

Original Research Article

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Screening of Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes for Resistance against Mungbean Yellow Mosaic Virus (MYMV) under Field Condition

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ABSTRACT

Mungbean [*Vigna radiata* (L.) Wilczek] is an important short duration grain legume which is grown in different parts of the country, for grain and green manure. It is an outstanding source of easily digestible proteins with low flatulence, which balances the staple rice diet in Asia. Mungbean yellow mosaic disease (MYMD) caused by whitefly (*Bemisia tabaci*) transmitted mungbean yellow mosaic virus (MYMV) is an important constraint of mungbean in India. Thirty five Indian mungbean genotypes were evaluated to identify the source of resistance against MYMV during *khari*f-2013. The per cent disease incidence (PDI) of MYMV among 35 mungbean genotypes was worked out up to ninth week after sowing and it varied from 0 to 84.96%. At maturity stage of crop (ninth week after sowing), mean PDI was 27.09% and mean disease severity index (DSI) was 2.73. Out of 35 mungbean genotypes, five were found highly resistant, six were resistant and seven were moderately resistant. While, eight genotypes were found moderately susceptible, seven were susceptible and two were highly susceptible. Five genotypes namely, Meha, Bada Mung 7, KM 2245, IPM 0205-7 and IPM 02-3 found highly resistant during present investigation which can be used for the development of mapping population for the development of MYMV resistant varieties.

Keywords

Mungbean [*Vigna radiata* (L.) Wilczek], MYMV, Field screening, Disease incidence

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Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is one of the most important pulse crops in India. In the traditional vegetarian diet of Indian

population, pulses occupy second place next to cereals and is the main source of protein, ranking after chickpea and pigeonpea. It is an important short duration grain legume which can be grown in varied environments, across

all three crop seasons viz., *kharif*, *rabi* and summer in different parts of the country, as sole or intercrop for grain and green manure (Robertson *et al.*, 2004). It is also known as greengram, green bean, moong, mash bean, golden gram and green soy. It is an excellent source of easily digestible proteins with low flatulence, which complements the staple rice diet in Asia (Saminathan, 2013). The center of origin for mungbean is not exactly known. However, according to Vavilov, (1926), it might have originated in India and the central Asiatic region (Dharajiyia *et al.*, 2017). Mungbean belongs to family *Leguminosae* and sub-family *Papilionaceae*. Mungbean is a self-pollinated diploid plant having $2n=2x=22$ chromosomes with a genome size of 0.60 pg/1C (579 Mb/1C) (Arumuganathan and Earle, 1991; Somta and Srinives, 2007).

Mungbean is grown throughout the Southern Asia, including India, Pakistan, Nepal, Burma, Bangladesh, Indonesia, Sri Lanka, Thailand, Vietnam, Malaysia, China and Philippines.

In India, the major mungbean growing states are Maharashtra, Gujarat, Tamil Nadu, Andhra Pradesh, Bihar, Uttar Pradesh, Rajasthan, Karnataka and Orissa (Singh *et al.*, 2010; Inbasekar, 2014). Mungbean was cultivated in about 3.38 million hectares during 2013-14 with a total production of 1.61 million tones and a productivity of 474 kg/ha in India (Anonymous, 2015). In Gujarat, the area under mungbean has been 1.83 lakh hectares with a total production of 1.06 lakh tones and a productivity of 579 kg/ha during 2013-14 (Anonymous, 2015).

India covers up to 55% of the total world acreage and 45% of total production and it leads Pakistan, Sri Lanka, Thailand and China. The average yield of mungbean is very low, not only in India but in the entire tropical and subtropical Asia (Rishi, 2009). The yield of mungbean has been stagnant over the years.

