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Research Paper

Response of mungbean genotypes for resistance against mungbean yellow mosaic virus

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ABSTRACT

Mungbean yellow mosaic virus (MYMV) is an important viral disease across mungbean growing areas and causes severe yield loss in mungbean especially during the spring/summer season. The present study was envisaged to identify MYMV donors in mungbean. A total of 104 mungbean genotypes were evaluated for MYMV under natural field conditions during summer, 2019. The results revealed that MYMV severity ranged from 0% to 100% among mungbean genotypes. Out of 104 genotypes, 32 genotypes were completely free from MYMV, two genotypes exhibited resistant reaction (R), 22 genotypes were found moderately resistant (MR) and the remaining 48 genotypes were susceptible to highly susceptible reaction to MYMV. Thus, the identified 34 promising lines of mungbean were further evaluated against MYMV along with susceptible check DGGV-2 under epiphytotic conditions during the summer of 2020 and 2021. Pooled data of MYMV over the two years indicated that six genotypes namely, IPM-1205-2, IPM-2-14, IPM-410-3, IPM-14-10, IPM-205-7 and IPM-1604-1 were showed stability for MYMV resistance. These identified stable resistant genotypes will serve as potential donors for the mungbean breeding program to develop resistance cultivars.

Key words: Mungbean, Genotypes, MYMV, Resistance source

INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek) commonly known as moong or green gram belongs to the family *Fabaceae*. It finds a unique place in different cropping systems across the world due to its shorter life cycle, and high per-day productivity. It can increase soil fertility through symbiotic nitrogen fixation (Singh *et al.* 2020). Mungbean has a wider adaptability being cultivated in spring, summer, and rainy seasons and contributes enormously in food and nutritional security for the vegetarian population (Abhimanyu and Revanappa 2021). The mungbean seeds have a high amount (up to 28%) of easily digestible quality proteins. Its grains are easy to cook and lack flatulence factors in contrast to other legumes (Sahoo *et al.* 2003). In addition, it also contains iron (5.9-7.6 mg), fat (1-3 %), carbohydrates (50.4 %), fibers (3.5-4.5 %) (Krishna and Modi 2023, Pratap *et al.* 2021) and calcium and phosphorus are 132 mg and 367 mg per 100 grams of seed, respectively (Dahiya *et al.* 2015). India is the leading producer and consumer of mungbean with around 55% of the world's total area and 45% of the world's total production (Kumar *et al.* 2023). The major growing states of the mungbean are Rajasthan, Maharashtra, Madhya Pradesh, Karnataka, Odisha, and Bihar. The crop yield is mainly affected by both biotic and abiotic stresses. Among the biotic factors, the Yellow Mosaic Disease (YMD) caused by the Mungbean Yellow Mosaic Virus (MYMV) is of major economic significance. YMD caused by Begomoviruses (family Geminiviridae, genus Begomovirus) has emerged as the major threat to mungbean cultivation especially during the spring-summer season. This disease currently is a major threat to the production of mungbean in India, Sri Lanka, Pakistan, Bangladesh, Philippines, and Thailand (Singh *et al.* 2020). The economic losses due to this virus account up to 85% in green gram which is spreading faster towards newer areas (Karthikeyan *et al.*, 2014). Losses due to YMD depend on the stage of infection, late infection causes a 32%–78% reduction in mungbean grain yield, and infection at early growth stages may even lead up to 100% yield loss (Khattak *et al.* 2000). Managing white flies through the use of insecticides is mostly practiced to manage this disease. However, achieving complete disease management through this approach remains unachievable. The wide host range, virus variation, and quantitative inheritance make it more challenging to breed YMD-resistant mungbean cultivars. Therefore, to contain the spread of the disease, identifying and growing resistant genotypes is a viable strategy. Therefore, the evaluation of genotypes for resistance against mungbean yellow mosaic virus (MYMV) is the need of the hour, which can compensate for the aforesaid problem through its use in developing new resistant MYMV varieties with that of susceptible high-yielding varieties by using different breeding methods. With this endeavor, the present investigation was carried out during the summer of 2019 - 2021 under natural field conditions at IIPR, Regional Centre, Dharwad to identify stable resistant sources for MYMV disease.

MATERIALS AND METHODS

The field experiment was conducted at ICAR-Indian Institute of Pulses Research, Regional Research Centre, Dharwad during the summer of 2019-21 under natural field conditions by following the recommended package of practices. The experiment was laid out in a randomized block design and each genotype was sown in two rows of four-meter length with a spacing of 30 × 10 cm. The plant material consisted of 104 genotypes received from IIPR, Kanpur. The yellow mosaic disease (YMD) severity was recorded by following a 0-9 scale (Mayee and Datar 1986). The recorded grade values were converted into percent Disease Index (PDI) by using the following formula proposed by Wheeler (1969).

$$\text{Percent disease index} = \frac{\text{Sum of the individual disease ratings}}{\text{No. of leaves observed} \times \text{Maximum disease grade}} \times 100$$

RESULTS AND DISCUSSION

Among the various diseases infecting mungbean, yellow mosaic disease (YMD) remains a major threat to mungbean production, thus identifying promising cultivars possessing resistance to mungbean yellow mosaic virus (MYMV) is a top priority for most *Vigna* crops (Mishra et al. 2020, Pratap et al. 2021, Singh et al. 2020). It is recognized as the most destructive and devastating viral disease. The affected plants flower sparsely and the pod contains shriveled seeds and yield loss up to 80-90% reported in susceptible cultivars. In several cases, leaves and other plant parts become completely yellow and the losses may be as high as 100% (Kirti and Vinod 2019, Pathak and Jhamaria 2004, Mohan *et al*. 2014).

