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Screening of Mungbean Genotypes for Resistance against *Mungbean yellow mosaic virus* (MYMV) during Kharif under Field Condition

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Authors' contributions

This work was carried out in collaboration between both authors. Author MM designed the study, performed the statistical analysis, wrote the protocol, literature searches and wrote the first draft of the manuscript. Author MK managed the analyses of the study. Both authors read and approved the final manuscript.

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ABSTRACT

Host resistance offers the cheapest way of disease management with no environmental concern of pesticide residues. This study was conducted during *kharif* to identify sources of resistant genotypes against *Mungbean yellow mosaic virus* (MYMV) in mungbean. Here, pre-released mungbean genotypes/lines were screened against MYMV and results showed that the incidence of MYMV among the genotypes evaluated varied from 3.44 to 69.12 per cent. Highest incidence was recorded in KM-13-71 (69.12%) followed by GG-13-8 (66.66%), NM-94 (62 %) and T30 (97/1) (56.75%). Lowest incidence was recorded for Jabalapuri (3.44%) followed by GM-20 (7%), TRCRM-141 (7.87%) and 116/01 (8%). Among 40 genotypes, eight genotypes showed resistance (R) reaction against MYMV with minimum disease score of 1. Eight genotypes showed moderate resistance (MR) reaction with disease score of 2 and two genotypes showed moderately

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susceptible responses (MS) with a disease score of 3. Eight genotypes were found susceptible (S) with a disease score of 4, and eleven genotypes were found highly susceptible (HS) to MYMV with the disease score of 5. Among these 40 genotypes, none of the genotypes were found to be highly resistant (HR) against MYMV.

Keywords: Mungbean; MYMV; resistant and genotypes.

1. INTRODUCTION

Mungbean (*Vigna radiata* (L.) Wilczek) also known as green gram or golden gram is the third most important pulse crop after chickpea and pigeon pea. The crop is native to the Indian subcontinent and cultivated in other South East Asian countries such as Pakistan, Bangladesh, Sri Lanka, Philippines, Taiwan, Nepal, Thailand, Laos, Kampuchea, Vietnam, Indonesia, Eastern Malaysia, Southern China and Java [1]. Mungbean seeds are used for consumption by cooking, fermenting, milling or sprouting and also used for making soups, curries, bread, sweets, noodles, salads, papad etc. [2]. It also exhibits antimicrobial and insecticidal activities [3] Being a leguminous crop, it plays an important role in improving the soil fertility through biological nitrogen fixation [4], checks soil erosion as a cover crop, used as green manure and fodder crop as well [5]. The crop is mainly cultivated during *Kharif* season under rainfed conditions and limited to irrigated conditions in *rabi*. Many biotic and abiotic stresses have hampered its cultivation. Among biotic stresses, mungbean yellow mosaic disease caused by *Mungbean yellow mosaic virus* (MYMV) is considered the most serious threat of mungbean, limiting the production and productivity. The virus is most destructive in the Indian subcontinent and adjacent areas of South-East Asia causing 100 per cent yield losses [6]. *Mungbean yellow mosaic virus* belongs to the family Geminiviridae [7] and genus Begomovirus which contains viruses that are transmitted by whitefly (*Bemisia tabaci* Genn.) [8]. In order to manage the MYMV, apart from controlling vectors by chemical and other measures, use of resistant cultivars is the most sought and cheapest option. For mungbean being cultivated on rainfed situations, development and identification of MYMV resistant cultivars is the need of the hour. Some mungbean cultivars like PDM-11, PDM-84, ML 267 and ML 220 have shown resistance in the northern states of India [9,10]. The present investigation focused on knowing suitable resistant source against MYMV in NEK.

2. MATERIALS AND METHODS

In order to know the response of new mungbean genotypes, 41 entries were evaluated against MYMV. The experiment was sown during *Kharif*, 2016. Each entry was sown in two rows of 5 m at 30 x 10 cm spacing. Local susceptible cultivar S-M (Shining Moong) was sown in two rows all around the plots as a susceptible check and also after every two entries to create a sandwich. Observations of per cent disease incidence in each entry were recorded following 0 to 5 disease scale (Table 1), and the ratings were designated accordingly [11].