Improvement in the yield of mungbean is becoming difficult, mainly due to the occurrence of pests and diseases (Karthikeyan *et al.*, 2014). Major biological stresses of mungbean are mungbean yellow mosaic virus, leaf crinkle virus, anthracnose, powdery mildew, *Cercospora* leaf spot, gram pod borer, bruchid and whitefly (Pande *et al.*, 2000). Plant viral diseases cause serious economic losses in many major crops by reducing seed yield and quality (Kang *et al.*, 2005). Mungbean yellow mosaic disease (MYMD) is reported to be the most destructive viral disease among the various viral diseases, caused by yellow mosaic virus. Among the various diseases, the MYMD was given special attention because of severity and ability to cause yield loss up to 85%, which is spreading faster towards newer areas (AVRDC, 1998). Mungbean yellow mosaic virus causes severe yield reduction in all mungbean growing countries in Asia, including India. MYMV belongs to the family *Geminiviridae*. It is transmitted by whitefly (*Bemisia tabaci* Genn.). The whitefly is one of the most economically important pests in many tropical and subtropical regions (Karthikeyan *et al.*, 2014).

Incidence and management of the MYMV disease depend on the vector (whitefly) population, which in turn depends on environmental conditions (Alam *et al.*, 2014). However, pesticides can provide temporary management of whitefly, but do not give effective control of MYMD. A more efficient and environmentally safe long-term solution is the development of mungbean cultivars resistant to both virus and its vector, *B. tabaci*. A good deal of research efforts has been directed towards the screening of mungbean germplasm against MYMD (Akhtar *et al.*, 2011). Mungbean genotype evaluation against MYMD through exposing them to high inoculum by planting in natural hot spots has been a principal method; it may be prone to

errors as different responses were observed for the same genotypes in different years. Resistance in mungbean germplasm against MYMV has been recognized earlier by different workers by using a common acceptable scale based on the severity of the disease (Panduranga *et al.*, 2011; Paul *et al.*, 2013; Suman *et al.*, 2015; Khaliq *et al.*, 2017; Abrol and Sharma, 2018). Hence, the present investigation was carried out for the identification of MYMV resistant mungbean genotypes of India by field screening to identify the source of resistance against MYMV.

Materials and Methods

Experimental materials

Total thirty five mungbean genotypes used in the experiment are given in Table 1 and were procured from Pulses Research Station, SDAU, Sardarkrushinagar, Gujarat, India.

Field evaluation of mungbean genotypes against MYMV

The field evaluation of mungbean genotypes against MYMV was carried out at Pulses Research Station, SDAU, Sardarkrushinagar, during *Kharif*-2013. In the field experiment, each genotype was sown in a single row of 4 m length with spacing of 45cm × 15cm in two replications using a randomized block design (RBD). Recommended cultural practices were followed to express genetic potential without insecticide sprays to maintain optimum whitefly (vector) population for high inoculum pressure of MYMV pathogen. The crop was regularly monitored for the development of symptoms of the disease. For recording MYMV incidence, observations were recorded at an interval of one week up to nine weeks after sowing. Based on the severity of the MYMV incidence, the genotypes were grouped into different categories based on 0 -

5 scale given in Table 2 (Bashir, 2005). The per cent disease incidence (PDI) and disease severity index (DSI) for MYMV were determined in all the mungbean genotypes at weekly interval. The equation for the PDI is as follow.

$$PDI = \frac{\text{Total no. of infected plants of the genotype}}{\text{Total no. of plants of the genotype}} \times 100$$

Spread of the per cent increase in the PDI was the difference between weekly observations. The number of genotypes infected per week was calculated. Weather data that consisted of maximum and minimum temperature (°C), rainfall (mm) and relative humidity (%) were recorded at Meteorological Station, Agronomy instructional farm, SDAU, Sardarkrushinagar.

Statistical analysis

The data obtained from field experiments conducted using RBD with two replications was subjected to the statistical analysis as per procedure of RBD (Gomez and Gomez, 2012). The data in percentages were transformed using arcsine transformation prior to analysis.

Results and Discussion

The set of 35 mungbean genotypes were screened against MYMV under field conditions during *kharif*, 2013 season. No disease symptoms were observed on any of the genotype till the crop was two weeks old. Afterwards, the symptoms of MYMV disease started to appear on the leaves of young plants of susceptible varieties which became more pronounced with time. After three weeks of sowing, four genotypes started to show symptoms of MYMV which increased with time up to seventh weeks and after seventh week total genotypes showing symptoms were 30 which were constant with time up to harvesting (Figure 1).

