Available online at www.ijpab.com

DOI: http://dx.doi.org/10.18782/2320-7051.2618

ISSN: 2320 – 7051

Int. J. Pure App. Biosci. **5 (2):** 1049-1056 (2017)

Research Article

International Journal of Pure & Applied Bioscience

OPEN ACCESS

Screening of Greengram Genotypes against Mungbean Yellow Mosaic Virus Diseases under Field Condition

Deepa, H.[1*], Govindappa, M. R.[1], Kenganal, M. [1], Kulkarni, S. A.[2] and Biradar, S. A.[3]

[1]Department of Plant Pathology, College of Agriculture, Raichur

[2]ARS, Bidar, UAS, Raichur

[3]AICRP on Linseed, MARS, Raichur

*Corresponding Author E-mail: deepah185@gmail.com

Received: 20.02.2017 | Revised: 24.02.2017 | Accepted: 25.02.2017

ABSTRACT

To identify sources of resistance against Mungbean Yellow Mosaic Virus (MYMV) screening was done under rainfed condition at MARS, Raichur during kharif 2015. Among one hundred and six genotypes tested, twenty five genotypes were procured from AVRDC (Asian Vegetable Research and Development Center), Legume section at ICRISAT (International Crops Research Institute for the Semi- arid Tropics) campus, Hyderabad and eighty one genotypes were collected from Agricultural Research Station, Bidar. The disease incidence varied from 12.4 to 86.4 per cent on tested genotypes. Further, tested genotypes were grouped into different categories based on 0-5 disease scale. None of the genotypes showed highly resistant and resistant reaction. But 19 genotypes showed moderate resistance reaction, 22 genotypes showed moderate susceptible reaction, 50 genotypes showed susceptible reaction and 15 genotypes showed highly susceptible reaction including susceptible check.

Key words: *MYMV, Screening, Genotypes, Begomovirus*

INTRODUCTION

Greengram (*Vigna radiata* (L.) Wilczek), it is also called as mungbean belongs to the family fabaceae, a good source of protein, carbohydrate, vitamin for human beings all over the globe. As greengram is an important short-duration grain legume, it is grown extensively in major tropical and subtropical countries of the world. Currently in India greengram is grown in an area of 34.4 lakh ha and production of 15 lakh tones with productivity of 407 kg ha-1 [2]. Although the crop is cultivated over a large extent, it is known to suffer by several biotic and abiotic factors which are considered as major yield limiting factors. Greengram suffers from several diseases with substantial losses in yield and it is affected with different fungal, bacterial and viral diseases[24], but viral diseases are serious threat to crop and among them, yellow mosaic disease caused by Mungbean Yellow Mosaic Virus (MYMV) appeared to be serious and widely spread in India, Pakistan, Bangladesh, New Guinea, Srilanka, Thailand, Philippines[1,5,9,12,13].

Cite this article: Deepa, H., Govindappa, M. R., Kenganal, M. , Kulkarni, S.A. and Biradar, S.A., Screening of Greengram Genotypes against Mungbean Yellow Mosaic Virus Diseases under Field Condition, *Int. J. Pure App. Biosci.* **5(2):** 1049-1056 (2017). doi: http://dx.doi.org/10.18782/2320-7051.2618

It was first reported by Nariani[17] at IARI (Indian Agricultural Research Institute), New Delhi with 20-30 per cent incidence. It was noticed that the crop infected at early stages, all the leaves exhibited yellow mosaic and complete yellowing with puckering symptoms[20]. MYMV causes irregular green and yellow patches in older leaves and complete yellowing of younger leaves. Infected plants produce fewer flowers and pods, pods often remain small contain few seeds that are malformed and discolour seeds that affecting yields qualitatively and quantitatively[7,19].

