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Screening of mungbean yellow mosaic virus resistant lines in greengram (*Vigna radiata* L. Wilczek) under natural conditions

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Abstract

Field screening of sixty green gram genotypes was conducted during two seasons in summer in order to identify resistant genotypes against Mungbean Yellow Mosaic Virus (MYMV). The screening for MYMV disease was done using infector row technique under natural field conditions. Modified scale of All India Coordinated Research Project on MULLaRP proposed by Alice and Nadarajan, 2007 was used for disease scoring. The results showed considerable variation among the genotypes for MYMV resistance. In the *kharif* season of 2019, seven genotypes PUSA-1432, Samrat, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3 are categorized as highly resistant genotypes. In the second season (2020) the genotypes, PUSA-1432, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3 were found as highly resistant and genotypes. Based on the average MYMV score, genotypes were categorized in to five groups in the first season *viz.*, 7 highly resistant, 10 resistant, 9 moderately resistant, 11 moderately susceptible, 14 susceptible and 9 highly susceptible. In the second season they are categorized 6 highly resistant, 9 resistant, 12 moderately resistant, 14 moderately susceptible, 9 susceptible and 10 highly susceptible.

Keywords: Mungbean, yellow mosaic virus, resistant lines, natural conditions

Introduction

Greengram or mungbean (*Vigna radiata* L. Wilczek) is the third most significant pulse crop in India after Redgram and Bengalgram. It can be grown throughout all crop seasons in various parts of the country (Raj *et al*, 2019) [9]. It is a popular short duration grain legume which can be grown in different environments, across all cropping seasons *viz.*, *kharif*, *rabi* and summer, as single or intercrop for grain or green manure (Robertson *et al.*, 2004) [12]. Mungbean is mostly grown in the Southern Asia, India, Pakistan, Bangladesh, Nepal, Burma, Indonesia, Sri Lanka, Thailand, Vietnam, China and Philippines (Dharajiya *et al*, 2018) [2].

The wider adaptability of greengram is affected by both biotic and abiotic stresses. The biotic stresses include the complex viral diseases that are being transmitted by their insect vectors. In India, the major viral diseases that affect the mungbean production are mungbean yellow mosaic virus disease (MYMV) transmitted by whitefly, Urdbean Leaf crinkle virus (ULCV) transmitted by both aphids and whitefly and Leaf curl virus disease (LCV) transmitted by thrips of which MYMV is the most destructive which can cause yield loss of upto 100% in severe cases (Ramaraio *et al*, 2023) [10].

The common method which is used to control MYMV is control of the vector population utilising insecticides. The major problem of this method is non availability of effective insecticides. Furthermore these chemicals cause health problems and have adverse impact on environment (Nariani, 1960) [8]. Furthermore, this method is not economical and environment friendly. Developing cultivars of green gram that are genetically resistant to this disease is the most effective method of preventing it from spreading. Developing YMD resistant mungbean cultivars is more challenging due to the extensive host range of virus, genetic variability and nature of complex quantitative inheritance. It is effective to control this disease by using resistant genotypes.

Hence, continuous research to develop mungbean genotypes with high resistance to the specific virus strain against YMD is a crucial breeding objective to breeders.

Materials and Methods

The current study was conducted at AB block during the kharif seasons of 2019 and 2020, Department of Plant Breeding and Genetics, BCKV, West Bengal, under natural field conditions. The sixty Greengram genotypes were planted in Randomized Block Design (RBD) with three replications. Each genotype was planted in a three meter long row with 30 cm x 10 cm spacing. After every two rows of the genotypes to be tested, MYMV susceptible variety, Sonamung was sown as infector row.

The recommended agronomical practices were adhered to in the field during the experiment. In order to maintain whitefly population insecticidal spray was avoided. When 90% of the plants in the infector row displayed the typical MYMV disease symptoms, genotypes were evaluated for MYMV resistance. Modified scale of All India Coordinated Research Project on MULLaRP (Alice and Nadarajan, 2007) was used for scoring the disease. Five plants from each genotype were randomly selected and evaluated for MYMV resistance by scoring these genotypes based on the visual observation of the disease symptoms. The mean value was calculated for these genotypes and based on these scores, the genotypes were categorized into different disease reaction groups.