Table.1 Mungbean genotypes used in the experiment

Sr. No.	Name of genotype	Centre responsible for developing
1	Vamban 2	National Pulses Research Centre (NPRC), Vambam
2	COGG 912	Tamil Nadu Agricultural University (TNAU), Coimbatore
3	AKM 9904	Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola
4	IPM 02-3	Indian Institute of Pulses Research (IIPR), Kanpur
5	VGG rsil 1	National Pulses Research Centre (NPRC), Vambam
6	LGG 460	Andhra Pradesh Agricultural University (APAU), Lam
7	SML 1082	Punjab Agricultural University (PAU), Ludhiana
8	IPM 02-17	Indian Institute of Pulses Research (IIPR), Kanpur
9	VGG rt 1	National Pulses Research Centre (NPRC), Vambam
10	Kopergaon	Agricultural Research Station, Kopergaon
11	VGG ru 1	National Pulses Research Centre (NPRC), Vambam
12	DGG 1	University of Agricultural Sciences (UAS), Dharwad
13	IPM 409-4	Indian Institute of Pulses Research (IIPR), Kanpur
14	MH 2-15	Chaudhary Charan Singh Agricultural University (CCSAU), Hisar
15	IPM 0205-7	Indian Institute of Pulses Research (IIPR), Kanpur
16	MH 3-18	Chaudhary Charan Singh Agricultural University (CCSAU), Hisar
17	M2 1451	Punjab Agricultural University (PAU), Ludhiana
18	Sona Mung 1	Bidhan Chandra Krishi Viswa Vidyalaya (BCKV), Mohanpur
19	Pusa 0871	Indian Agricultural Research Institute (IARI), New Delhi
20	Pusa 672	Indian Agricultural Research Institute (IARI), New Delhi
21	IPM 02-19	Indian Institute of Pulses Research (IIPR), Kanpur
22	KM 2245	Chandra Shekhar Azad University of Agriculture and Technology(CSAUAT), Kanpur
23	MH 521	Chaudhary Charan Singh Agricultural University (CCSAU), Hisar
24	RMG 991	Rajasthan Agricultural Research Institute (RARI), Durgapura
25	Pusa 9531	Indian Agricultural Research Institute (IARI), New Delhi
26	HUM 1	Banaras Hindu University (BHU), Varanasi
27	Vamban 1	National Pulses Research Centre (NPRC), Vambam
28	Pusa Ratna	Indian Agricultural Research Institute (IARI), New Delhi
29	Bada Mung 7	INA
30	TM 96-2	Bhabha Atomic Research Centre (BARC), Mumbai
31	VC 1997-17	INA
32	Pant M 5	Govind Ballabh Pant University of Agriculture and Technology (GBPUAT), Pantnagar
33	Meha (IPM 99-125)	Indian Institute of Pulses Research (IIPR), Kanpur
34	GM 4	Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar
35	GM 3	Sardarkrushinagar Dantiwada Agricultural University (SDAU), Sardarkrushinagar

INA: Information not available

Table.2 Disease rating scale used for categorization of mungbean genotypes against MYMV (Bashir, 2005)

Disease scale	Percent infection	Infection category	Reaction group
0	All plants free of disease symptoms	Highly resistant	HR
1	1-10% infection	Resistant	R
2	11 - 20% infection	Moderately resistant	MR
3	21 - 30% infection	Moderately susceptible	MS
4	30 - 50% infection	Susceptible	S
5	More than 50% infection	Highly susceptible	HS

Table.3 Genotype wise appearance of MYMV disease

Weeks after sowing	Genotypes in which disease appeared for the first time	Total no. of genotypes
1	None of the genotype showed disease symptoms	-
2	None of the genotype showed disease symptoms	-
3	Vamban 2, AKM 9904, Sona Mung 1, Pusa Ratna	04
4	COGG 912, VGG rsil 1, SML 1082, IPM 02-17, Kopergaon, DGG 1, IPM 409-4, MH 2-15, MH 3-18, Pusa 0871, IPM 02-19, MH 521, HUM 1, Vamban 1, TM 96-2, VC 1997-17, Pant M 5, GM 3	18
5	VGG rt 1, M2 1451, Pusa 672, Pusa 9531	04
6	LGG 460, RMG 991, GM 4	03
7	VGG ru 1	01
Genotypes namely, Meha, Bada Mung 7, KM 2245, IPM 0205-7 and IPM 02-3 showed no disease symptoms up to 9th week		05
Total		35

