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RESEARCH PAPER

Assessment of mungbean genotypes for durable resistance to mungbean yellow mosaic virus (MYMV)

D. M. KIRANAKUMARA[1], SUMANGALA BHAT[1*], O. SRIDEVI[1], P. U. KRISHNARAJ [2] AND PARASAPPA R. SAABLE[3]

[1]Department of Genetics and Plant Breeding, [2]Department of Microbiology, College of Agriculture, Dharwad
[3]Department of Plant Pathology, ICAR-IIPR, Regional Research Station
University of Agricultural Sciences, Dharwad - 580 005, India
*E- mail: bhatsumangala@uasd.in

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Abstract: Mungbean (*Vigna radiata* (L.) Wilczek) is a vital pulse crop in India, often constrained by biotic stresses, among which Mungbean Yellow Mosaic Virus (MYMV) is the most devastating, capable of causing up to 85 per cent yield loss. The present study was undertaken to identify stable sources of resistance to MYMV by evaluating 60 mungbean genotypes along with four checks under natural epiphytotic conditions during the summer seasons of 2023 and 2024 at the University of Agricultural Sciences, Dharwad. The experimental design followed was an augmented block layout and disease scoring was performed at 45, 60 and 75 days after sowing using a standard rating scale. Significant variation was observed among genotypes, with disease incidence (DI) ranging from 0 to 63.38 per cent in 2023 and 0 to 70 per cent in 2024. Analysis of variance indicated significant differences among entries, confirming genetic variability in disease response. Genotypes were classified into six disease response classes, from highly resistant to highly susceptible. Resistant checks, *Vigna trilobata* and IPM 2-14, exhibited consistent resistant to moderately resistant responses, while susceptible checks DGGV 2 and TARM 1 showed highly susceptible and moderately susceptible reactions, respectively. Among the test entries, 'Virat' and '8-BRD-9' consistently exhibited resistant reactions across both seasons, indicating their potential as stable MYMV-resistant sources. DGGV 251-1 showed a moderately resistant response, likely due to its parentage involving the resistant cultivar IPM 2-14. The observed variation in disease response was attributed to genetic diversity among genotypes, seasonal variability and differential vector pressure. These findings contribute valuable insights into utilization of MYMV-resistant genotypes for future mungbean improvement programs.

Key words: Disease incidence**,** Mungbean, MYMV, Resistance

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek), commonly known as green gram, is one of the major pulse crops cultivated in India, alongside pigeon pea and chickpea. It belongs to the family *Fabaceae*, subfamily *Papilionoideae*, genus *Vigna*, with a diploid chromosome number of 2n = 2x = 22 (Karpechenko, 1925). Nutritionally, 100 grams of raw mungbean contains approximately 10 g moisture, 24 g protein, 60 g carbohydrates, 1 g fat, 3 g minerals, 1 g fibre and provides 348 kcal of energy. It is also rich in essential micronutrients, including vitamin A (83 mg), thiamine (0.82 mg), riboflavin (0.15 mg), nicotinic acid (2.4 mg), calcium, phosphorus and iron. Mungbean is a valuable source of essential amino acids, such as tryptophan (260 mg), lysine (1664 mg), methionine (252 mg), phenylalanine (1421 mg), threonine (758 mg), valine (1246 mg), leucine (1687 mg) and isoleucine (1058 mg) (Dahiya *et al.,* 2015).

According to the Department of Agriculture and Farmers Welfare (2024), mungbean was cultivated over an area of 3.787 million hectares during the 2023–24 agricultural year, with a total production of 2.916 million tonnes and an average productivity of 770 kg/ha. Despite its nutritional and economic importance, mungbean production is constrained by several agronomic and biotic factors, including pod shedding, pod shattering, indeterminate growth habit, unproductive plant types and low harvest index. Among biotic stresses, viral diseases are particularly detrimental, with Mungbean Yellow Mosaic Virus (MYMV) being the most destructive, capable of causing yield losses of up to 85 per cent. MYMV a major constraint in mungbean cultivation across South and Southeast Asia, belongs to the genus *Begomovirus* (family *Geminiviridae*) and possesses a bipartite single-stranded DNA genome. It is transmitted persistently by the whitefly (*Bemisia tabaci*), enabling rapid disease spread under favorable conditions (Mishra *et al.,* 2020). Typical symptoms include yellow mosaic patterns on leaves, stunting, reduced flowering, and malformed pods with shrivelled seeds, resulting in substantial yield losses (Karthikeyan *et al*., 2014 and Mishra *et al*., 2020). In light of these challenges, the present study aimed to screen a diverse set of mungbean genotypes to identify stable sources of resistance against MYMV.