The use of host plant resistance is the most viable approach to alleviate viral disease in mungbean. Continuous evaluation of mungbean genotypes against MYMV disease is very much essential to identify stable sources of resistance (Mohan *et al*. 2014).

In the present investigation, 104 mungbean genotypes were screened against mungbean yellow mosaic viral disease (MYMV) incidence under natural field conditions during summer 2019-2021. The genotypes used in the present study showed a varied range of disease reactions. The percent disease severity ranged from 0 to 100%. These results are in confirmation with the previous studies conducted by Karthikeyan *et al*. (2014) and Vijaya Bhaskar (2017) they also reported that MYMV disease incidence in green gram germplasm lines ranged from 0% to 100%.

The response of tested mungbean genotypes varied differently against MYMV, 32 genotypes viz., PDM-139, IPM-205-7, IPM 410-3, SML-668, ML-2056, IPM 2-14, ML818, TMB-37, CO-5, TARM-1, VBN -3, Pant Mung-6, AVMU 1617, AVMU 1635, AVMU 1649, AVMU 1655, AVMU 1656, AVMU 1659, AVMU 1676, AVMU 1683, AVMU 1688, AVMU 1689, AVMU 1690, BARI MUNG-2, BARI MUNG-3, BARI MUNG-4, BARI MUNG-5, BARI MUNG-6, BARI MUNG-7, IPM-14-10, IPM-1604-1, IPM-1205-2 was free from infection (Scale 0), While, two genotypes viz., MH 3-18 and AVMU-1657 showed resistant (R) reaction with less than 1 % disease severity (scale 1) (Table 1) and 22 genotypes found moderately resistant (MR) reaction (scale 2-3) to MYMV disease (Table 2). It was previously reported that the same genotypes showed different reactions to MYMV in different locations, due to the existence of different strains of the virus (Mohan *et al*, 2014). Other possible causes for different responses might be due to the heavy load of vector populations (white fly), climatic conditions, and genetic behavior of different genotypes. Similar resistance responses against YMD were reported by Pathak and Jhamaria (2004), who evaluated fourteen mung bean varieties for MYMV resistance and identified two resistant lines (ML-5 and MUM-2). Vijaya Bhaskar *et al. (*2017) reported five resistant entries viz., KMP-35, MGG-360, MGG-373, MGG-385 and MGG 395 for YMD. In the present study, a total of 48 genotypes were showed susceptible to highly susceptible reactions (Table 2 & 3). Further,

Table. 1. List of mungbean genotypes with immune or resistance reaction to MYMV during 2019

Genotypes	Disease score	Reaction
PDM-139	0	I
IPM 205-7	0	I
IPM 410-3	0	I
SML-668	0	I
ML-2056	0	I
IPM 2-14	0	I
ML818	0	I
TMB-37	0	I
CO-5	0	I
TARM-1	0	I
VBN (Gg)-3	0	I
Pant Mung-6	0	I
AVMU 1617	0	I
AVMU 1635	0	I
AVMU 1649	0	I
AVMU 1655	0	I
AVMU 1656	0	I
AVMU 1659	0	I
AVMU 1676	0	I
AVMU 1683	0	I
AVMU 1688	0	I
AVMU 1689	0	I
AVMU 1690	0	I
BARI MUNG-2	0	I
BARI MUNG-3	0	I
BARI MUNG-4	0	I
BARI MUNG-5	0	I
BARI MUNG-6	0	I
BARI MUNG-7	0	I
IPM-14-10	0	I
IPM-1604-1	0	I
IPM-1205-2	0	I
MH 3-18	1	R
AVMU 1657	1	R

Table 2. A list of mungbean genotypes revealed moderate resistant or moderately susceptible reactions to MYMV in 2019

Genotypes	scale	Reaction
Pant Mung-2	3	MR
YEZIN MUNGBEAN 11	3	MR
AVMU 1613	3	MR
AVMU 1648	3	MR
BARI MUNG-8	3	MR
AVMU 1650	3	MR
LGG-460	3	MR
AVMU 1647	3	MR
CELERA	3	MR
SML-1115	3	MR
MH-421	3	MR
Pusa Vishal	3	MR
AVMU 1604	3	MR
AVMU 1633	3	MR
Vamban-2	3	MR
AVMU 1619	3	MR
AVMU 1654	3	MR
AVMU 1641	3	MR
YEZIN MUNGBEAN 6	3	MR
AVMU 1606	3	MR
AVMU 1642	3	MR
AVMU 1626	3	MR
AVMU 1614	5	MS
MGG-351	5	MS
AVMU 1607	5	MS
GREEN DIAMOND	5	MS
AVMU 1643	5	MS
AVMU 1622	5	MS
AVMU 1627	5	MS
AVMU 1623	5	MS
AVMU 1651	5	MS
AVMU 1608	5	MS
AVMU 1609	5	MS
AVMU 1652	5	MS
CELRALL-AU	5	MS
YEZIN MUNGBEAN 14	5	MS
AVMU 1646	5	MS
AVMU 1645	5	MS