MYMV belongs to the genus begomovirus of the family Geminiviridae consists of viruses with circular, single-stranded (ss) DNA genomes. These are transmitted from plant-to-plant by whitefly (*Bemisia tabaci*). This virus cannot be transmitted through sap, seed, soil or mechanically but Thailand strain of this virus can be transmitted by mechanical inoculation[4,9,18,22]. Management through chemicals (insecticides, pesticides) control the population of whitefly inturn reduce disease incidence to some extent but complete destruction of virus is difficult and continuous use of these chemicals create a hazardous impact on surrounding environment. So, in this regard, identification of varieties that shows resistance to both virus and vector served as economically feasible approach in alleviation of disease severity and placed a prominent value in breeding programmes. Several efforts have been directed towards screening of greengram germplasm against MYMV to identify the resistant sources by using scale based disease severity[10,14,16,25].

MATERIALS AND METHODS

Screening was undertaken to test the reaction of various greengram germplasms against MYMV incidence under rainfed condition at MARS, Raichur during *kharif* 2015. Among one hundred and six genotypes tested, twenty five were procured from AVRDC (Asian Vegetable Research and Development Center), Legume section at ICRISAT (International Crops Research Institute for the Semi- arid Tropics) campus, Hyderabad and eighty one were collected from Agricultural Research Station, Bidar. These were sown in 30 x 10 cm spacing with Selection - 4 as a susceptible check (Infector row) after every 10 test entries. The recommended agronomic practices were followed and plots were irrigated whenever necessary except that insecticide sprays were not applied in order to encourage the population of whitefly for natural disease spreading . Per cent incidence of disease in each genotype/variety was calculated as below

$$\text{Per cent Disease Incidence (PDI)} = \frac{\text{Number of plants infected in a row}}{\text{Total number of plants in a row}} \text{x } 100$$

The genotypes were grouped into different categories based on 0 to 5 scale from highly resistant to highly susceptible according to Bashir[3].

Percent Disease Incidence	Infection Category	Reaction Group
All plants free of disease symptoms	Highly resistant	HR
1 - 10%	Resistant	R
11 -20%	Moderately resistant	MR
21-30%	Moderately susceptible	MS
30-50 %	Susceptible	S
More than 50%	Highly susceptible	HS

RESULTS

Evaluation of one hundred six greengram germplasms under natural conditions in UAS, Raichur against mungbean yellow mosaic virus (MYMV) was carried out on the basis of arbitrary scoring scale. The results revealed that there was a great variation among genotypes they showed differential disease reaction. All the genotypes were categorized into six classes based upon disease severity. Twenty five genotypes from AVRDC were screened for their reaction against MYMV disease during *kharif*, 2015 under field condition. The per cent disease incidence was recorded at every 15 days interval from 15 days after sowing. The symptoms of yellow mosaic started to appear on the susceptible check lines about 15-20 days after planting. Initially it produces scattered yellow specks of mild intensity were observed on young leaves in susceptible lines. After few days, alternate yellow and green patches developed on the first fully-formed trifoliate leaf. The intensity of disease increased with passage of time. In severe infection at the end of August, all the check lines turned completely yellow with 5-10 white flies per plant. Similar spread of yellow mosaic pattern has been reported by Jalaluddin and Sheikh[11]. The infected pods also turned yellow and a few shriveled seeds were observed. The results are presented in Table 1. The disease incidence varied from 13.8 to 86.4 per cent on tested genotypes. Further, tested genotypes were grouped into different categories based on 0-5 disease scale. None of the genotypes showed highly resistant and resistant reaction. The genotypes 18/01, 71/01, 116/01, 17/01, 70/01 and 29/01 showed 16.2, 15.1, 13.9, 14.8, 13.8 and 15.9 per cent disease incidence respectively and were grouped under moderately resistant and 39/01, 65/01, 87/01, 116/02, 37/01, EC693376, ML1628, NM94, 44/01, 118/01, 90/01, R2/116/01(12) showed moderately susceptible reaction. While 86/01, 97/01, 1-Dec, 111/01, ML 818, 42/01 and 42/02 were found to be susceptible for yellow mosaic disease with disease incidence of 33.2, 47.2, 41.3, 31.8, 43.7, 31.9 and 53.1 (Table 2) respectively. The variety Selection-4 was found highly susceptible with 86.4 per cent disease incidence. Due to planting of susceptible check between test entries it encourages good build-up of white fly. There were good chances of spread of disease minimizing the chances of disease escape. At the end of the experiment, all the check lines turned completely yellow showing maximum disease severity ensuring good evaluation of greengram germplasms against yellow mosaic.