Results and Discussion

Among all the genotypes examined YMV score ranged from 0 to 9 (Table 1 and 2). YMV score was noticed higher for Sonamung-2 in both seasons i.e., 8.83 and 8.91 in 2019 and 2020 *kharif* respectively, followed by KM-16-97 (8.60), TM-2000-2 (8.3) in the first season. In second season Sonamung-2 was followed by KM-16-119 (8.6), PM-11-9 and TMB-140 (8.5). The lowest score was observed for IPM-2-3 (0.29), BCM-18-3 (0.31), MH-421(0.43), ML-1008 (0.46) and IPM-4-10-3 (0.56) in season 1(2019). Lowest YMV score in season 2 is recorded for IPM-2-3 (0.26), IPM-410-3(0.32), BCM-18-3

(0.34), ML-1008 (0.43) and MH-421 (0.44). The genotypes were grouped into six disease reaction categories as highly resistant, resistant, moderately resistant, susceptible, moderately susceptible and highly susceptible on the basis of their YMV scores given in the Table 3 and 4. Mishra *et al.* (2020) [6] has also classified 53 genotypes into 6 disease reaction categories. Darshan *et al.* (2018) [3] in a similar way investigated the resistance and susceptibility of 35 mungbean genotypes.

In the *kharif* season of 2019 (Table 3), seven genotypes (PUSA-1432, Samrat, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3) exhibited YMV scores ranging from 0-1, categorized as highly resistant genotypes, comprising 12% of the total. Approximately 17% of genotypes (PUSA-1431, PUSA Vishal, HUM-16, Meha, HUM-B, Virat, IPM-512-1, IPM-2-14, TMB-37, HUM (6)) fell into the resistant category with scores ranging from 1.1 to 2.0. Genotypes scoring between 2.1 and 4.0 were classified as moderately resistant, with 15% frequency represented by 9 genotypes. Eleven genotypes scored between 4.0 and 5.0 were categorized as moderately susceptible, making up 18% of the total. Highly susceptible genotypes, scoring between 7 and 9, comprised 15% of the genotypes, totaling 9 genotypes. But, in *kharif* 2020 (Table 4), six (6) genotypes namely, PUSA-1432, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3 had MYMV score of 0-1 and were categorized into highly resistant genotypes with a frequency of 10%. Approximately 15% of genotypes (KM-16-103, TMB-124, IPM-521-1, KM-16-116, SML-832, IPM-410-3, DGG-5, IPM-2-23, OUM-11-5) exhibited resistance, scoring between 1.1 and 2.0. Genotypes scoring from 2.1 to 4.0 were classified as moderately resistant, comprising 20% of the total with 12 genotypes. Darshan *et al.* (2018) [3] identified IPM 02-03 under highly resistant category in his study similar to this. Scoring between 4 and 5, included IPM-410-9, Bireswar, Sonali, TMB-17, IPM-522-1, PM-11-10, Shwetha, MGG-347, MH-1142, EC-496841 and were categorized as moderately susceptible, totaling 23%. Highly susceptible genotypes, scoring between 7 and 9, consisted of 15% of the genotypes, totaling 9 varieties.