34 identified promising genotypes were evaluated during the summer of 2020 and 2021 under epiphytotic conditions to confirm the resistance to MYMV disease. The results revealed (Pooled data over the years) that, 25 genotypes showed susceptible reactions and four genotypes revealed moderately resistant reactions to MYMV during subsequent evaluation may be due to low disease pressure during the previous year of evaluation. Further, six genotypes namely IPM-2-14, IPM-410-3, IPM-14-10, IPM-1604-1, IPM-1205-2, and IPM-205-7) in subsequent years of evaluation showed stability in resistance. The genetic makeup of genotypes, and prevailing favorable environmental conditions such as varied temperature, rainfall, and dry spell experienced during the period under investigation can be cause for the susceptibility of most of these studied genotypes. It was previously reported (Bashir *et al.* 2006, Singh *et al.* 2000, Mohan *et al.* 2014) that large variability in the incidence and severity of YMD depends on variety, location, and year.

Table 3. List of mungbean genotypes revealed susceptible or highly susceptible reactions to MYMV in 2019

Genotypes	Scale	Reaction
AVMU 1618	7	S
AVMU 1636	7	S
AVMU 1625	7	S
AVMU 1616	7	S
DGGS-1	7	S
BU-MUNG-4	7	S
DGGS-4	7	S
AVMU 1610	7	S
AVMU 1612	7	S
AVMU 1653	7	S
AVMU 1602	7	S
AVMU 1603	7	S
AVMU 1637	7	S
YEZIN MUNGBEAN 1	7	S
AVMU 1644	7	S
AVMU 1640	7	S
AVMU 1621	9	HS
WHITE GOLD	9	HS
AVMU 1628	9	HS
AVMU 1629	9	HS
AVMU 1634	9	HS
EMERALD	9	HS
YEZIN MUNGBEAN 9	9	HS
AVMU 1611	9	HS
AVMU 1631	9	HS
AVMU 1632	9	HS
AVMU 1638	9	HS
DELT	9	HS
SATIMILL	9	HS
AVMU 1620	9	HS
CRYSTAL	9	HS
DGGV-2 (Suceptible check)	9	HS

CONCLUSION

Yellow mosaic disease is a major virus disease in mungbean and its incidence has become severe in the past three years, particularly in the southern zone. It was reported that the MYMV strain (Mungbean Yellow Mosaic Virus) primarily occurs in the southern region of India, while the MYMIV strain (Mungbean Yellow Mosaic Indian Virus) prevails in the northern, central, and eastern regions of India (Mishra *et al.* 2020). In the present investigation, most of the genotypes showed susceptible reactions to MYMV, and six mungbean genotypes IPM-2-14, IPM-410-3, IPM-14-10, IPM-1604-1, IPM-1205-2, and IPM-205-7 identified as resistance to MYMV. These stable resistant genotypes could be utilized as donors in disease-resistance breeding programs to develop MYMV-resistant cultivars.

Table 4. Evaluation of selected mungbean genotypes against MYMV over the years (pooled data)

Genotypes	Disease score		Avg. score	Disease reaction
	2020	2021		
PDM-139	3	3	3	MR
IPM 205-7	1	1	1	R
IPM 410-3	1	1	1	R
SML-668	5	7	6	S
ML-2056	3	3	3	MR
IPM 2-14	1	1	1	R
ML818	3	3	3	MR
TMB-37	3	5	4	MS
CO-5	3	3	3	MR
TARM-1	3	5	4	MS
VBN (Gg)-3	3	5	4	MS
Pant Mung-6	3	5	4	MS
AVMU 1617	5	7	6	S
AVMU 1635	5	7	6	S
AVMU 1649	5	7	6	S
AVMU 1655	5	5	5	MS
AVMU 1656	5	7	6	S
AVMU 1659	7	7	7	HS
AVMU 1676	5	7	6	S
AVMU 1683	5	5	5	MS
AVMU 1688	5	7	5	MS
AVMU 1689	5	7	6	S
AVMU 1690	7	9	8	HS
BARI MUNG-2	5	7	6	S
BARI MUNG-3	5	5	5	MS
BARI MUNG-4	5	7	6	S
BARI MUNG-5	5	5	5	MS
BARI MUNG-6	3	7	5	MS
BARI MUNG-7	3	5	4	MS
MH 3-18	5	5	5	MS
AVMU 1657	5	5	5	MS
IPM-14-10	1	1	1	R
IPM-1604-1	1	1	1	R
IPM-1205-2	1	1	1	R
DGGV-2 (Susceptible check)	9	9	9	HS

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