Material and methods

A total of 60 test genotypes, including advanced breeding lines and some released varieties were evaluated for Mungbean Yellow Mosaic Virus (MYMV). The test genotypes, along with four check entries DGGV2 and TARM 1 (susceptible checks) and IPM 2-14 and *Vigna trilobata* (resistant checks) were evaluated under field conditions during the summer seasons of 2023 and 2024 at the University of Agricultural Sciences, Dharwad. The trials were laid out in an augmented block design, and screening was conducted under natural epiphytotic conditions. To ensure uniform disease pressure, the susceptible genotype DGGV2 was planted after every ten test genotypes as an infector row.

Table 1. Disease rating scale used for scoring MYMV (Bashir *et al.*, 2005)

Disease scale	Visual symptoms	Per cent disease incidence	Category	Disease reaction
0	Complete absence of symptoms	0	Highly Resistant	HR
1	Few small yellow specks or spots on few leaves seen after careful observation	1-10	Resistant	R
2	Bright yellow specks or spots common on leaves, easily observed and some coalesce	11-20	Moderately Resistant	MR
3	Mostly coalesced bright yellow specks or spots common on leaves, . but no or minor reduction in yield	21-30	Moderately Susceptible	MS
4	Plants showing coalesced bright yellow specks or spots on all leaves, with no or minor stunting and set fewer normal pods	31-50	Susceptible	S
5	Yellowing or chlorosis of all leaves on flowers & deformed pods produced with small, immature and shrivelled seeds.	>50	Highly susceptible	HS

The field was monitored regularly for MYMV symptoms. The incidence of disease on the leaves of mungbean genotypes was scored during 45 DAS, 60 DAS and 75 DAS. The per cent disease incidence (DI) was calculated by using the formula given by Bashir *et al*. (2005). Based on the per cent disease incidence, the genotypes were categorized into different groups (Table 1) given by Bashir *et al.* (2005).

$$DI = \frac{\text{Number of diseased plants in a row}}{\text{Total number of plants in a row}} \times 100$$

The DI values were subjected to arcsine transformation, and the transformed values were used for subsequent statistical analyses.

Results and discussion

Analysis of variance (ANOVA) and estimation of genetic parameters

Analysis of variance (Table 2) revealed that there was no significant block difference indicating that the homogeneity was maintained across the experimental plot and the significant differences were observed among the entries and checks indicating the sufficient variation in the material used for this study. This variation can be attributed to the test material which consists of different genotypes and some advanced breeding lines. Genetic parameters such as mean, range, coefficient of variation, critical difference arepresented in Table 3. The DI range varies from zero to 63.38 per cent and zero to 70 per cent in summer 2023 and summer 2024 respectively. The disease reaction ranged from highly resistant to highly susceptible classes. These results are in confirmation with the previous studies conducted by Karthikeyan *et al.* (2014), Bhaskar (2016) and Saable *et al.* (2024) who also reported the high variation in MYMV disease response. The yield per plant ranged from 1.10 to 3.98 g and 4.16 to 14.30 g in summer 2023 and summer 2024 respectively.

Identification of resistant genotypes for MYMV

This study identified resistant genotypes against MYMV and represented in Table 4 and Table 5. The resistant check *V. trilobata* showed the highly resistant response,confirming earlier findings (Gautam *et al.,* 2014; Mogali *et al.,* 2017; Kumari *et al.,* 2021 and Dharani, 2022). Similarly, another check IPM 2-

Table 2. ANOVA for Disease incidence of MYMV

Sources of variation	d.f.	DI (MYMV)	
		Summer 2023	Summer 2024
Block (eliminating Check+Var.)	3	1.46	0.67
Entries (ignoring Blocks)	63	185.18**	394.91**
Checks	3	1437.14**	2030.65**
varieties	59	121.77**	318.32**
varieties vs. Check	1	170.19**	6.75*
Error	9	5.77	6.03

