

## Evaluation of Mung Bean (*Vigna Radiate L.*) Germplasm for Mung Bean Yellow Mosaic Virus Disease

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### Abstract

Mung bean yellow mosaic virus (MYMV) is one of the most important diseases affecting mung beans, transmitted by the whitefly (*Bemisia tabaci*). MYMV poses a significant threat to mung bean production, emphasizing the need to identify resistant genotypes for the development of effective disease control strategies. In this study, we screened 60 mung bean germplasm under field conditions during the Yala season of 2022 to identify stable MYMV-resistant lines. Infector rows were planted alongside the test entries, and disease incidence and severity were observed under natural conditions. The genotypes studied were categorized as highly resistant to highly susceptible, with none of the test entries appearing to be highly resistant. We identified MIMB 909, MIMB 913, MIMB 916, MIMB 918, MI 7, MIMB 907, MIMB 908, MIMB 911, MIMB 912, MIMB 914, MIMB 923, MIMB 926, MIMB 933, MIMB 937, MIMB 938, MIMB 941, MIMB 945, MIMB 982, and MIMB 983 as resistant and moderately resistant genotypes, respectively. These genotypes could serve as parental lines in a mung bean breeding program focused on developing more MYMV-resistant varieties. Further studies are needed to evaluate the stability of resistance in these genotypes across multiple growing seasons and locations. The research contributes Valuable insight into the dynamics of MYMV infection in mung bean providing a foundation for developing disease-resistant varieties and sustainable crop management strategies. Consequently, in the near future, the improved varieties may surfeit the sustainable agriculture production in the biotic stress prone areas.

**Keywords:** Germplasm, Mung bean, Mung bean Yellow Mosaic Virus, Resistance, Screen

### I. INTRODUCTION

The mung bean (*Vigna radiata L.*) is one of the most important edible legume crops, grown on more than 6 million ha worldwide (about 8.5% of the global pulse area) and consumed by most households in Asia. Due to its characteristics of relatively drought-tolerant, low-input crop, and short growth cycle (70 days or so), the mung bean is widely cultivated in many Asian countries (concentrated mainly in China, India, Bangladesh, Pakistan, and some Southeast Asian countries) as well as in dry regions of southern Europe and warmer parts of Canada and the United States (Dahiya et al., 2015). In the predominantly cereal-based diets of China and India, the mung bean has been consumed as a common food for centuries. The mung bean contains balanced nutrients, including protein, dietary fiber, minerals, vitamins, and significant amounts of bioactive compounds (Gan et al., 2017)

In mung bean, yellow mosaic disease (YMD) caused by yellow mosaic viruses (YMV) is of key importance especially in South and Southeast Asia. Besides mung bean, YMD also affect various leguminous crops including black gram (*Vigna mungo*), moth bean (*Vigna aconitifolia*), Lima bean (*P. lunatus*), pigeon pea (*Cajanus cajan*), French bean (*Phaseolus vulgaris*), cowpea (*Vigna unguiculata*), Dolichos (*Lablab purpureus*), horse gram (*Macrotyloma uniflorum*), and soybean (*Glycine max*) (Ramesh, Chouhan and Ramteke, 2017; Dikshit et al., 2020).

In India, MYMV was first reported from the mung bean fields of Indian Agricultural Research Institute (IARI), New Delhi during 1950s (Nariani, 1960). In general, MYMV is the major isolate infecting mung bean crop in western and

southern India, Thailand, and Indonesia; whereas, MYMIV isolate in central, eastern and northern India, Pakistan, Bangladesh, Nepal, and Vietnam (Malathi and John, 2009). With this background, this review systematically deals with the scientific developments about YMV's infecting mung bean, its vector and also various YMD management challenges including the prospective use of recent tools like omics approaches and translational genomics, across the world.

One of the main reasons for insufficient production is low productivity due to the high incidence of diseases, the unavailability of suitable mung bean varieties for rain-fed conditions for third-season cultivation, and the unavailability of quality seeds.

Aphids, whiteflies, leafhoppers, trips, stem flies, pod bugs, and pod borer complexes are the most significant pests that attack mung beans. Among these, whiteflies act as vectors of mung bean yellow mosaic virus (MYMV) (Sekar and Nalini, 2017). It is found to spread the Begomo viruses, the major hazard to the flourishing production of mung bean in India, Sri Lanka, Pakistan, Bangladesh, Papua New Guinea, Philippines, and Thailand (Haq et al., 2011).