Fig.1 Number of mungbean genotypes infected at weekly interval and in progressive mode

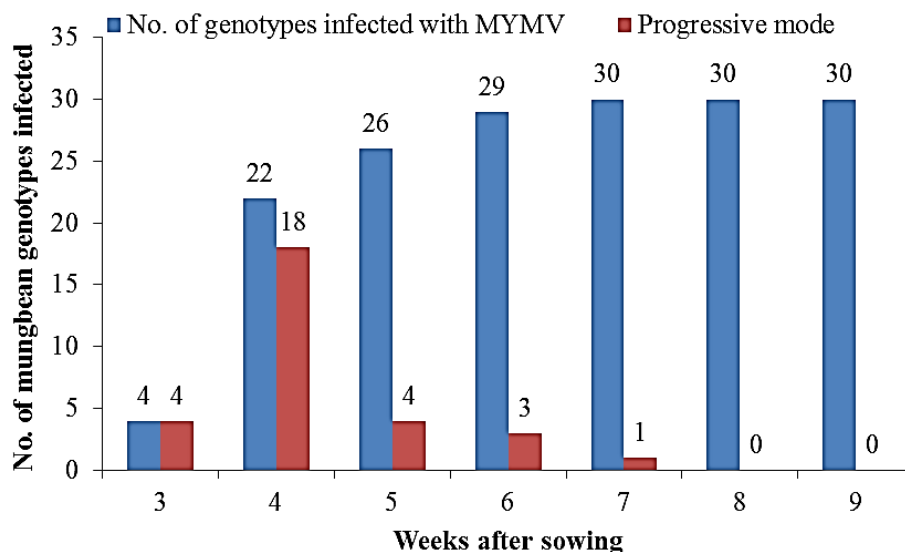


Table.4 PDI of MYMV on mungbean genotypes

Sr. No.	Name of genotype	PDI at maturity (after 9 weeks)*	Sr. No.	Name of genotype	PDI at maturity (after 9 weeks)*
1	Vamban 2	49.42 (44.67)	21	IPM 02-19	21.59 (27.67)
2	COGG 912	22.88 (28.56)	22	KM 2245	00.00 (04.06)
3	AKM 9904	39.94 (39.20)	23	MH 521	43.49 (41.26)
4	IPM 02-3	00.00 (04.06)	24	RMG 991	05.63 (13.72)
5	VGG rsil 1	36.90 (37.40)	25	Pusa 9531	19.09 (25.90)
6	LGG 460	02.91 (09.65)	26	HUM 1	43.51 (41.27)
7	SML 1082	24.61 (29.73)	27	Vamban 1	13.27 (21.36)
8	IPM 02-17	18.27 (25.27)	28	Pusa Ratna	84.96 (67.19)
9	VGG rt 1	28.65 (32.36)	29	Bada Mung 7	00.00 (04.06)
10	Kopergaon	27.51 (31.63)	30	TM 96-2	38.97 (38.62)
11	VGG ru 1	04.35 (12.01)	31	VC 1997-17	16.11 (23.66)
12	DGG 1	47.16 (43.37)	32	Pant M 5	19.53 (26.22)
13	IPM 409-4	09.20 (17.63)	33	Meha	00.00 (04.06)
14	MH 2-15	27.56 (31.66)	34	GM 4	07.92 (16.34)
15	IPM 0205-7	00.00 (04.06)	35	GM 3	12.13 (20.37)
16	MH 3-18	29.12 (32.65)	Mean PDI		27.09
17	M2 1451	09.94 (18.30)	S.Em.±		1.16
18	Sona Mung 1	59.25 (50.33)	CD (0.01)		3.45
19	Pusa 0871	29.39 (32.82)	CD (0.05)		2.57
20	Pusa 672	19.52 (26.19)	CV (%)		4.78