3. RESULTS AND DISCUSSION

Breeding for disease resistance is a continuous process, and in the present research, apart from the evaluation of resistant cultivars, green gram genotypes were also screened for their resistance against MYMV. In total 41 genotypes of mungbean were screened against MYMV during *Kharif*, 2016 under natural infestation of virus in field conditions. The per cent disease

Table 1. Descriptive chart used to score incidence of MYMV on mungbean genotypes

Disease severity	Percent infection	Infection category	Reaction group
0	All plants free of disease symptoms	Highly 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

incidence was recorded in each genotype. The incidence of MYMV among the genotypes evaluated varied from 3.44 to 69.12 per cent. Highest was recorded in KM-13-71 (69.12%) followed by GG-13-8 (66.66%), NM-94 (62 %) and T30 (97/1) (56.75%). Lowest incidence was recorded in Jabalapuri (3.44%) followed by GM-20 (7%), TRCRM-141 (7.87%) and 116/01 (8%) (Table 2). Among 40 genotypes, eight genotypes *viz.*, Jabalpuri, TRCRM-118, TMB-37(c), TRCRM-141, GM-20, 17/01, 116/01 and KMB-39 showed resistance (R) reaction against MYMV with minimum disease score of 1. Eight genotypes TRCRM-127, TM-96-2-(c), BGS-9, TRCRM-143, TRCRM-147, TRCRM-4, DGGV-2 and Selection-4 showed moderate resistance (MR) reaction with disease score of 2 and two genotypes TRCRM-144 and TRCRM-115 were moderately susceptible (MS) with disease score of 3. Eight genotypes *viz.*, BG-1, BG-4, 1-Dec, TJM-3, 70/01, BG-2, BG-3 and TRCRM-24 were found susceptible (S) with a disease score of 4 and eleven genotypes *viz.*, 65/01, TRCRM-17, GG-13-8, 39/01, TRCRM-37, 730 (97/01), KMS-13-17, 42/02, KM-13-8, NM-94 and KM-13-30 were found highly susceptible (HS) to MYMV

Table 2. Response of mungbean genotypes against MYMV incidence during *Kharif* 2016

Sl. no.	Entries	PDI (%)	Disease severity scale	Disease reaction
1	TRCRM-144	26.66	3	MS
2	TRCRM-127	17.87	2	MR
3	TRCRM-115	25.00	3	MS
4	TM-96-2-(c)	11.66	2	MR
5	Jabalpuri	3.44	1	R
6	BGS-9	16.00	2	MR
7	TRCRM-143	17.86	2	MR
8	TRCRM-147	14.44	2	MR
9	TRCRM-4	15.86	2	MR
10	TRCRM-118	8.88	1	R
11	TMB-37(c)	8.86	1	R
12	TRCRM-141	7.87	1	R
13	DGGV-2	18.23	2	MR
14	GM-20	7.00	1	R
15	BG-1	32.45	4	S
16	17/01	8.92	1	R
17	116/01	8.00	1	R
18	KMB-39	10.00	1	R
19	65/01	50.20	5	HS
20	BG-4	39.76	4	S
21	TRCRM-17	55.22	5	HS
22	1-Dec	34.88	4	S
23	TJM-3	48.40	4	S
24	GG-13-8	66.66	5	HS
25	39/01	18.00	5	HS
26	70/01	42.40	4	S
27	TRCRM-37	52.00	5	HS
28	97/01	56.75	5	HS
29	KMS-13-71	53.48	5	HS
30	BG-2	48.50	4	S
31	42/02	51.00	5	HS
32	BG-3	39.42	4	S
33	KM-13-8	69.12	5	HS
34	NM-94	62.00	5	HS
35	KM-13-30	52.00	5	HS
36	TRCRM-24	48.10	4	S
37	KM-13-13	NG	_	_
38	29/01	NG	_	_
39	Selection-4	15.52	2	MR
40	TRCRM-26	NG	_	_

Table 3. Grouping of mungbean genotypes based on their response against MYMV incidence during *Kharif*, 2016