## II. METHODOLOGY

### A. Study Area

This experiment was conducted at Field Crop Research and Development Institute (FCRDI), Mahailippallama (8.1152° N and 80.47199° E) during Yala season of 2022 (May to September). It is in the DL1b agro ecological region, at elevation of 138 m above mean sea level in the North Central Province of Sri Lanka. The average annual rainfall of this area is less than 1750 mm and the temperature range is 25 °C to 35 °C.

### B. Planting Materials

Exotic and local mung bean germplasms (including recommended variety MIMB 07) available in Field Crops Research and Development Centre, were evaluated under field condition.

### C. Land Preparation and Mung Bean Planting

The mung bean germplasms were planted with the spacing of 30 cm X 10 cm on the plots having the

size of 3 m X 3 m in Randomized Complete Block Design (RCBD) with two replications.

One row of the most MYMV susceptible species called "*Lathoroid*" was planted in every other row of tested entries as infester rows. Plants of the trial were not treated with chemicals to obtain the maximum chance of primary infection. To estimate the yield reduction due to viral infestation, infested as well as non-infested plants of the same genotype should be available.

All the genotypes were established in a nearby field with no viral infestation achieved by chemical control of whitefly only in the central region as estimation in yield reduction in all three regions becomes tedious. The genotypes in the non-infested field was established as similar to the infested field but without the susceptible check in every other row.

### D. Crop Management Practices

All management practices including fertilizer application were performed as per the Department of Agriculture (DOA) recommendations. Urea, Muriate of potash (MOP) and Triple superphosphate (TSP) were applied as basal dressing before seed planting at the rate of 30 kg/h, 75 kg/h and 100 kg/h respectively. Top dressing was done 5 weeks after planting using urea at the rate of 35 kg/h, and weeding was done manually at two weeks interval after planting.

### E. Data Collection

#### 1) Weather data:

Daily weather data of rain fall, maximum and minimum temperature relative humidity and wind velocity were collected.

#### 2) Disease incidence:

Disease reaction of germplasms were recorded using 1 – 9 scale (Singh et al, 2004) at two weeks interval after first symptom observed. To offer a comprehensive overview of disease incidence across all genotypes, it was calculated the mean Disease Incidence (DI) and mean Disease severity index (DSI) values. DI reflects the percentage of plants exhibiting disease symptoms out of the total number of plants evaluated. Meanwhile, the mean DSI value furnishes an average measure of disease symptom severity encompassing all genotypes. DSI and percentage disease incidence (PDI) were recorded using the following formulas.

$$PDI = \frac{\text{Total number of infected plants of genotype}}{\text{Total number of plants of genotype}} \times 100$$

$$DSI = \frac{\text{Sum of the numerical rating}}{\text{total no. of leaves observed} \times \text{maxi. grade}} \times 100$$

#### F. Data Analysis

Rank or/and scale data were pre-transformed before analysis using a pre-transformed scale. When interactions were significant, they were further evaluated using response curves or further analysis using variance component methods. DMRT was used to separate means wherever necessary and other relevant statistical tools such as Microsoft Excel were used.

### III. RESULTS AND DISCUSSION

According to the analysis results in the Table 01 there has been significant ( $p \leq 0.05$ ) differences between the genotypes. Variety MIMB 913 (7.10) was very effective in mung bean yellow mosaic virus and it showed the lowest Disease Severity Index Percentage (7.10). Variety NIMB 910 showed the highest Disease Severity Index Percentage (52.24) and it was highly susceptible in mung bean yellow mosaic virus under field conditions. The genotypes classified into six categories based on the severity of disease infection recorded. Out of the 60 genotypes studied, none were classified as highly resistant to disease, while four were classified as resistant and fifteen as moderately resistant.

Meanwhile, twenty-one genotypes were moderately susceptible to disease, eighteen were susceptible, and two were highly susceptible. The severity of disease infection varied among the genotypes, with some showing high disease severity and others showing low disease severity. The genotypes with the highest disease severity were identified as MIMB 909, MIMB 913, MIMB 916, and MIMB 918, as shown in Table 01.