* = Mean of two replications; PDI = Per cent Disease Incidence; S.Em.± = Standard Error of mean; CV = Coefficient of Variation; CD (0.01) = Critical Difference at 1% level of significance; CD (0.05) = Critical Difference at 5% level of significance; Figures in parenthesis are square root transformation values

Fig.2 Weekly progress of mean PDI and mean DSI of MYMV in mungbean genotypes

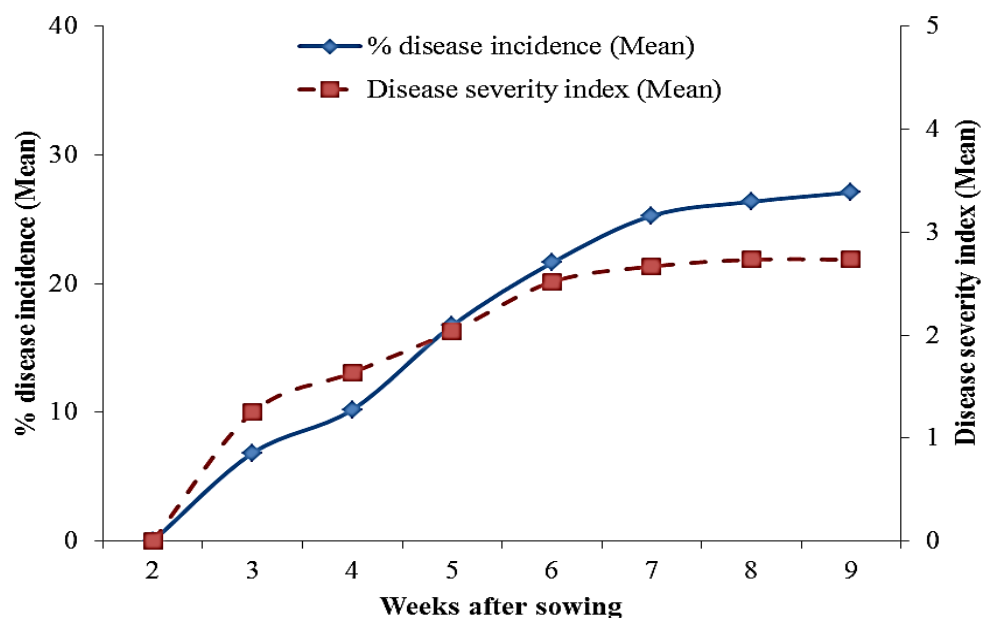


Table.5 Information on some environmental factors and occurrence of MYMV in mungbean genotypes

