



## Inheritance of resistance to Mungbean Yellow Mosaic India Virus (MYMIV) in mungbean (*Vigna radiata*)

MURALEEDHAR ASKI<sup>1</sup>, H K DIKSHIT<sup>2</sup>, D SINGH<sup>3</sup>, A SINGH<sup>4</sup> and PRAPTI P<sup>5</sup>

ICAR-Indian Agricultural Research Institute, New Delhi 110 012

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### ABSTRACT

Improvement in production and productivity of mungbean is difficult mainly due to major viral disease; Yellow Mosaic Disease (YMD) caused by Mungbean Yellow Mosaic India Virus (MYMIV) more prevalent in Northern Indian subcontinent and MYMV more prevalent in Southern Indian subcontinent. Management of plant diseases through host resistance is considered as one of the best options available for crop protection hence breeding for YMD is essentially required in case of pulses. In case of MYMV, conflicting reports are available on the mode of inheritance of resistance and but there is a need to know the genetics of MYMIV for use of host resistance in breeding programme. In this present study, we studied mode of inheritance for resistance against MYMIV. Four crosses between resistant and susceptible genotypes were made. The six generation P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, BC<sub>1</sub>, BC<sub>2</sub> and F<sub>2</sub> were grown along with infector row for evaluation against MYMIV resistance. The segregation of resistance responses in F<sub>2</sub> populations in ratios of 9 S: 3 MS: 3 MR: 1 R suggested that the resistance was governed by two recessive genes. The study of test crosses/back cross BC<sub>1</sub> with all susceptible plants and in BC<sub>2</sub> ratio of 1S: 1MS: 1MR: 1R also supported that two recessive genes are involved in imparting resistance against MYMIV.

**Key words:** Inheritance, Mungbean, Mungbean Yellow Mosaic India Virus (MYMIV), Resistance

Almost 90% of world's mungbean [*Vigna radiata* (L.) Wilczek] production comes from Asia and India is the world's largest mungbean producer with an area of 2.71 m ha with production of 1.19 m tonnes and productivity of 469 kg/ha (Gupta 2014). However, in general yield of mungbean in India is very low (469 kg/ha). The main cause for the low yield is the susceptibility of the crop to insects, weeds and diseases of which yellow mosaic disease (YMD) is one of the most prevalent and destructive viral agent in mungbean (Anupam and Malathi 2003). Yellow mosaic disease of cultivated legumes in South-East Asia, is caused by *Mungbean yellow mosaic India virus* (MYMIV) and *Mungbean yellow mosaic virus* (MYMV) belonging to the genus *Begomovirus* of the family *Geminiviridae* (Haq *et al.* 2010). MYMV is widely distributed, causing 10–100% yield losses depending on the crop stage at which the plants becoming infected (Nene 1969, Nene *et al.* 1972, Chenulu *et al.* 1979, Marimuthu *et al.* 1981). Two virus species causing YMD are reported from Indian sub continent, Mungbean Yellow Mosaic India Virus (MYMIV) occurs in northern region and Mungbean Yellow Mosaic

virus (MYMV) in southern region of Indian sub continent (Naimuddin *et al.* 2011 and Sanjeev *et al.* 2013). The epidemics have been attributed to their ability to undergo genetic recombination and their transmission by polyphagous whitefly (*Bemisia tabaci*) pests that act as an efficient vector (Butler 1977). YMD control is often based on limiting the vector population with insecticides, which are ineffective under severe whitefly infestations. The use of host resistance is the most efficient and ecologically friendly approach to reduce MYMIV damage in mungbean. For breeding resistant cultivars, information on inheritance of resistance to MYMV disease is useful in breeding for resistant cultivars. Inheritance of resistance to MYMV in mungbean has been studied extensively using different resistant sources but results were contradictory. Therefore the present investigations were conducted to understand the inheritance pattern of resistance to MYMIV in our mungbean plant material as mentioned below.

### MATERIALS AND METHOD

The plant material in the present study consisted of eight mungbean genotypes, viz. four resistant (UPM 99-03, PM 4, PDM 139 and IPM 99-125) and four susceptible (Pusa 9531, K 851, BDYR 1 and EC 398885). The resistant lines used are released commercial cultivars. Pusa 9531 and K 851 are released varieties and BDYR 1 and EC 398885 are the promising germplasm lines introduced from AVRDC,

<sup>1</sup>Scientist (e mail: murali2416@gmail.com), <sup>2</sup>Principal Scientist (e mail: hk\_dikshit@rediffmail.com), <sup>3</sup>Senior scientist (e mail: dsingh@iari.res.in), <sup>4</sup>Research Associate (e mail: a\_singh1388@yahoo.in), <sup>5</sup>Senior Research Fellow (e mail: prapti62@gmail.com), Division of Genetics

Taiwan. UPM 99-03 and PM 4 are promising varieties of North West plain zone and PDM 139, IPM 99-125 are recommended for North East plain zone. All resistant lines except PDM 139 are relatively late in maturity.