Conversely, the genotypes with the lowest disease severity were identified as MIMB 919 and MIMB 910. Overall, the study provides insights into the disease resistance of different mung bean genotypes and can help guide future efforts to develop more disease-resistant varieties of mung bean. Screened a set of 60 genotypes and observed the absence of disease symptoms in these genotypes until the crops reached five weeks of age under field conditions during the Yala season in 2022. Subsequently, symptoms of MYMV

disease began to manifest on the leaves of young plants of susceptible varieties, and these symptoms progressively intensified over time. By the fifth week of planting, a few genotypes exhibited initial signs of MYMV symptoms, which escalated in prevalence up to the eighth week, at which juncture, all genotypes displayed symptomatic features. The study assessed the Disease Severity Index (DSI) values across the genotypes, ranging from 0 to 9, signifying the extent of MYMV disease symptom severity. DSI values were ascertained by evaluating the disease symptom levels on each genotype, utilizing a scale from 0 (indicating no symptoms) to 9 (indicating severe symptoms).

The mean DI and mean DSI values, have been visually depicted in Figure 01. Altogether, this study provides valuable insights into the resistance of mung bean genotypes to MYMV disease under field conditions. These insights can offer guidance for the development of mung bean varieties that are more resistant to this disease.

In Figure 02, the illustration portrays the impact of variations in climate parameters on disease incidence (DI) and disease severity index (DSI). The results reveal that minimum temperature, maximum temperature, and wind velocity exerted no significant influence on DI and DSI. Conversely, both rainfall and relative humidity exhibited a highly significant effect on both DI and DSI.

The study discerned that whiteflies thrived and were most prevalent during periods of elevated rainfall and reduced humidity, potentially contributing to an escalated disease spread rate.

In a similar study conducted by S. Mohan, A. Sheeba, E. Murugan, and S. M. Ibrahim in India, several mung bean genotypes were identified as displaying resistance to MYMV. These genotypes, which encompass TM-11-07, TM-11-34, PDM-139, IPM-02-03, IPM-02-14, Pusa-0672, Pusa-0871, CO-7, and MH-521, hold promise as potential donors for the development of MYMV-resistant lines. This discovery bears significant implications, as it offers valuable insights for the advancement of mung bean varieties with enhanced disease resistance.

IV. CONCLUSION

This study has successfully pinpointed various mung bean genotypes showcasing diverse levels of resistance to MYMV. Among the genotypes analyzed, MIMB 909, MIMB 913, MIMB 916, and MIMB 918 have demonstrated high resistance, while MI 7, MIMB 907, MIMB 908, MIMB 911, MIMB 912, MIMB 914, MIMB 923, MIMB 926, MIMB 933, MIMB 937, MIMB 938, MIMB 941, MIMB 945, MIMB 982, and MIMB 983 have been categorized as moderately resistant genotypes. These identified genotypes hold significant promise as potential parental lines

within a mung bean breeding program aimed at cultivating more MYMV-resistant varieties.

Such an endeavor has the potential to substantially mitigate the occurrence and severity of the disease, ultimately resulting in improved crop yields and enhanced food security. Nevertheless, it is imperative to conduct further research to assess the stability of resistance in these genotypes across various growing seasons and geographical locations.

