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Evaluation of Mungbean (*Vigna radiata* L.) genotypes for resistance to Mungbean Yellow Mosaic Virus (MYMV) under natural conditions

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Abstract— *Mungbean (Vigna radiata (L.) R. Wilczek) is an essential grain legume crop valued for its nutritional profile, rich protein content, and soil-enriching nitrogen-fixing capacity. Despite the crop's adaptability and rapid growth cycle, Mungbean Yellow Mosaic Virus (MYMV) remains the most economically devastating biotic threat to commercial mungbean production. Consequently, identifying resistant genotypes is essential to develop sustainable disease management strategies n this study, 64 mungbean genotypes, comprising 62 testing entries and two standard checks were evaluated under natural field conditions during summer 2023 to identify potential sources of genetic resistance. Based on disease severity scores, the genotypes were categorized into distinct resistance categories. The screening revealed that 6 entries (GGG 156, GGG 163, GGG 168, GGG 169, GGG 170, and GGG 171) were completely free/immune to the virus. Additionally, 8 genotypes exhibited a highly resistant (HR) reaction, including the resistant check IPM 2-14, while 15 and 12 genotypes were classified as resistant (R) and moderately resistant (MR), respectively. Conversely, 9 genotypes showed moderate susceptibility (MS), 14 genotypes were found susceptible (S) including the susceptible check LGG-450), and no entries fell under the highly susceptible (HS) category. The identification of these stable resistant sources provides valuable donor material for marker-assisted selection and breeding programs aimed at developing MYMV resistant mungbean cultivars.*

Keywords— ***Mungbean (Vigna radiata), Mungbean Yellow Mosaic Virus (MYMV), screening/, Disease resistance***

I. INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek) is a fast-growing pulse crop with high nutritional and economic importance, widely cultivated across South and Southeast Asia (Mukhtar, S. and Mohamad, E.A.A, 2022). Its grains contain approximately 51% carbohydrates, 24–26% protein, 4% minerals, and 3% vitamins, making it an important dietary protein source in predominantly cereal-based, subtropical diets (Shilpa *et. al.,* 2024). Beyond nutrition, mungbean fixes atmospheric nitrogen through symbiotic root rhizobia, enriching soil fertility In India alone, it was cultivated over 3.787 million hectares during 2023–24 with a total production of 2.916 million tonnes (Kiranakumara *et. al.,* 2025). Mungbean yellow mosaic virus (MYMV) belongs to the genus *Begomovirus* (family *Geminiviridae*) and cause yellow mosaic disease (YMD) across Asian mungbean-growing regions, with MYMV predominant in southern India and MYMIV in northern, central, and eastern India (Bharsakale *et.al.,* 2024).

Yield losses from MYMV range from 10% to 100% depending on the crop growth stage at infection,

virus strain, mungbean genotype, and environmental interactions (Shilpa *et. al.,* 2024). Chemical management of MYMV relies on reducing whitefly vector populations through insecticide sprays which is economically unsustainable and ecologically harmful. Consequently, identifying and breeding inherently resistant host genotypes is the most viable, eco-friendly, and cost-effective strategy to mitigate these viral diseases. This study aims to evaluate and screen diverse mungbean entries to identify reliable sources of resistance against MYMV.

II. MATERIALS AND METHODS

The experiment was conducted under natural field conditions during the summer, 2023. A total of 62 mungbean genotypes along with resistant check (IPM 2-14) and one susceptible check (LGG-450) were evaluated for resistance to mungbean yellow mosaic virus (MYMV) using an Augmented Completely Randomized Block Design (ACRBD) and an infector-row technique, with no insecticide application to allow natural vector build-up and disease spread.

2.1 Disease rating Scale for Scoring Yellow Mosaic Virus Disease (1-9 scale)

Disease severity is typically scored using 1-9 scale to categorize genotypes reaction based on the extent of yellow mosaic symptoms observed on the foliage. The scoring criteria were as follows.

Table 1: The rating scale for scoring Mungbean Yellow Mosaic Virus disease (Alice and Nadarajan, 2007)

Grade	Description	Reaction
1	No visible symptoms on leaves or very minute yellow specks on leaves	Free
2	Small yellow specks with restricted spread covering 0.1-5% leaf area	Highly Resistant (HR)
3	Mottling of leaves covering 6-10% leaf area	Resistant (R)
4	Yellow mottling covering 11-15% leaf area	Moderately resistant (MR)
5	Yellow mottling and discolouration of 15-20% leaf area	Moderately susceptible (MS)
6	Yellow coloration of 21-30% leaves and yellow pods	Susceptible (S)
7	Pronounced yellow mottling and discoloration of leaves and pods, reduction in leaf size and stunting of plants covering 30-50% 0f foliage	Susceptible (S)
8	Severe yellow discoloration of leaves covering 50-75% of foliage, stunting of plants and reduction in pod size	Highly susceptible (HS)
9	Severe yellowing of leaves covering above of foliage, stunting of plants and no pod formation	Highly susceptible (HS)