*Significant at 5% **Significant at 1%,
d.f.-Degrees of freedom, DI- Per cent disease incidence, MYMV – Mungbean yellow mosaic virus

Table 3. Estimates of mean, range, coefficient of variation andCritical difference during summer 2023and 2024

Traits	DI (MYMV)			
	Mean ± SE	Range	CV	CD
Summer 2023	39.27 ± 1.44	0.00 - 63.38	6.2	6.79
Summer 2024	32.35 ± 2.24	0.00 – 70.12	7.56	6.94

SE – Standard error, DI- Per cent disease incidence, MYMV – Mungbean yellow mosaic virus, CV- Coefficient of variation, CD-Critical difference @ 5%

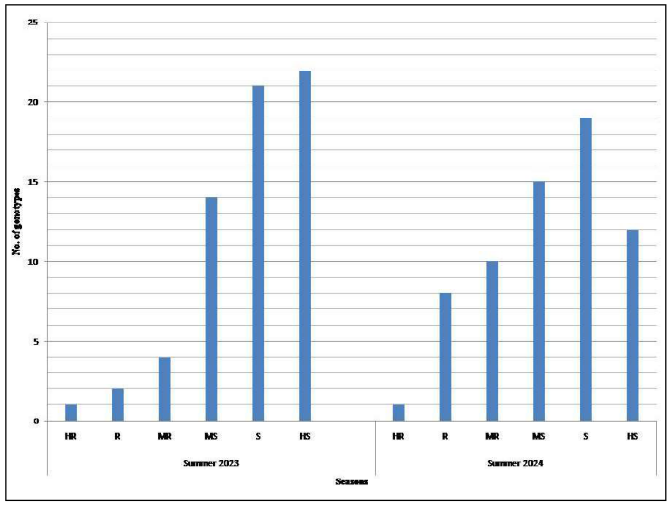
Table 4. Response of mungbean genotypes to Mungbean yellow mosaic virus diseases during summer 2023 and summer 2024

Sl No	Genotypes	MYMV			
		Summer 2023		Summer 2024	
		DI	Class	DI	Class
1	IPM 2-14 (C-1)	15.00	MR	19.11	MR
2	DGGV 2 (C-2)	53.33	HS	63.43	HS
3	TARM 1(C-3)	25.00	MS	37.32	S
4	*Vignatrilobata*(C-3)	0.00	HR	0.00	HR
5	DGGV 231	53.85	HS	29.33	MS
6	DGGV 12	40.00	S	18.43	MR
7	DGGV 213-1	27.78	MS	27.31	MS
8	GG-K-21-3	47.06	S	47.87	S
9	5-BRD-11	50.00	HS	54.74	HS
10	DGGV 96	36.00	S	13.63	MR
11	DGGV 119	57.14	HS	30.71	MS
12	8 BRD 9	6.25	R	2.13	R
13	DGGV 128	70.00	HS	35.26	S
14	DGGV 73	16.67	MR	21.57	MS
15	Karihesaru	22.22	MS	52.51	HS
16	DGGV 21	72.22	HS	45.00	S

