Research Article
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Screening mungbean [*Vigna radiata* (L.) wilczek] genotypes for *mungbean yellow mosaic virus* resistance under natural condition

Abstract

Mungbean Yellow Mosaic Virus (MYMV), transmitted through the white fly (*Bemisia tabaci*) in the persistent manner is one of the most pernicious diseases of Vigna species. Twenty-five genotypes of mungbean [*Vigna radiata* (L.) Wilczek] were sown in randomized block design with two replications during the summer season in 2015. The test entries were evaluated against the *mungbean yellow mosaic virus (MYMV)* under natural field conditions. Screening for *MYMV* resistance was done by planting infector rows along with the test entries. Percent Disease Incidence (PDI) was calculated. The differential response against *MYMV* observed and the results revealed that most of the genotypes studied were characterized as moderately susceptible to highly susceptible. In spite of the variable response to *MYMV*, IPM 02-03, KM 2241, PDM 139, Pusa 0672, HUM 16, ML 1464 and TARM-1 of the mungbean genotypes exhibited resistance during the summer, 2015. The present investigation suggests that these genotypes could possibly be utilized as donors to develop *MYMV* resistant lines *MYMV* resistance by introgressing in agriculturally important but *MYMV* susceptible genotypes. Consequently, in the near future, the improved varieties may surfeit the sustainable agriculture production in the biotic stress prone areas.

Keywords: genotype, mungbean, screening, yellow mosaic virus, percent disease incidence

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Introduction

Legumes are vital, environment-friendly food grain crops with a rich source of proteins, minerals and vitamins besides carbohydrates. They are next to cereals in terms of their nutritive and economic value. In addition, they play a pivotal role in the restoration of soil fertility by atmospheric nitrogen fixation through symbiosis with *Rhizobium* species, and also play an important part in the sustainability of agricultural production system. Besides this, characteristics like rapid growth, early maturity and easily digestibility without flatulence further add to their value in various cropping systems.[1] Per contra, the total production and productivity of legumes are affected by a number of biotic (viral, fungal, bacterial pathogens and insects) and abiotic (temperature, drought, salinity, water logging etc.) stresses.[2] Among the biotic factors, *Mungbean yellow mosaic virus (MYMV)* is one of the most destructive and devastating diseases that limits the mungbean production throughout Asia, including India.[3,4]

The virus is a member of the Gemini viridae family, belonging to the Begomovirus genus with bipartite genome,[5] and is transmitted by the insect vector, white fly (*Bemisia tabaci*) in a persistent (calculative) manner.[3,6] The early symptoms of the virus become evident with the development of yellow specks along the veins which progressively spreads and turns the entire leaf yellow. In the severe cases, the entire leaf may become chlorotic which later turns in to necrotic regions.[7] The affected plants flower sparsely and the pods formed are curled with reduced size and increased percent of the shrivelled seeds.[3,8] The yield loss from the viral diseases in pulses accounts upto 80 percent, while the *MYMV* alone causes losses upto 80 to 100 percent in mungbean.[9] Management of this disease is only possible by the way of reducing the vector *viz.*, white fly population using insecticides which are ineffective under severe infestations making a complete destruction of the virus knotty. Therefore, development and use of the virus resistant cultivars turn out to be the most effective and economical strategy against *MYMV*.[10] Keeping this background information into consideration, the present investigation was envisaged with the objective to identify the mungbean resistant genotypes against *MYMV* based on the field screening to evaluate its expediency in breeding for *MYMV* resistance.