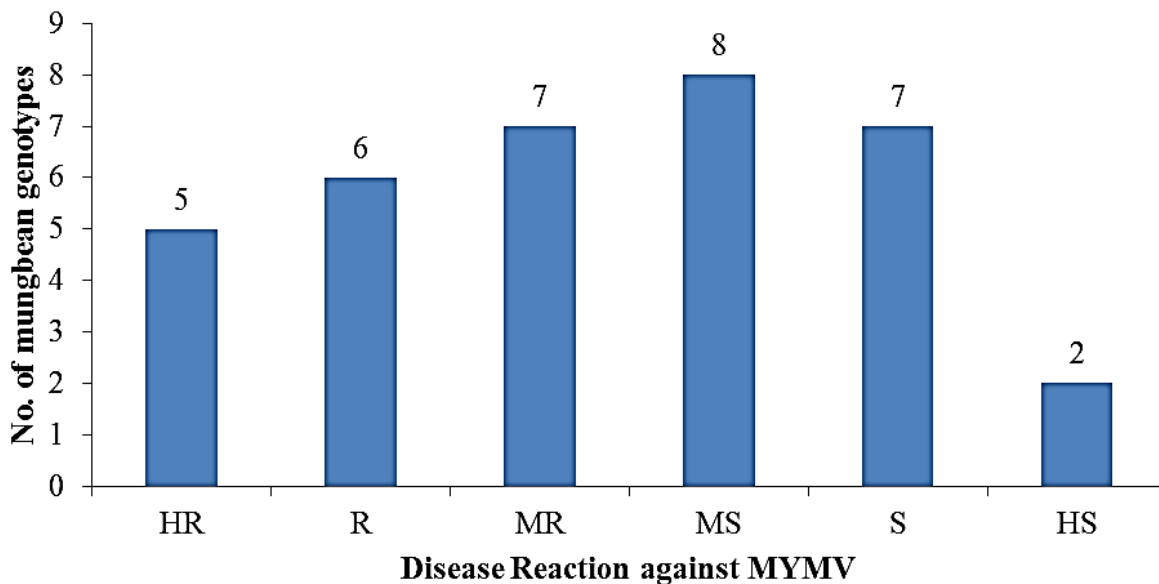
SMW	Weeks after sowing	Temperature (°C)			RH%		Rainfall (in mm)	Mean DSI	% incidence (mean PDI) of MYMV	% weekly increase in mean PDI	Remark/observation
		Max.	Min.	Avg.	RH1	RH2					
29	1	33.69	27.46	30.57	88	66	0	0.0	0	-	Sowing and germination
30	2	32.10	25.86	28.98	93	82	211.4	0.0	0	-	Landing of whitefly
31	3	31.26	25.21	28.24	96	86	43.4	1.25	6.84	-	Appearance of disease in susceptible genotypes
32	4	30.70	25.49	28.09	93	76	9.3	1.64	10.21	3.38	Spreading of disease in other genotypes
33	5	30.63	26.00	28.31	93	84	80.8	2.04	16.74	6.53	Maximum % weekly increase in PDI and severity
34	6	31.80	25.87	28.84	87	63	0	2.52	21.62	4.88	Fast increase in PDI and DSI
35	7	32.71	25.77	29.24	87	65	0	2.67	25.27	3.65	Fast spreading of disease
36	8	34.24	25.76	30.00	86	56	0	2.73	26.37	1.09	Very slow spreading of MYMV
37	9	37.20	27.14	32.17	90	46	0	2.73	27.09	0.73	Highest and regular infection at maturity of crop

Max.: Maximum; Min.: Minimum; Avg.: Average; RH: Relative Humidity (%); RH1: Relative Humidity (0700 LMT Obs.); RH2: Relative Humidity (1400 LMT Obs.); PDI: Per cent Disease Incidence; DSI: Disease Severity Index; SMW: Standard Meteorological Week

Table.6 Distribution of mungbean genotypes in various infection categories of MYMV

Reaction category	Disease severity	No. of genotypes	Genotypes
Highly Resistant (HR)	0	5	Meha, Bada Mung 7, KM 2245, IPM 0205-7, IPM 02-3
Resistant (R)	1	6	LGG 460, VGG ru 1, IPM 409-4, M2 1451, RMG 991, GM 4
Moderately Resistant (MR)	2	7	IPM 02-17, Pusa 672, Pusa 9531, Vamban 1, VC 1997-17, Pant M 5, GM 3
Moderately Susceptible (MS)	3	8	COGG 912, SML 1082, VGG rt 1, Kopergaon, MH 2-15, MH 3-18, Pusa 0871, IPM 02-19
Susceptible (S)	4	7	AKM 9904, VGG rsil 1, DGG 1, MH 521, HUM 1, TM 96-2, Vamban 2
Highly Susceptible (HS)	5	2	Pusa Ratna, Sona Mung 1

Fig.3 Number of mungbean genotypes categorized in different disease reaction against MYMV



However, the disease incidence was recorded up to nine weeks after sowing but disease score did not vary that much after seven weeks, though, the number of plants infected increased with time.

The symptoms of MYMV disease in different genotypes appeared at different time/weeks.