Eighty one genotypes from ARS, Bidar were screened for their reaction against MYMV disease. The results are presented in Table 3. The disease incidence varied from 12.4 to 86.4 per cent. Among the tested once, 13 genotypes KMS 13-26, KM 13-13, KM 13-12, KMS 13-76, KMS13-73, KM 13-48, KM 13-26, TM 96-2, CO-6, DGGV-4, Local mung (more pods), TRCRM-24 and TRCRM-111 showed 15.1, 14.1, 18.8, 16.7, 18.3, 13.8, 18.4,13.9,14.6, 12.4, 15.8, 14.6 and 16.2 per cent disease incidence, respectively and were grouped under moderately resistant and 10 entries, GG 13-12, KMS 13-59, KGS-5, KM 13-44, KM 13-37, KM 13-16, KM 13-22, KM 13-08, KM 13-36, GG 13-8 showed moderately susceptible reaction to disease. While 43 entries (GG 13-11, KMS 13-26, KMS-13-61, KMS 13-57, Pusa Baisakhi, GG 13-9, TRCRM -4, GG 13-3, KM 13-32, SML-668, Bengaluru local, GG 13-7, GG 13-4, CG 13-1, KM 13-55, KM 13-18, KM 13-47, KM 13-54, KM 13-20, KM 13-30, KM 13-48, KM 13-41, KM 13-39, KM 13-23, MH 709, KMS 13-29, GG 13-10, GG 13-5, KMS 13-55, KMS 13-71, KM 13-02, KM 13-45, KM 13-09, KM 13-19, KM 13-42, KM 13-11, KM 13-05, Gangavati, TRCRM-26, TRCRM-17, TRCRM-36, TJM-3, TRCRM-37) showed susceptible and 15 entries (Shiningmung, GG 13-6, Chinamung, BGS-9, COGG-973, COGG-912, LGG-460, Selection-4, Pusa Baisakhi Sel, Local Mung (Tall), Local Mung (Vaddanakera), Shiningmung Sel, Yellow Mung Sel-1, Mung Sel-2, Yellow Mung Sel-2, Selection-4) showed highly susceptible reaction (Table 4).

DISCUSSION

Mungbean Yellow Mosaic Virus (MYMV) disease is the most destructive, which takes heavy toll in Indian subcontinent and adjacent areas of South-East Asia, causing upto 100 per cent losses in yield. So, identification of promising material through screening is one of the most ideal and durable method for exploiting resistance in disease management especially to virus diseases. In the present investigation a total of one hundred and six genotypes were screened during *kharif*, 2015 under rainfed conditions. None of the genotypes showed highly resistant and resistant reaction. nineteen genotypes showed moderate resistance reaction, twenty two genotypes showed moderates susceptible reaction, fifty genotypes showed susceptible reaction and fifteen genotypes showed highly susceptible reaction including susceptible check. Such a susceptible or resistant reaction was attributed to the genes present in the respective genotypes[17].