Sl. no.	Disease severity	Percent infection	Infection category	Reaction group	Cultivars
1	0	All plants free of disease symptoms	Highly Resistant	HR	-
2	1	1 - 10% Infection	Resistant	R	Jabalpuri,TRCRM-118, TMB-37(c), TRCRM-141, GM-20, 17/01, 116/01, KMB-39
3	2	11 -20% infection	Moderately Resistant	MR	TRCRM-127, TM-96-2-(c), BGS-9, TRCRM-143, TRCRM-147, TRCRM-4, DGGV-2, Selection-4
4	3	21-30% infection	Moderately Susceptible	MS	TRCRM-144, TRCRM-115
5	4	30-50 % infection	Susceptible	S	BG-1, BG-4, 1-Dec, TJM-3, 70/01, BG-2, BG-3, TRCRM-24
6	5	More than 50%	Highly Susceptible	HS	65/01, TRCRM-17, GG-13-8, 39/01, TRCRM-37, 730 (97/01), KMS-13-17, 42/02, KM-13-8, NM-94, KM-13-30

with the disease score of 5 (Table 3). Differential response of MYMV severity might be due to vector load, climatic conditions and genetic character of varieties.

Paul et al. [12] screened 18 germplasm against MYMV, one was found resistant (ML-818), and one was susceptible (Pusa baisaki). Remaining nine were moderately resistant and seven were moderately susceptible. ML-818, IPM-99-125, PANT-M-4, PDM-139, UPM-9903, Pusa-2072, SML-668, Asha, PS-16 and MH-96-1 were found prominent lines against mosaic infection. The diverse resistance among the genotypes necessitates their screening and grouping for further selection and release as variety. In the present investigation also eight of each genotype were found to be resistant and moderately resistant. Mondal et al. [13] screened 102 mungbean lines against MYMV in Bangladesh and reported ACC-12840014 most promising with minimum infection and high yield (2888 kg ha^{-1}) followed by VC-1007A (2844 kg ha^{-1}) and VO-1319 (B-G) (2788 kg ha^{-1}). These were also recommended as MYMV resistant genetic material for further breeding programmes. In another screening experiment by [14], they reported that none of the test entries was immune. Genotypes EC-398897, TM-11-07, TM-11-34, PDM-139, IPM-2-3, IPM-2-14, Pusa-0672, Pusa-0871 and MH-521 exhibited resistance. Similarly, 12 genotypes of mungbean were screened by [15] who found only two genotypes, Meha and ML-1477, were resistant at Jharkhand region. Another report studied in North Eastern Karnataka by [16] revealed none of the genotypes as highly resistant or resistant. But, 19 genotypes were found moderately resistant, 22 genotypes were moderately susceptible, 50 were susceptible and 15 highly susceptible. Screening of mungbean entries against MYMV was carried by [17] who also failed to find any entry under the category of highly resistant. However, there were six entries (BRM-325, BRM-345, BRM-363, BRM-364, BRM-366 and NM-2011) found resistant, 10 (BRM-311, BRM-312, BRM-321, BRM-331, BRM-335, BRM-365, BRM-378, BRM-382, BRM-343 and BRM-353) moderately resistant. 5 (Chakwal-06, BRM-334, BRM-348, BRM-354 and BRM-356) moderately susceptible and two entries BRM-349 and BRM350 showed susceptible and highly susceptible response respectively. It is clear from the present findings that pre-breeding material will have a diverse genetic background and their response against MYMV will vary. The stable genotypes with highly resistant and resistant character are suitable for promotion as cultivars. Viruses such as the single-stranded (ss) DNA begomoviruses, are emergent problems worldwide [18,19]. They have higher mutation rates than other pathogens, and distinct evolutionary dynamics compared to bacterial and fungal phytopathogens. Therefore breeding and screening of mungbean for

resistance against MYMV should be carried out regularly for identification of suitable cultivars.

4. CONCLUSION

The yellow mosaic disease caused by MYMV is limiting the production of green gram across the world. The varied incidence of this virus is reported from various parts of green gram cultivating countries including India. Mungbean of genotypes *viz.,* Jabalpuri, TRCRM-118, TMB-37(c), TRCRM-141, GM-20, 17/01, 116/01 and KMB-39 which showed resistance against MYMV shall be elevated for release after agronomical and yield evaluation studies and may also be used in breeding programmes.

DISCLAIMER

As per pathological screening, in this work authors have done the check row sandwich method of sowing and for each check row, authors had sown two rows of genotypes. Hence here in this kind of experiment authors can only calculate the per cent disease incidence and tell directly the host response to the pathogen based on the per cent incidence in each row of genotypes and conclude its resistance and susceptibility. Hence no statistical methods are done here. Since this paper is based on the preliminary dataset and the authors wanted to publish the initial data as early as possible, the authors recommend detailed statistical analysis for similar future studies

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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