Materials and methods

A total of 25 diverse genotypes of mungbean [*Vigna radiata* (L.) Wilczek] were obtained from Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, BHU, Varanasi, India for the screening of mungbean yellow mosaic disease under natural conditions. The investigation was carried out at the Agriculture Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India which is located in the South-Eastern part of Varanasi city at 25' 18" N latitude, 83' 03" E longitude. The field screening trials were laid in randomized block design with two replications during the summer season of 2015. Each plot consisted of a single row of three-meter length with 30cm and 10cm row to row and plant to plant spacing, respectively. The infector row method was adopted in which one-row infector line of Co 5 (urdbean) was raised after every two-test entries to evaluate *MYMV* infection. Disease scoring was done on the basis of the visual symptoms. Plants were randomly selected and their leaves showing clear symptoms (veinal yellowing and scattered bright yellow spots) and total leaves were counted and percent disease incidence was calculated by using the formula given by Wheeler.[11] The disease was scored on 0-5 arbitrary scale, as suggested by Bashir[12] and Akhtar et al.,[13] and the genotypes were scored as Highly resistant (HR), Resistant (R), Moderately Resistant (MR), Susceptible (S) and Highly Susceptible (HS) based on disease severity (Table 1).

$$Percent\ incidence\ (PI) = \frac{Total\ number\ of\ infected\ leaves}{Total\ number\ of\ leaves\ observed} \times 100$$

$$Percent\ incidence\ index\ (PDI) = \frac{Sum\ of\ numarical\ rating}{Total\ number\ of\ leaves\ observed \times Max.grade} \times 100$$

Results and discussion

Legume viruses consisting of both RNA and DNA viruses infect legumes severely, thus have been a major threat to the production of several crops e.g. mungbean, urdbean, cowpea etc. In mungbean, *Mungbean Yellow Mosaic Virus* (*MYMV*), which is a DNA begomovirus is the most severe one due to its persistent nature of transmission. In addition, the rapid development of the viral recombinant strains and the presence of wide host range for the vector Bemesia tabaci possess a serious constraint to the mungbean production in India. Akhtar et al.,[14] reported that identification of the resistance source is the most reliable and economical method for the management of this virus as no virucide is available for the management of *MYMV* disease. Even though several genotypes and varieties have been identified showing resistance against *MYMV*, lack of durable resistance has been observed in most of the cases. Continuous screening during the year is required for the identification of the resistance source against *MYMV*.

Consequently, screening for identification of *MYMV* resistance source in the mungbean germplasm has been performed by a number of the scientists,[15–17] but with a little success. In the present study, the difference in the level of resistance shown by different mungbean genotypes based on the visual symptoms in response to *MYMV* infection was studied for all the 25 mungbean genotypes, and percent disease incidence was worked out. Due to the planting of the most susceptible check Co 5 (urdbean) after every two test entries and due to a good build-up of the white fly population (5-10 whiteflies plant-1) there were good chances of the spread of disease minimizing the chances of disease escape. At the end of the experiment, all the check lines turned completely yellow, showing maximum disease severity, ensuring a good evaluation of mungbean germplasm against the yellow mosaic disease.

On the basis of percent disease index recorded, the mungbean genotypes were classified into six groups (Table 1). The percent disease incidence varied from 4.45 to 70.35 percent in summer, 2015. Out of the 25 mungbean genotypes, 7 genotypes viz. IPM-02-03, Pusa 0672, ML 1464, KM 2241, PDM-139, TARM-1, and HUM 16 were found to be resistant (Table 2). Three genotypes i.e., ML 1465, IPM 02-17, and ML 1296 were categorized as moderately resistant. Three genotypes namely, HUM 1, HUM 7, and ML 717 were categorised under moderately susceptible. Similarly, susceptible and highly susceptible consisted of 3 (ML 712, Pusa 95-31, and AKM 9904) and 9 (HUM 12, LG 460, K 851, Pusa Vishal, COGG 902, MH 84-1, SML 1455, China mung and Kopergaon) genotypes, respectively (Table 2). It is evident from the results that only 7 genotypes out of the 25 appeared as resistant in mungbean, which indicated the existence of small amount of resistance in genotypes against *MYMV*. None of the genotypes was highly resistant, showing the uniform prevalence of disease in the field. The results of the present screening were in close agreement with the previous findings. Shad et al.,[18] found no immunity or resistance in 254 lines; all lines were susceptible to highly susceptible to the virus.