Table 1: Scoring of greengram genotypes for mungbean yellow mosaic virus resistance for *kharif* 2019

S. No.	Genotype	YMV score (0-9)	Disease reaction
1	SML-668	6.41	Susceptible
2	PUSA 1432	0.82	Highly resistant
3	TMB 120	5.81	Susceptible
4	TM 153	5.63	Susceptible
5	KM -16-103	3.55	Moderately resistant
6	KM-16-97	8.64	Highly susceptible
7	PUSA-1431	1.62	Resistant
8	TM-2000-2	8.34	Highly susceptible
9	TMB-124	3.46	Moderately resistant
10	SUKUMAR	6.53	Susceptible
11	SIKHA	6.32	Susceptible
12	PUSA VISHAL	1.54	Resistant
13	HUM-16	1.84	Resistant
14	IPM-410-9	4.52	Moderately susceptible
15	MH-1315	7.63	Highly susceptible
16	IPM-521-1	2.62	Moderately resistant
17	IMP-103-3	3.94	Moderately resistant
18	MEHA	1.30	Resistant
19	KM-16-119	7.83	Highly susceptible
20	SML-832	3.25	Moderately resistant
21	SAMRAT	0.94	Highly resistant
22	HUM(B)	1.82	Resistant
23	BIRESWAR	4.88	Moderately Susceptible
24	VIRAT	0.95	Resistant

25	SONALI	4.65	Moderately susceptible
26	IPM-512-1	1.97	Resistant
27	TMB-17	4.65	Moderately susceptible
28	IPM-2-14	1.56	Resistant
29	PM-11-9	7.86	Highly susceptible
30	SML-1741	7.32	Highly susceptible
31	TMB-37	1.22	Resistant
32	IPM-522-1	4.82	Moderately susceptible
33	TMB-117	6.53	Susceptible
34	PM-11-10	4.84	Moderately Susceptible
35	IPM-410-3	3.43	Moderately resistant
36	TMB-112	6.84	Susceptible
37	SHWETHA	4.34	Moderately Susceptible
38	TMB-136	6.33	Susceptible
39	TMB-140	5.84	Susceptible
40	Sonamung-2	8.83	Highly susceptible
41	MH-421	0.43	Highly resistant
42	IPM-2-3	0.29	Highly resistant
43	IPM-4-10-3	0.56	Highly resistant
44	ML-1008	0.46	Highly resistant
45	BCM-18-3	0.31	Highly resistant
46	HUM(6)	1.92	Resistant
47	OBGG-52	6.53	Susceptible
48	ADT-03	5.82	Susceptible
49	MGG-347	6.33	Moderately Susceptible
50	KM-16-92	6.52	Susceptible
51	DGG-5	3.42	Moderately resistant
52	EC-391178	6.41	Susceptible
53	DGG-1	4.64	Moderately susceptible
54	PUSA M-1721	5.63	Susceptible
55	MH-1142	4.84	Moderately susceptible
56	IPM-2-23	3.42	Moderately resistant
57	ML-1464	7.84	Highly susceptible
58	EC-496841	4.56	Moderately susceptible
59	OUM-11-5	3.82	Moderately resistant
60	DGG-54	8.44	Highly susceptible

Raj *et al.* (2019) ^[9], Mishra *et al.* (2020) ^[6], Nainu *et al.* (2020) ^[7], Hithesh *et al.* (2022) ^[4], Thakur *et al.* (2022) ^[13], Choudhary *et al.* (2023) ^[1] and Kolloju *et al.* (2023) ^[5] have conducted screening against yellow mosaic disease and classified the genotypes into different reaction categories in a similar way.

The present investigation indicated significant variation in YMV resistance among different genotypes. Six genotypes which have exhibited high resistance in both seasons (PUSA-1432, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3) could be utilized as resistant donors in future breeding programmes.

Table 2: Scoring of greengram genotypes for mungbean yellow mosaic virus resistance for *kharif* 2020