The disease symptoms were observed in some genotypes during early stage of the crop (third week after sowing); considered as susceptible to highly susceptible, based on observations up to nine weeks. The genotypes showing early symptoms were Vamban 2, AKM 9904, Sona Mung 1 and Pusa Ratna. Besides this, some genotypes *viz.*, LGG 460, RMG 991,

GM 4 and VGG ru 1 showed disease symptoms during later stage (sixth to seventh week). Overall genotype wise appearance of MYMV disease during each week of *kharif*, 2013 is given in Table 3. The PDI of the 35 mungbean genotypes was worked out up to ninth week and it varied from 0 to 84.96% after nine weeks. The PDI of each genotype after ninth week is given in Table 4. After nine weeks, maximum PDI was observed in Pusa Ratna (84.96%) followed by Sona Mung 1 (59.25%) indicating that they were highly susceptible to MYMV whereas, minimum PDI was recorded in Meha, IPM 02-3, KM 2245, Bada Mung 7 and IPM 0205-7 having 0% incidence of MYMV which lead them to categorize under highly resistant or immune genotypes among all the genotypes screened.

During *kharif*, 2013, different genotypes showed DSI between 0-5, in which, maximum DSI (5) was observed in Pusa Ratna and Sona Mung 1. However, no disease symptoms were observed in five genotypes namely, Meha, IPM 02-3, KM 2245, Bada Mung 7 and IPM 0205-7. To find out overall disease incidence of all the genotypes against MYMV, mean PDI and mean DSI were calculated and represented in Figure 2.

Results showed that MYMV disease appeared during third week after sowing and increased with time up to seventh week, after that PDI and DSI were almost constant. At ninth week after sowing, mean PDI was 27.09% and mean DSI was 2.73. Results showed that increase in mean DSI was higher during third and fourth weeks, followed by decreased rate of increase in DSI up to seventh week, which was increased up to a small degree after seventh week.

The results indicated that symptoms of MYMV on mungbean plants started to appear during third week, initiating development of the disease among the population. During

fourth week, per cent weekly increase in PDI was 3.38% indicating slow increase in disease incidence. Maximum per cent weekly increase in PDI was during fifth week (6.53%) due to increase in minimum temperature, mean temperature, relative humidity and rain fall. During sixth week, per cent weekly increase in PDI was 4.88% which might be due to increase in temperature. Per cent weekly increase in PDI during seventh week was 3.65% as the temperature and relative humidity were increased. Hence, conclusion may be drawn that increase in temperature and relative humidity increased the PDI of MYMV which resulted in fast spreading of MYMV disease in mungbean. Rainfall was observed during second week to fifth week of crop growth followed by no rainfall till ninth week of crop growth. It can be concluded that increase in PDI during third to fifth week might be due to limited rainfall coupled with high humidity and favourable environment for vector of MYMV. The information on the development of MYMV disease and some environmental factors during the experimental period is shown in Table 5.

On the basis of disease severity recorded, the mungbean genotypes were classified into six disease infection categories (Table 6). Out of 35 mungbean genotypes, five were found highly resistant, six were resistant and seven were moderately resistant. While, eight genotypes were found moderately susceptible, seven were susceptible and two were highly susceptible (Figure 3).

In the present study, out of 35 mungbean genotypes, developed from the different parts of the country, five genotypes namely, Meha, Bada Mung 7, KM 2245, IPM 0205-7, IPM 02-3 found highly resistant. These genotypes can be utilized in breeding program for the development of MYMV resistant varieties. Some researchers have tried to find out the

source of resistance against MYMV in mungbean but most of them got little success in India (Singh *et al.*, 1996; Awasthi and Singh, 2008; Salam *et al.*, 2009; Mohan *et al.*, 2014; Deepa *et al.*, 2017 and Nair *et al.*, 2017). Further work should be carried out at the different agro-climatic zones of India for more consecutive seasons to check the stable reaction of mungbean genotypes against MYMV. The number of genotypes should be increased for the field screening to find out more number of resistant genotypes. But the present study will provide the source of resistance against MYMV to carry out further breeding work to develop MYMV resistant variety.

Five genotypes namely, Meha, Bada Mung 7, KM 2245, IPM 0205-7, IPM 02-3 found highly resistant during present investigation which can be used for the selection of mungbean genotypes for the development of mapping population for molecular breeding, development of molecular markers, QTL identification for MYMV resistance, as well as development of MYMV resistant varieties. The present investigation also gives idea about the effect of weather conditions on the MYMV incidence.

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