The variety selection-4 was found highly susceptible with 86.4 per cent disease incidence which is used as a susceptible check. The susceptible check lines after test entries resulted in enhanced vector population. The MYMV vector, whitefly (*Bemisia tabaci* Genn) appeared to inhabit plant soon after the emergence and remained till maturity and with the passage of time, disease severity increased significantly and favourable ernvironmental conditions for the disease development owing to the presence of enormous vector population in the field. High temperature from June to August favours the spread of the vector, which provides greater opportunity to multiply on the host. Due to inadequate plant protection measures, greengram is infested by whitefly and additional damage to this crop is caused by the MYMV transmitted by the whitefly vector[23]. Which makes the screening in natural field condition successful. Use of resistant varieties is one of best method which reduces both insect population and also diseases incidence. The results of present investigation was supported by Munawwar *et al*.[16] who tested 64 mungbean lines under field conditions, 6 were found resistant and 35 moderately resistant. Remaining lines exhibited susceptible reaction. Further, Mohan *et al.*[15] screened 120 germplasm lines under field condition during *kharif* 2013, among them none of the test entries appeared to be immune and genotypes EC 398897, TM-11-07, TM-11-34, PDM-139, IPM-02-03, IPM-02-14, Pusa-0672, Pusa-0871, CO-7 and MH-521 exhibited resistance reaction. Sudha *et al*.[25] found that out of 78 mungbean genotypes evaluated, only 28 genotypes were found resistant and 77 genotypes were found susceptible to MYMV. Iqbal *et al*.[10] evaluated and categorized one hundred genotypes/lines of mungbean germplasm, the differential response of mungbean lines to MYMV was determined and none of the genotype/line was found highly resistant to disease. However four genotypes/lines *i.e*., 014043, 014133, 014249, 014250 were found resistant. Eight were moderately resistant and 30 were moderately susceptible. Remaining 30 were classified as susceptible and 43 as highly susceptible. Similar type of the varietal evaluations were previously documented by several workers [6,8,14,1520,22] .

In general, considering the overall performance of genotypes during the season, none of the them exhibited highly resistant or immune reaction, majority of genotypes tested have recorded susceptible and highly susceptible reaction against MYMV. However the genotypes showing some degree of resistance should be tested again by artificial inoculation or at the hot spot areas like Koppal and Bidar districts that recorded high incidence during survey before including them in resistant breeding programme or recommending directly as resistant varieties. Selection-4 and chinamung greengram varietites popularly grown all over Karnataka was found highly susceptible during in recent year with incidence of 86.4 and 60 per cent during survey. The genotypes which showed resistant reaction may be used in MYMV resistance breeding programme and can be viewed as alternatives to selection-4 and chinamung in Karnataka.

Table 1: Screening of AVRDC greengram genotypes against MYMV during *kharif*, 2015

Sl. No.	Lines/ genotypes	Disease incidence (%)	Host reaction	Sl. No.	Lines/ genotypes	Disease incidence (%)	Host reaction
1	18/01	16.2	MR	14	90/01	22.3	MS
2	39/01	24.2	MS	15	111/01	31.8	S
3	65/01	28.1	MS	16	R2/116/01	24.8	MS
4	71/01	15.1	MR	17	118/01	29.1	MS
5	86/01	33.2	S	18	ML 818	33.7	S
6	87/01	22.5	MS	19	29/01	15.9	MR
7	97/01	37.8	S	20	42/01	31.9	S
8	116/01	13.9	MR	21	42/02	33.1	S
9	116/02	27.1	MS	22	44/01	21.9	MS
10	1-Dec	31.3	S	23	NM94	24.1	MS
11	17/01	14.8	MR	24	ML1628	21.9	MS
12	37/01	29.1	MS	25	EC693376	23.8	MS
13	70/01	13.8	MR	26	Selection-4	86.4	HS

S = Susceptible
MR = Moderately resistant
MS = Moderately susceptible
HS = Highly susceptible

Table 2: Grouping of AVRDC greengram genotypes screened against MYMV disease during *kharif*, 2015

Percent Infection	Infection Category	Reaction Group	Genotypes
All plants free of disease symptoms	Highly resistant	HR	-
1 - 10% Infection	Resistant	R	-
11 -20% infection	Moderately resistant	MR	18/01, 71/01, 116/01, 17/01, 70/01, 29/01(6)
21-30% infection	Moderately susceptible	MS	39/01, 65/01, 87/01, 116/02, 37/01, EC693376, ML1628, NM94, 44/01, 118/01, 90/01, R2/116/01(12)
30-50% infection	Susceptible	S	86/01, 97/01, 1-Dec, 111/01, ML 818, 42/01, 42/02 (7)
More than 50%	Highly susceptible	HS	Selection-4 (1)

Table 3: Screening of ARS, Bidar greengram genotypes against MYMV during *kharif*, 2015