S. No.	Genotype	YMV score (0-9)	Disease reaction
1	SML-668	1.62	Resistant
2	PUSA 1432	0.93	highly resistant
3	TMB 120	4.52	moderately susceptible
4	TM 153	5.61	Susceptible
5	KM -16-103	3.55	moderately resistant
6	KM-16-97	7.74	highly susceptible
7	PUSA-1431	1.96	Resistant
8	TM-2000-2	4.68	moderately susceptible
9	TMB-124	4.82	moderately susceptible
10	SUKUMAR	6.24	Susceptible
11	SIKHA	1.73	Resistant
12	PUSA VISHAL	2.76	moderately resistant
13	HUM-16	1.35	Resistant
14	IPM-410-9	4.34	moderately susceptible
15	MH-1315	4.63	moderately susceptible
16	IPM-521-1	2.57	moderately resistant
17	IMP-103-3	7.98	highly susceptible
18	MEHA	3.59	moderately resistant
19	KM-16-119	8.62	highly susceptible
20	SML-832	4.64	moderately susceptible
21	SAMRAT	4.81	moderately susceptible
22	HUM(B)	3.45	moderately resistant

23	BIRESWAR	4.64	moderately susceptible
24	VIRAT	3.72	moderately resistant
25	SONALI	1.93	Resistant
26	IPM-512-1	1.24	Resistant
27	TMB-17	4.82	Moderately Susceptible
28	IPM-2-14	1.53	Resistant
29	PM-11-9	8.56	highly susceptible
30	SML-1741	7.96	highly susceptible
31	TMB-37	1.67	Resistant
32	IPM-522-1	3.58	moderately resistant
33	TMB-117	7.69	highly susceptible
34	PM-11-10	3.41	moderately resistant
35	IPM-410-3	5.82	Susceptible
36	TMB-112	5.74	Susceptible
37	SHWETHA	8.38	highly susceptible
38	TMB-136	5.77	Susceptible
39	TMB-140	8.56	highly susceptible
40	Sonamung-2	8.91	highly susceptible
41	MH-421	0.44	highly resistant
42	IPM-2-3	0.26	highly resistant
43	IPM-4-10-3	0.32	highly resistant
44	ML-1008	0.43	highly resistant
45	BCM-18-3	0.34	highly resistant
46	HUM(6)	4.65	Moderately Susceptible
47	OBGG-52	4.57	moderately susceptible
48	ADT-03	1.65	Resistant
49	MGG-347	3.81	Moderately resistant
50	KM-16-92	6.34	Susceptible
51	DGG-5	4.65	moderately susceptible
52	EC-391178	4.36	moderately susceptible
53	DGG-1	2.81	moderately resistant
54	PUSA M-1721	6.54	Susceptible
55	MH-1142	3.82	moderately resistant
56	IPM-2-23	5.82	Susceptible
57	ML-1464	3.95	Moderately resistant
58	EC-496841	4.64	moderately susceptible
59	OUM-11-5	7.81	highly susceptible
60	DGG-54	6.86	Susceptible

Table 3: Frequency of greengram genotypes classified for MYMV scores for *kharif* 2019

YMV Score	Category	Genotypes	No.	Frequency (%)
0-1	Highly resistant	PUSA-1432, Samrat, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3.	7	12
1-2	Resistant	PUSA-1431, PUSA Vishal, HUM-16, Meha, HUM-B, Virat, IPM-512-1, IPM-2-14, TMB-37, HUM(6).	10	17
2-4	Moderately resistant	KM-16-103, TMB-124, IPM-521-1, IMP-103-3, SML-832, IPM-410-3, DGG-5, IPM-2-23, OUM-11-5.	9	15
4-5	Moderately susceptible	IPM-410-9, Bireswar, Sonali, TMB-17, IPM-522-1, PM-11-10, Shwetha, MGG-347, MH-1142, EC-496841.	11	18
5-7	Susceptible	SML-668, TMB-120, TM-153, Sukumar, Sikha, TMB-117, TMB-112, TMB-136, TMB-140, OBGG-52, ADT-03, KM-16-92, PUSA M-1721.	14	23
7-9	Highly susceptible	KM-16-97, TM-2000-2, MH-1315, KM-16-119, PM-11-9, SML-1741, Sona Mung-2, ML-1464, DGG-54.	9	15