III. RESULTS AND DISCUSSION

3.1. Phenotypic Evaluation and Disease Progress

Total 62 mungbean entries along with two checks (IPM 2-14 as the resistant check and LGG-450 as the susceptible check) were evaluated under natural field screening conditions during summer, 2023. Phenotypic reactions against the Mungbean Yellow Mosaic Virus (MYMV) were categorized using the 1–9 modified disease rating scale proposed under AICRP on MULLaRP. Disease scoring commenced when more than 80% of the susceptible plants exhibited clear, systemic visual symptoms, ensuring that the phenotypic expressions captured reflected accurate genetic responses under high disease pressure.

The performance of IPM 2-14 as a resistant check (Score 2) validates the reliability of the screening set, as this line has repeatedly been reported as stably resistant across diverse studies and seasons (Kiranakumara *et al.,* 2025). By contrast, the high score of LGG-450 as a susceptible check aligns with standard MYMV screening protocols, where susceptible controls are intentionally included to ensure adequate disease pressure and to discriminate resistance classes reliably (Ramarao *et al.,* 2021).

The evaluation revealed wide phenotypic variation among the tested material, spanning from complete immunity to high susceptibility. Total 62 genotypes were partitioned into different distinct reaction categories (Table 2).

Table 2. Screening of mungbean entries against viral diseases during Summer, 2023

S. No.	Entry	MYMV score (1-9 scale)	S.No.	Entry	MYMV score (1-9 scale)
1	GGG 95	3	33	GGG 144	5
2	GGG 101	3	34	GGG 145	5
3	GGG106	5	35	GGG 146	6
4	GGG107	3	36	GGG 147	3
5	GGG108	3	37	GGG 148	2
6	GGG109	5	38	GGG 149	2
7	GGG110	4	39	GGG 150	3
8	GGG 113	6	40	GGG 151	3
9	GGG 118	6	41	GGG 152	3
10	GGG 119	6	42	GGG 153	4
11	GGG 116	6	43	GGG 154	4
12	GGG 120	6	44	GGG 155	2
13	GGG 121	6	45	GGG 156	1
14	GGG 123	6	46	GGG 157	2
15	GGG 122	5	47	GGG 158	5
16	GGG 124	6	48	GGG 159	4
17	GGG 127	3	49	GGG 160	4
18	GGG 128	4	50	GGG 161	4
19	GGG 129	4	51	GGG 162	7
20	GGG 130	3	52	GGG 163	1
21	GGG 131	6	53	GGG 164	6
22	GGG 132	4	54	GGG 165	5
23	GGG 133	4	55	GGG 166	4
24	GGG 134	3	56	GGG 167	2
25	GGG 136	2	57	GGG 168	1
26	GGG 137	3	58	GGG 169	1
27	GGG 138	2	59	GGG 170	1
28	GGG 139	3	60	GGG 171	1
29	GGG 140	3	61	LGG-460	5
30	GGG 141	3	62	TM 96-2	6
31	GGG 142	5		LGG-450 (S. Check)	7
32	GGG 143	4		IPM 2-14 (R. Check)	2

3.2. Grouping and Distribution of Genotypes based on MYMV Reaction

Among the 62 test entries, 6 entries (GGG 156, GGG 163, GGG 168, GGG 169, GGG 170, and GGG 171) were found to be completely Free/Immune (Grade 1) from the disease, showing no visible symptoms on their foliage. Exceptional field resistance was noted in 7 test entries along with the resistant check IPM 2-14, which were classified as Highly Resistant (Grade 2) due to highly restricted, minor yellow specks occupying less than 5% of the individual leaf

area (GGG 136, GGG 138, GGG 148, GGG 149, GGG 155, GGG 157, and GGG 167) (Table 3).

The largest segment of the resistant block fell under the Resistant (Grade 3) designation, comprising 15 entries that exhibited mottling of leaves covering 6-10% leaf area. Additionally, 12 entries exhibited Moderately Resistant (Grade 4) profiles with scattered yellow patches covering 11–15% of the leaf surfaces.

Table 3. Grouping of mungbean genotypes based on their reaction to MYMV during summer, 2023 under natural field conditions.