Among the 146 lines screened, only one line was found to be resistant to the virus, which showed that this virus is a severe problem.[13] The resistance nature of the genotypes IPM-02-03, PDM-139, Pusa 0672, and HUM 16 have also been reported by several scientists.[19–23] However, in a recent report where 63 mungbean entries were evaluated under the natural conditions, ten entries viz., KMP-13, 19, 20, 22, 23, 24, 40, 45, MLGG-8 and WGG-42 have been found immune to *mungbean yellow mosaic virus* disease.[24] On the other hand, in evaluation of 106 genotypes of mungbean none of the genotypes showed highly resistant and resistant reaction[25] which suggests that great variation in genotype response to *MYMV* represents variability in their genetic makeup.

The absence of the highly resistant lines from the test germplasm population of mungbean highlights the need for extensive work for exploring new sources of germplasm collection. Lack of resistant varieties necessitates the development of virus resistant varieties through inter-specific hybridization and biotechnology in the future. However, critical investigations like forced feeding method, agro inoculation method, etc., are necessary to ascertain the resistance level in these germplasm lines. Indirect selection of using molecular markers linked to *MYMV* resistant genes would facilitate precision plant breeding and the high-throughput marker-assisted selection (MAS) of the resistant genotypes.

Table 1 Disease scoring scale (0-5) for MYMV based on the percentage of disease incidence (PDI)

Disease Scale	Percent infection	Visual symptoms	Category	Reaction group
0	All plants free of virus symptoms	Complete absence of symptoms	Highly Resistant	HR
1	1-10 % infection	Small yellowish spots scattered on some leaves	Resistant	R
2	11-20 % infection	Yellowish bright spots common on leaves, easy to observe	Moderately Resistant	MR
3	21-30% infection	Yellowish bright specks common on leaves, easy to observe with larger patches of symptoms	Moderately Susceptible	MS
4	30-50% infection	Bright yellow specks or spots on all leaves, minor stunting of plants and less number of pods	Susceptible	S
5	50 % and more infection	Yellowing or chlorosis of all leaves on whole plant, shortening of internode, severe stunting of plants with no yield or few flowers and deformed pods produced with small, immature and shrivelled seeds	Highly Susceptible	HS

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Table 2 Reaction of mungbean genotypes against *MYMV* in agricultural research station, BHU, Varanasi during the summer, 2015

S. No.	Genotypes	Percentage of disease incidence	Disease scale	Disease reaction
1.	IPM-02-03	4.25	1	R
2.	Pusa 0672	4.45	1	R
3.	ML 1464	5.1	1	R
4.	KM 2241	5.35	1	R
5.	PDM-139	5.85	1	R
6.	TARM-1	6.6	1	R
7.	HUM 16	7.8	1	R
8.	ML 1465	11.34	2	MR
9.	IPM 02-17	12.8	2	MR
10.	ML 1296	14.76	2	MR
11.	HUM 1	26.45	3	MS
12.	HUM 7	27.3	3	MS
13.	ML 717	27.64	3	MS
14.	ML 712	37.86	4	S
15.	Pusa 95-31	38.65	4	S
16.	AKM 9904	47.27	4	S
17.	HUM 12	53.35	5	HS
18.	LG 460	58.75	5	HS
19.	K 851	61.4	5	HS
20.	Pusa Vishal	62.55	5	HS
21.	COGG 902	63.2	5	HS
22.	MH 84-1	63.55	5	HS
23.	SML 1455	64.55	5	HS
24.	China mung	66.7	5	HS
25.	Kopergaon	70.35	5	HS
26.	Co 5*	75.5	5	HS

*Co 5 genotype of urdbean was used as the infector row.

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Conflict of interest

The author declares no conflict of interest.

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