In the first season (2019) the genotypes, PUSA-1432, Samrat, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3 were found as highly resistant and genotypes, PUSA-1431, PUSA Vishal, HUM-16, Meha, HUM-B, Virat, IPM-512-1, IPM-2-14, TMB-37, HUM(6) were resistant. The genotypes which exhibited moderate resistance are KM-16-103, TMB-124, IPM-521-1, IMP-103-3, SML-832, IPM-410-3, DGG-5, IPM-2-23, OUM-11-5. IPM-410-9, Bireswar, Sonali, TMB-17, IPM-522-1,

PM-11-10, Shwetha, MGG-347, MH-1142, EC-496841 were noticed as moderately susceptible. Susceptible reaction to YMV includes SML-668, TMB-120, TM-153, Sukumar, Sikha, TMB-117, TMB-112, TMB-136, TMB-140, OBGG-52, ADT-03, KM-16-92, PUSA M-1721. KM-16-97, TM-2000-2, MH-1315, KM-16-119, PM-11-9, SML-1741, Sonamung-2, ML-1464, DGG-54 were highly susceptible (Table 3).

Table 4: Frequency of greengram genotypes classified for MYMV scores for *kharif* 2020

YMV Score	Category	Genotypes	No.	Frequency (%)
0-1	Highly resistant	PUSA-1432, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3.	6	10
1-2	Resistant	SML-668, PUSA-1431, Sikha, HUM-16, Sonali, IPM-512-1, IPM-2-14, TMB-37, ADT-03.	9	15
2-4	Moderately resistant	KM-16-103, Pusa Vishal, IPM-521-1, Meha, HUM-B, Virat, IPM-522-1, PM-11-10, MGG-347, DGG-1, MH-1142, ML-1464.	12	20
4-5	Moderately susceptible	TMB-120, TM-2000-2, TMB-124, IPM-410-9, MH-1315, SML-832, Samrat, Bireswar, TMB-17, HUM-6, OBG-52, DGG-5, EC-391178, EC-496841.	14	23
5-7	Susceptible	TM-153, Sukumar, IPM-410-3, TMB-112, TMB-136, KM-16-92, PUSA M-1721, IPM-2-3, DGG-54.	9	15
7-9	Highly susceptible	KM-16-97, IMP-103-3, KM-16-119, PM-11-9, SML-1741, TMB-117, Shwetha, TMB-140, Sona Mung-2, OUM-11-5.	10	17

In season two (2020) the genotypes, PUSA-1432, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3 were found as highly resistant and genotypes, SML-668, PUSA-1431, Sikha, HUM-16, Sonali, IPM-512-1, IPM-2-14, TMB-37, ADT-03 were resistant. The genotypes which showed moderate resistance are KM-16-103, Pusa Vishal, IPM-521-1, Meha, HUM-B, Virat, IPM-522-1, PM-11-10, MGG-347, DGG-1, MH-1142, ML-1464. Moderately susceptible reaction was observed in TMB-120, TM-2000-2, TMB-124, IPM-410-9, MH-1315, SML-832, Samrat, Bireswar, TMB-17, HUM-6, OBG-52, DGG-5, EC-391178 and EC-496841. The genotypes which showed susceptibility to YMV include TM-153, Sukumar, IPM-410-3, TMB-112, TMB-136, KM-16-92, PUSA M-1721, IPM-2-3 and DGG-54. The genotypes KM-16-97, IMP-103-3, KM-16-119, PM-11-9, SML-1741, TMB-117, Shwetha, TMB-140, Sonamung-2 and OUM-11-5 were highly susceptible (Table 4).

Conclusion

The present investigation indicated significant variation in YMV resistance among different genotypes. Among the 60 genotypes studied under two seasons during kharif 2019 and 2020 it is found that Six genotypes which have exhibited high resistance in both seasons (PUSA-1432, MH-421, IPM-2-3, IPM-4-10-3, ML-1008, BCM-18-3) could be utilized as resistant donors in future breeding programmes. Sonamung-2 was identified as highly susceptible and could be used as susceptible parent.

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