Table 01: Reaction of Mung Bean Lines to Mung Bean Yellow Mosaic Virus

Lines name	DSI %	Reaction	Lines name	DSI %	Reaction
MIMB 913	7.10	R	MIMB 939	26.03	MS
MIMB 918	9.50	R	MIMB 974	26.52	MS
MIMB 909	9.69	R	MIMB 924	26.74	MS
MIMB 916	9.89	R	MIMB 903	27.81	MS
MIMB 914	11.51	MR	MIMB 927	28.34	MS
MIMB 908	14.66	MR	MIMB 940	28.48	MS
MIMB 937	15.32	MR	MIMB 972	28.80	MS
MIMB 945	16.60	MR	MIMB 986	28.96	MS
MIMB 923	17.81	MR	MIMB 978	30.03	MS
MIMB 926	17.83	MR	MIMB 905	30.70	MS
MIMB 911	17.90	MR	MIMB 988	32.12	S
MIMB 941	17.92	MR	MIMB 981	33.18	S
MIMB 982	18.15	MR	MIMB 944	33.68	S
MIMB 938	19.00	MR	MIMB 936	33.72	S
MIMB 912	19.61	MR	MIMB 930	33.96	S
MI 07	19.76	MR	MIMB 920	35.21	S
MIMB 933	20.15	MR	MIMB 979	36.23	S
MIMB 983	20.17	MR	MIMB 917	36.24	S
MIMB 907	20.28	MR	MIMB 942	36.61	S
MIMB 922	21.33	MS	MIMB 931	37.21	S
MIMB 943	21.88	MS	MIMB 921	37.45	S
MIMB 932	22.18	MS	MIMB 985	39.03	S
MIMB 991	22.72	MS	MIMB 901	39.81	S
MIMB 973	23.27	MS	MIMB 906	40.48	S
MIMB 952	23.57	MS	MIMB 902	41.83	S
MIMB 929	24.45	MS	MIMB 980	43.08	S
MIMB 934	25.31	MS	MIMB 915	44.30	S
MIMB 935	25.50	MS	MIMB 987	47.91	S
MIMB 904	25.75	MS	MIMB 919	51.84	HS
MIMB 990	25.99	MS	MIMB 910	52.24	HS

R= Resistant, MR= Moderate resistant, MS= moderate susceptible, S= Susceptible, HS= Highly susceptible

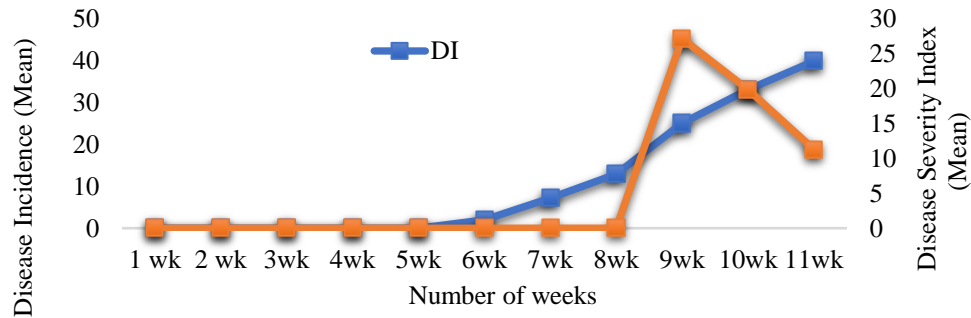


Figure 01: Weekly progress of mean percentage disease incidence (PDI) and mean Disease severity index (DSI) of MYMV in mung bean genotype

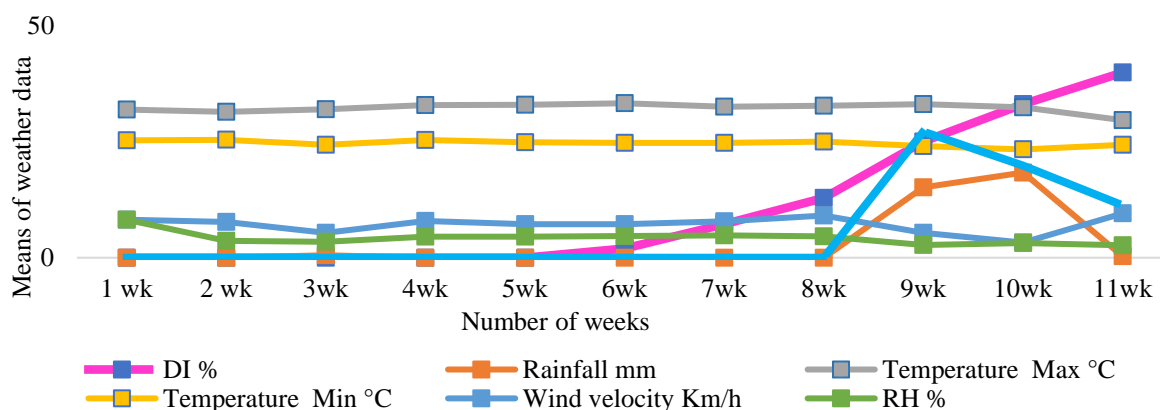


Figure 02: Effect of the climate parameters on Disease incident (DI) and Disease Severity index (DSI) during field evaluation

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