Sl. No.	Genotypes/ lines	Disease incidence (%)	Host reaction	Sl. No	Genotypes/ lines	Disease incidence (%)	Host reaction
1	Shiningmung	53	HS	31	KMS 13 -76	16.7	MR
2	GG 13-12	28.1	MS	32	KM 13-22	29.8	MS
3	GG 13-6	58	HS	33	KMS 13-73	18.3	MR
4	GG 13-2	21.9	MS	34	GG 13-5	34.8	S
5	Chinamung	60	HS	35	GG 13-10	38.1	S
6	BGS-9	68.2	HS	36	KMS 13-29	35.8	S
7	GG 13-11	31.8	S	37	MH 709	49.1	S
8	KMS 13-26	15.1	MR	38	KM13-23	38.2	S
9	KMS 13-61	36.8	S	39	KM 13-I6	28.1	MS
10	KMS 13-57	39.1	S	40	KM 13-39	41.8	S
11	Pusa Baisakhi	37.7	S	41	KM 13-41	44.9	S
12	GG 13-9	42	S	42	KM 13 48	13.8	MR
13	TRCRM-4	41.9	S	43	KM 13-30	45.1	S
14	GG 13-3	35.8	S	44	KM 13-20	48.2	S
15	KM13 -32	32.9	S	45	KM 13-54	39.1	S
16	KMS 13 -24	15.4	MR	46	KM 13-47	34.3	S
17	SML- 668	34.1	S	47	KM 13-26	18.4	MR
18	Bengaluru local	38.2	S	48	KM13-18	34.8	S

19	GG 13-7	41.8	S	49	KM 13-37	29.1	MS
20	GG 13 -4	32.9	S	50	KM 13-55	48.5	S
21	KMS 13-59	29.1	MS	51	KM 13-02	32.5	S
22	CG 13-1	33.8	S	52	TM 96-2	13.9	MR
23	KM 13-13	14.1	MR	53	COGG-973	68.1	HS
24	KGS 5	25.8	MS	54	COGG-912	71.9	HS
25	KM 13-44	24.1	MS	55	CO-6	14.6	MR
26	KM 13-36	28.8	MS	56	GG 13-8	21.2	MS
27	KMS 13 -71	31.3	S	57	KM 13-45	46.3	S
28	KMS 13 -55	34.8	S	58	KM 13-09	41.2	S
29	KM 13-12	18.8	MR	59	LGG-460	58.8	HS
30	KM 13-08	25.4	MS	60	DGGV-4	12.4	MR

Contd…..

Sl. No.	Genotypes/ lines	Disease incidence (%)	Host reaction	Sl. No.	Genotypes/ lines	Disease incidence (%)	Host reaction
61	KM 13-19	32.8	S	72	Yellow mung Sel-1	70.9	HS
62	KM 13-42	38.00	S	73	TRCRM-26	35.8	S
63	KM 13-11	41.8	S	74	Mung Sel-25	64.7	HS
64	KM 13-05	44.8	S	75	TRCRM-17	35.4	S
65	Selection-4	86.4	HS	76	TRCRM-36	39.1	S
66	Pusa Baisakhi Sel	62.8	HS	77	Yellow mung Sel-2	63	HS
67	Local mung (Tall)	72.8	HS	78	TJM-3	32.8	S
68	Local mung (more pods)	15.8	MR	79	TRCRM-111	16.2	MR
69	Local mung (Vaddankera)	69.2	HS	80	TRCRM-37	35.8	S
70	Shiningmung Sel	59.1	HS	81	TRCRM-24	14.6	MR
71	Gangavati	41.2	S	82	Selection – 4	86.4	HS

S = Susceptible
MR = Moderately resistant
MS = Moderately susceptible
HS = Highly susceptible

Table 4: Grouping of ARS, Bidar greengram genotypes screened against MYMV disease during *kharif*, 2015

