was reported that two recessive genes are responsible for the control of resistance mechanism in mungbean (Shukla and Pandya, 1985), whereas in case of susceptibility it was controlled by single recessive gene. From this it is evident that susceptibility is dominant over resistance. An essential measure for an efficient disease control is the use of virus resistant genotypes but the success obtained was not much.

In field, after every five test entries there should be susceptible check lines which can enhance the vector population. The vector can appear as soon after the emergence of the plant and can remain till maturity also the disease severity will worsen with time. In the field most of the plants showed MYMV incidence. The scoring of the test materials was done on the basis of MYMV disease rating scale. According to the mean disease scoring by Bashir *et al*., (2005) the mungbean genotypes were categorized into six groups highly resistant (HR), resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS)(Table 2).It is noticeable from the results table 3 and Fig. a-c that only seven genotypes (IC76361, IC119020 1, PLM490, IC75200, IC119020-2, CO7, CO8) appeared as resistant, which indicated the existence of small amount of resistance in genotypes against MYMV Fig. 1. None of the genotype is highly resistant, showing the consistent occurrence of disease in the field. Whereas fifteen showed moderately resistance. Similar studies conducted by Ahmed (1975) evaluated 157 local and exotic mungbean varieties, but no resistant variety was found, however 6 out of 34 local collections showed moderate resistance response to disease. Singh *et al.,* (1996) observed partial resistance in mungbean. A single variety of mungbean (Plant-U30) was only resistant to whitefly and yellow mosaic disease (Sahoo & Hota, 1991). Bashir (2003) screened 276 lines of mungbean and out of which 10 show résistance. Similarly, nine resistant lines were observed from the study of Awasthi & Shyam (2008) in field conditions for 83 lines against MYMV. Results obtained from the present screening were in close agreement with the above studies mentioned. The genotypes clustered under resistant category would be employed as donors to develop MYMV resistant lines. These resistant genotypes will be further screened through artificial screening methods like forced feeding method, agroinoculation method, etc., to confirm MYMV resistance.

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