Grade	Disease Severity / Reaction	No. of Entries	Entries
1	Free / Immune	6	GGG 156, GGG 163, GGG 168, GGG 169, GGG 170, GGG 171
2	Highly Resistant (HR)	8	GGG 136, GGG 138, GGG 148, GGG 149, GGG 155, GGG 157, GGG 167, **IPM 2-14 (R. Check)**
3	Resistant (R)	15	GGG 95, GGG 101, GGG 107, GGG 108, GGG 127, GGG 130, GGG 134, GGG 137, GGG 139, GGG 140, GGG 141, GGG 147, GGG 150, GGG 151, GGG 152
4	Moderately Resistant (MR)	12	GGG 110, GGG 128, GGG 129, GGG 132, GGG 133, GGG 143, GGG 153, GGG 154, GGG 159, GGG 160, GGG 161, GGG 166
5	Moderately Susceptible (MS)	9	GGG 106, GGG 109, GGG 122, GGG 144, GGG 142, GGG 145, GGG 158, GGG 165, LGG-460
6	Susceptible (S)	12	GGG 113, GGG 116, GGG 118, GGG 119, GGG 120, GGG 121, GGG 123, GGG 124, GGG 131, GGG 146, GGG 164, TM 96-2,
7	Susceptible (S)	2	GGG 162, **LGG-450 (S. Check)**
8-9	Highly Susceptible (HS)	0	None
	Total	**64**	**(62 Entries + 2 Checks)**

Vulnerability to the virus expanded within the remaining germplasm lines. Eight genotypes including the commercial line LGG-460 manifested moderately susceptible (Grade 5) symptoms, showcasing severe chlorotic patches across 15–20% of their canopy. Definitive, heavy systemic breakdown was verified in 14 genotypes clustered into the Susceptible (Grades 6 and 7) group. Genotypes in Grade 6 suffered from vast chlorosis (21–30% leaf area) alongside distinct yellowing of the pods, whereas GGG 162 and the check LGG-450 (Grade 7) exhibited severe plant stunting and drastic leaf shrinkage. Notably, no genotype advanced into the Highly Susceptible bounds (Grades 8 and 9), indicating the absence of total reproductive failure or absolute biomass collapse among the screened entries.

The identification of a distinct subset of resistant genotypes within a broader population characterized by intermediate and susceptible reactions is a central finding of this study. This pattern aligns with repeated field evaluations demonstrating that natural MYMV resistance is relatively uncommon, with the majority of germplasm tending to cluster into susceptible, highly susceptible, or intermediate categories under natural epiphytotic conditions (Jyothi *et al.,* 2020).

The presence of entries scoring 1 and 2 holds considerable agricultural importance because host resistance remains the most practical and economical strategy for managing MYMV, a begomovirus transmitted by *Bemisia tabaci* that is capable of causing severe yield losses in mungbean. Multiple studies therefore recommend that field-identified resistant lines be advanced as donor parents for breeding programs, quantitative trait locus (QTL) discovery, marker development, and multi-location validation, rather than being judged from a single season alone (Ambarish *et al.,* 2023).

Some genotype-specific disagreements with existing literature are nevertheless expected. For example, LGG-460 has been reported as susceptible in one inheritance study but moderately resistant in another field screening, demonstrating that genotypic reactions can shift with location, season, inoculum load, and vector pressure

(Saable *et al.,* 2024). Similar instability has been documented more broadly, field resistance often weakens under cage inoculation, whitefly-mediated artificial transmission, graft inoculation, or diverse hotspot environments, indicating that symptom-based field resistance typically reflects partial resistance rather than complete immunity (Madhumitha *et al.,* 2020).

Although the biological basis of resistance in the superior entries cannot be inferred directly from the score table alone, prior work suggests that resistant genotypes frequently combine favorable morphological and biochemical traits. These include higher levels of phenolics, tannins, trichome density, and stronger antioxidant responses, coupled with lower sugar content and reduced stomatal density-related susceptibility signals (Kamireddy *et al.,* 2025). Recent marker studies further show that field resistance can be strengthened through molecular confirmation, as phenotypically identified resistant genotypes have been successfully validated using linked markers or resistance gene analogs (Dharajiya *et al.,* 2021).

Finally, inheritance studies explain why stable resistance is difficult to recover consistently. Evidence remains mixed across genetic backgrounds, with reports supporting either two dominant genes or a single recessive gene. This indicates that resistance architecture is genotype-dependent, which likely contributes to variable expression across populations and environments (Mahalingam *et al.,* 2018). This complexity, together with virus variation and quantitative effects, is a key reason why repeated screening across years and locations is necessary before nominating entries as durable MYMV-resistant donors (Saable *et al.,* 2024).

IV. CONCLUSION

In summary, the MYMV screening identified multiple resistant entries, most notably, six entries (GGG 156, GGG 163, GGG 168, GGG 169, GGG 170, and GGG 171) demonstrated complete immunity (Grade 1) with zero visible symptoms under high natural vector pressure while, confirming strong susceptibility in GGG 162 and LGG-450. These elite immune lines, alongside the seven highly resistant genotypes, are prime candidates for direct field deployment and parental selection. Utilizing these genetic resources in upcoming hybridization programs will accelerate the development of high-yielding, climate-resilient mungbean cultivars with durable resistance to MYMV. These preliminary resistant sources that warrant replicated, multi-season, and multi-location validation with phenotypic and molecular confirmation before use in resistance breeding.

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