Disease Severity	Percent Infection	Infection Category	Reaction Group	Genotypes
0	All plants free of disease symptoms	Highly resistant	HR	-
1	1 - 10% Infection	Resistant	R	-
2	11 -20% infection	Moderately resistant	MR	KMS 13-26, KM 13-13, KM 13-12, KMS 13-76, KMS13-73, KM 13-48, KM 13-26, TM 96-2, CO-6, DGGV-4, Localmung (more pods), TRCRM-24, TRCRM-11(13)
3	21-30% infection	Moderately susceptible	MS	GG 13-12, KMS 13-59, KGS-5, KM 13-44, KM 13-37, KM 13-16, KM 13-22, KM 13-08, KM 13-36, GG 13-8 (10)
4	30-50 % infection	Susceptible	S	GG 13-11, KMS 13-26, KMS-13-61, KMS 13-57, Pusa Baisakhi, GG 13-9, TRCRM -4, GG 13-3, KM 13-32, SML-668, Bengaluru local, GG 13-7, GG 13-4, CG 13-1, KM 13-55, KM 13-18, KM 13-47, KM 13-54, KM 13-20, KM 13-

				30, KM 13-48, KM 13-41, KM 13-39, KM 13-23, MH 709, KMS 13-29, GG 13-10, GG 13-5, KMS 13-55, KMS 13-71, KM 13-02, KM 13-45, KM 13-09, KM 13-19, KM 13-42, KM 13-11, KM 13-05, Gangavati, TRCRM-26, TRCRM-17, TRCRM-36, TJM-3, TRCRM-37(43)
5	More than 50%	Highly susceptible	HS	Shiningmung, GG 13-6, Chinamung, BGS-9, COGG-973, COGG-912, LGG-460, Selection-4, Pusa Baisakhi Sel, Local Mung (Tall), Local Mung (Vaddanakera), Shiningmung Sel, Yellow Mung Sel-1, Mung Sel-2, Yellow Mung Sel-2, Selection-4 (15)

Acknowledgements

The above authors are highly thankful to Dr. Ramakrishnan M. Nair, Vegetable Breeder-Legume AVRDC, ICRISAT campus, Hyderabad and Dr. C. R. Konda, Professor (Genetics and plant breeding) and Head, ARS, Bidar for providing genotypes to my research work.

REFERENCES

1. Ahmad, M. and Harwood, R. F., Studies on a whitefly-transmitted yellow mosaic of urdbean (*Phaseolus mungo*). *Pl. Dis.,* **57:** 800-802 (1973).
2. Anonymos, 2014, *www. Indiastat.com*.
3. Bashir, M., Studies on viral disease of major pulse crops and identification of resistant sources. *Tech. Annu. Rep.* (April 2004 to June 2005) *of ALP*, p. 76 (2005).
4. Bos, L., Plant Viruses: Unique and Intriguing Pathogens: A Text Book of Plant Virology, Back huys Publishers, the Netherlands (1999).
5. Chenulu, V. V. and Verma, A., Virus and virus-like diseases of pulse crops commonly grown in India. In: Baldev, B., Ramajunam, S., Jain, H.K. (Eds.), Pulse Crops. Oxford and IBH, New Delhi, pp. 338-370 (1988).
6. Chenulu, V. V., Venateswaralu, V. and Rangaraju, R., Studies on yellow mosaic diseases of mungbean. *Indian Phytopath.*, **32:** 230-235 (1979).
7. Dhingra, K. L. and Chenulu, V. V., Effect of yellow mosaic on yield and nodulation of soybean. *Indian Phytopath*, **38:** 248-251 (1985).
8. Ganapathy, T. Karuppaih, R. and Gunasekaran, K., Identifying the source of resistance for mungbean yellow mosaic virus (MYMV), urd bean leaf crinkle virus and leaf curl virus disease in urdbean (Vigna mungo (L.) Hepper). In *Annual Meeting and Symposium on recent Developments in the diagnosis and Management of Plant Diseases for Meeting Global Challenges*, December 18-20, 2003, University of Agricultural Sciences, Dharwad. Germplasm for resistance to mungbean yellow mosaic virus. *Sabrao J.*, **13(1):** 61- 68 (2003).
9. Honda, Y., Iwaki, M. and Saito, Y., Mechanical transmission, purification and some properties of whitefly-borne mungbean yellow mosaic virus in Thailand. *Pl. Dis*., **67:** 801-804 (1983).
10. Iqbal, U., Iqbal, S. M., Afzal, R., Jamal, A., Farooq, M. A. and Zahid, A., Screening of mungbean germplasm against mungbean yellow mosaic virus (MYMV) under field conditions. *Pakistan J. Phytopath.*, **23(1):** 48-51 (2011).
11. Jalaluddin, M., and Sheikh M. A. Q., Evaluation of mungbean (*Vigna radiata* (L.) Wilczek) germplasm for resistance to mungbean yellow mosaic virus. *Sabrao J.*, **13(1):** 61- 68 (1981).
12. Jones, D. R., Plant viruses transmitted by whiteflies. *Eurupean J. Pl. Pathol*., 195-219 (2003).
13. Malik, B. A. and Bashir, M., Major diseases of food legume crops of Islamic countries. *In: Jamil, F. F., Naqvi, S.H.M. (Eds.), Proceedings of COMSTECH-NIAB International Workshop of Agroclimatology Pests and Disease and Their Control*, 25-38 (1992).