17	DGGV 188	69.23	HS	35.26	S
18	DGGV 252	40.00	S	32.31	S
19	IPM 2-03	35.00	S	34.67	S
20	DGGV 215-1	15.79	MR	12.60	MR
21	IPM 2-17	30.43	MS	60.00	HS
22	GPM 19	50.00	HS	41.41	S
23	DGGV 184	30.00	MS	36.14	S
24	DGGV 191	52.00	HS	54.74	HS
25	DGGV 225	39.13	S	70.53	HS
26	DGGV 229	26.67	MS	30.71	MS
27	DGGV 223	33.33	S	70.53	HS
28	DGGV 228	66.67	HS	62.11	HS
29	DGGV 178	72.22	HS	58.05	HS
30	Virat	1.00	HR	1.78	R
31	IPM 19-9	44.44	S	19.86	MR
32	DGGV 75	30.00	MS	29.59	MS
33	DGGV 1	34.78	S	23.28	MS
34	DGGV 251	33.33	S	38.72	S
35	DGGV 126	50.00	HS	26.10	MS
36	DGGV 84	45.00	S	56.60	HS
37	DGGV 219	57.89	HS	58.52	HS
38	DGGV 59	21.74	MS	33.21	S
39	5MBRD 98	38.89	S	47.97	S
40	PDM 54	13.04	MR	25.49	MS
41	PANT MUNG 4	24.00	MS	33.21	S
42	PUSA 9531	50.00	HS	5.20	R
43	PUSA VISHAL	30.43	MS	35.26	S
44	IPM 99-125	45.00	S	13.26	MR
45	TMB 37	26.09	MS	45.00	S
46	HUM 16	48.00	S	51.67	HS
47	MH 2-15	52.63	HS	25.24	MS
48	PANT MUNG 6	46.67	S	12.92	MR
49	KM 2241	53.85	HS	9.00	R
50	IPM 2-3	44.00	S	24.09	MS
51	PUSA 0672	73.91	HS	15.79	MR
52	IPM 410-3 (SHIKHA)	34.62	S	20.70	MR
53	LGG 460	27.78	MS	43.75	S
54	PANT MUNG 5	39.13	S	31.09	S
55	TM 96-2	40.00	S	39.23	S
56	SML 832	65.22	HS	22.21	MS
57	MH 3-18	30.00	MS	8.10	R
58	CO-4	47.37	S	25.88	MS
59	CO-6	53.85	HS	23.41	MS
60	HUM 1	61.54	HS	11.54	MR
61	COGG 912	60.00	HS	8.60	R
62	VARSHA 2K-14-9	23.08	MS	27.79	MS
63	TBG 104	28.00	MS	3.00	R
64	SAMRAT(PDM 139)	50.00	HS	47.33	S

C1, C2, C3, C4 – Checks, HR- Highly resistance, R- Resistant, MR- Moderately Resistant, MS- Moderately Susceptible, S- Susceptible, HS- Highly Susceptible, DI – Per cent disease incidence.

14 showed moderately resistant response. IPM 2-14 is MYMV resistant variety released by IIPR, Kanpur during 2011. However, complete resistance of IPM 2-14 to MYMV was reported by several workers (Mohan *et al.,*2014;Suman *et al.,* 2015; Dharani, 2022 and Saable *et al.*, 2024). In contrast, the susceptible checks, DGGV 2 displayed highly susceptible response to MYMV indicating strong disease incidence during both the summer seasons. Susceptibility of DGGV2 to MYMV was reported earlier by several workers *viz.*, Mogali *et al.* (2017);



HR- Highly Resistant, R- Resistant, MR- Moderately Resistant, MS- Moderately Susceptible, S- Susceptible, HS- Highly Susceptible

Fig.1. Number of genotypes in different classes of MYMV during summer 2023 and summer 2024

Virat (Resistant) | **8 BRD 9 (Resistant)** | ***Vignatrilobata* (Resistant check)** | **DGGV 2 (Susceptible check)**

Plate 1. Images showing response of identified resistant genotypes along with checks

Dharani, (2022) and Amita, (2024). Another susceptible check, TARM 1 showed moderately susceptible response to MYMV as reported earlier by Saable *et al.*, (2024). The consistent disease response of check genotypes confirms their roles as reference genotypes for screening test genotypes for MYMV resistance.

Evaluation of test genotypes to MYMV resistance during both summer 2023 and summer 2024 (Table 4 and Table 5) revealed that only two genotypes *viz,*Virat and 8-BRD-9 consistently demonstrated resistant response to MYMV, highlighting their potential as stable sources of MYMV resistance. Virat was released by Indian Institute of Pulse Research (IIPR) Kanpur, for resistance against MYMV and recently Dharani (2022) also reported that Virat showed resistant against MYMV which supported our study. 8-BRD-9 was also released for its resistance against MYMV by Banaras Hindu University (BHU) Varanasi. DGGV 251-1 maintained a moderately resistant response, since it is developed by crossing IPM 2-14 with IPM 2-17 where, one of its parents IPM 2-14 is resistant against MYMV. The previous researchers were also identified some of the MYMV resistant genotypes *viz.,*Pathak and Jhamaria (2004) found two resistant lines (ML-5 and MUM 2) among fourteen mungbean varieties, while screening against

Table 5. Grouping of genotypes based on their response to MYMV disease during summer 2023 and summer 2024

	MYMV	
	Summer 2023	Summer 2024
Highly resistant0 (0 - 00%)	*Vigna trilobata* (1)	*Vigna trilobata* (1)
Resistant 1(1 - 10%)	8 BRD 9, Virat (2)	Virat, PUSA 9531, KM 2241, MH 3-18, COGG 912, TBG 104, 8 BRD 9. (8)
Moderately resistant 2(11-20%)	PDM 54, IPM 2-14, DGGV 215-1, DGGV 73. (4)	HUM 1, DGGV 215-1, PANT MUNG 6, IPM 99-125, DGGV 96, PUSA 0672, DGGV 12, IPM 2-14, IPM 19-9, IPM 410- 3 (SHIKHA), (10)
Moderately susceptible 3(21-30%)	TARM 1, DGGV 59, Karihesaru, VARSHA 2K-14-9, PANT MUNG 4, TMB 37, DGGV 229, DGGV 213-1, LGG 460, TBG 104, DGGV 184, DGGV 75, MH 3-18, IPM 2-17, PUSA VISHAL. (14)	DGGV 73, SML 832, DGGV 1, CO-6, IPM 2-3, MH 2-15, PDM 54, CO-4, DGGV 126, DGGV 213-1, VARSHA 2K-14-9, DGGV 231, DGGV 75, DGGV 119, DGGV 229. (15)
Susceptible 4(31 – 50%)	DGGV 223, DGGV 251, IPM 410-3 (SHIKHA), DGGV 1, IPM 2-03, DGGV 96, TARM 1, 5MBRD 98, DGGV 225, PANT MUNG 5, DGGV 12, DGGV 252, TM 96-2, IPM 2-3, IPM 19-9, DGGV 84, IPM 99-125, PANT MUNG 6, DGGV 128, DGGV 188, PUSA VISHAL, GG-K-21-3, CO-4, HUM 16. (21)	PANT MUNG 5, DGGV 252, DGGV 59, PANT MUNG 4, TARM 1, IPM 2-03, DGGV 184, TARM 1, DGGV 251, TM 96-2, GPM 19, LGG 460, DGGV 21, TMB 37, SAMRAT (PDM 139), GG-K-21-3, 5MBRD 98. (19)
Highly susceptible 5(>50%)	5-BRD-11, GPM 19, DGGV 126, PUSA 9531, SAMRAT (PDM 139), DGGV 191, MH 2-15, DGGV 231, KM 2241, CO-6, DGGV 119, DGGV 219, DGGV 2, COGG 912, HUM 1, SML 832, DGGV 228, DGGV 188, DGGV 128, DGGV 21, DGGV 178, PUSA 0672. (22)	HUM 16, Karihesaru, 5-BRD-11, DGGV 191, DGGV 84, DGGV 178, DGGV 219, IPM 2-17, DGGV 2, DGGV 228, DGGV 225, DGGV 223. (12)

Values in the parenthesis in second and third column indicates the number of genotypes
MYMV - Mungbean Yellow Mossaic Virus, HR- Highly Resistant, R- Resistant, MR- Moderately Resistant, MS- Moderately Susceptible, S- Susceptible, HS- Highly Susceptible.

MYMV. Similarly, Bhaskar *et al*. (2016) also identified five entries (KMP-35, MGG-360, MGG-373, MGG-385 and MGG 395) which are resistant to MYMV.The rest of the genotypes showed varied response to MYMV incidence during summer 2023 and summer 2024 (Table 4). During summer 2023, fourteen genotypes showed moderately susceptible, twenty one genotypes showed susceptible and twenty two genotypes showed highly susceptible reaction. Similarly in summer 2024, ten genotypes were moderately resistant, fifteen were moderately susceptible, nineteen were susceptible and twelve were highly susceptible to MYMV (Fig. 1). The variation in disease response (Fig. 1) among the mungbean genotypes attributed to seasonal and regional differences. According to Mohan *et al.* (2014), different strains of MYMV can cause different reactions from the same genotypes in different locations. The disease response was also depends on vector populations (white fly), climatic conditions, and genetic behaviour of the genotypes. Hence identification of genotypes with stable resistance across the different seasons and different locations is prerequisite for improvement of mungbean genotypes with durable MYMV resistance.

Conclusion

In breeding programs the multi-seasonal evaluation of different accessions helps to identify the selection of stable resistant sources. The identified genotypes *viz*, Virat and 8-BRD-9 could be used as a prime resistant donor in breeding program aiming for MYMV resistance. The highly susceptible accessions can be used as susceptible checks in screening programs.

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