14. Marappa, N., Savithramma, D. L., Nagaraju, Prameela, H. A. and Krishnamurthy, R. A., Evaluation of mungbean genotypes against powdery mildew, yellow mosaic virus and bacterial blight diseases at Bangalore. *In: Annual Meeting and Symposium on Recent Developments in the Diagnosis and Management of Plant Diseases for Meeting Global Challenges*, December 18-20, 2003, University of agricultural sciences Dharwad. p.31 (2003).
15. Mohan, S., Sheeba, A., Murugan, E. and Ibraihm, S. M., Screening of Mungbean germplasm for resistance to Mungbean Yellow Mosaic Virus under Natural Condition. *Indian J. Sci and Technol.*, **7(7):** 891-896 (2014).
16. Munawwar, M. H., Ali, A. and Malik, S. R., Identification of resistance in mungbean and mashbean germplasm against mungbean yellow mosaic virus. *Pakistan J. Agric. Res.*, 27(2): 129-133 (2014).
17. Nagaraj, N.C., *Indian J. Genet.*, **41:** 426-428 (1981).
18. Nene, Y. L., A survey of viral diseases of pulse crops in Uttar Pradesh. G. B. Pant University Press, Pantanagar, India. pp. 191 (1972).
19. Nene, Y. L., Viral diseases of some warm weather pulse crops in India; *Plant Dis. Rep*. **57:** 463–467 (1973).
20. Salam, S. A., Studies on Mungbean yellow mosaic virus disease on greengram. *M. Sc (Agri) Thesis*, Univ. Agril. Sci., Dharwad, Karnataka, India (2005).
21. Shad, N., Mughal, S. M. and Bashir, M., Transmission of mungbean yellow mosaic Begomovirus (MYMV). *Pakistan J. Phytopath.* **17(2):** 141-143 (2005).
22. Shad, N., Mughal, S. M., Farooq, K. and Bashir, M., Evaluation of mungbean germplasm for resistance against mungbean yellow mosaic begomovirus. *Pakistan J. Bot.* **38(2):** 449-457 (2006).
23. Shakoor, A., Haq, M. A., Sadiq, M. S. and M. Sarwar. Induction of resistance to yellow mosaic virus in mungbean through induced mutation. *Plant Dis.,* **214:** 293-302 (1977).
24. Singh, D. P., Breeding for resistance to diseases in greengram and blackgram. *Theor. Appl.Genet.*, **59:** 1-10 (1981).
25. Sudha, M., Karthikeyan, A., Nagarajan, P., Raveendran, M., Senthil, N., Pandiyan, M., Angappan, K., Ramalingam, J., Bharathi, M., Rabhindran, R., Veluthnbhi, K. and Balasubramaniyan, P., Screening of mungbean (*Vigna radiata* L.) germplasm for resistance to *Mungbean yellow mosaic virus* using agroinoculation. *Can. J. Pl. Pathol.*, **35(3):** 424–430 (2013).