The maximum incidence of MYMIV has been in *kharif* (July-Sept) in north Indian subcontinent. Parents were crossed in four combinations (*kharif* 2010) and half of the F<sub>1</sub> seeds of the four crosses were used for inheritance study (*kharif* 2011), and test crosses (BC<sub>1</sub> and BC<sub>2</sub>) were carried out and F<sub>1</sub> were advanced to F<sub>2</sub>. The six basic populations, namely P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, BC<sub>1</sub>, BC<sub>2</sub> and F<sub>2</sub> were grown in compact family block design with three replications in *kharif* season 2013 at Experimental Field Facility of Indian Agriculture Research Institute (IARI), New Delhi, which is a hot spot for MYMIV disease. Each plot consisted of 3-m rows with inter and intra row spacing of 30 and 10 cm, respectively. After every five rows, one row of the highly susceptible genotype PS 16 was grown as infector row. All recommended cultural practices were followed, except insecticide spraying to allow the growth and development of vector *Bemecia tabaci*. Disease reaction was scored when 95% of the infector rows (PS 16) showed MYMIV incidence under field conditions. The resistant plants did not show any mosaic symptoms on leaves or pods during the entire growth period, while the susceptible plants showed various grades of yellowing depending on the stages at which infection occurred. The disease rating was done using modified rating scale of Singh *et al.* 1988 (Table 1). Segregating populations were classified into four reactions that is, susceptible (S), moderately susceptible (MS), moderately resistant (MR) and highly resistant (R) on the basis of disease scores and type of symptoms (Table 1). F<sub>2</sub> populations and test cross progenies were classified as segregating and non-segregating for MYMV disease reaction. The chi-square test was performed to determine the goodness of fit of observed segregation for MYMV disease reaction in F<sub>2</sub> and test cross generations.

## RESULTS AND DISCUSSION

The susceptible parents, viz. Pusa 9531, K 851, BDYR 1, EC 398885 and infector row PS 16 and F<sub>1</sub> plants of all four crosses showed highly susceptible reaction (S) that is; disease symptoms were observed on both leaves and pods.

Table 1 Reaction rating for mungbean yellow mosaic virus

Types of symptoms	Reaction
No visible symptoms or yellow specks on leaves or pods	R (Resistant)
Minute yellow specks on leaves without any symptoms on pods	MR (Moderately Resistant)
No visible symptoms on leaves till flowering and showing yellowing and mottling of pods at maturity	MS (Moderately Susceptible)
Pronounced yellow mottling of foliage and discoloration of leaves and yellowing of pods and seeds	S (Susceptible)

No disease symptoms were observed in resistant parents (UPM 99-03, PM 4, PDM 139 and IPM 99-125) and hence, they were scored as highly resistant (R). In all the four F<sub>2</sub> populations, four reactions were recorded. Resistant (R) with no visible symptoms or yellow specks and susceptible(S) pronounced yellow mottling of foliage and discoloration of foliage, pod and seeds; two more classes were observed, viz. MR plants with minute yellow specks on leaves without any symptoms on pods and MS plants with no visible symptoms on leaves till flowering and yellow mottling symptoms on pods only (Table 1). The F<sub>2</sub> segregation ratio of 9(S): 3(MS): 3(MR): 1(R) was observed in all four crosses (Table 2) and test cross segregation in BC<sub>1</sub> indicated that all are susceptible to MYMV and in case of BC<sub>2</sub> segregation was in the ratio of 1S:1MS: 1MR: 1R. In F<sub>1</sub>, F<sub>2</sub>, and test crosses X<sup>2</sup> value and p value showed goodness of fit to the expected ratios.

Yellow Mosaic Disease (YMD) is the most important viral disease in mungbean reported from entire India. The key symptoms are bright yellow patches on the leaves interspersed with green areas, and slight puckering; seed production is affected (Naraini 1960). It attacks mungbean crop in an epidemic form and is severe in areas between 24 and 32° N latitude. Mungbean Yellow Mosaic Virus (MYMV) is more prevalent in southern Indian subcontinent compared to MYMIV (India Virus) which is more prevalent in northern Indian subcontinent (Gupta *et al.* 2013). In spring/summer season, this disease is reported from northern plains and central India. In winter season mungbean is grown in south zone; here also this disease is a major problem. Yield loss depends on the time of infection and severity of disease. Growing MYMIV resistant mungbean varieties will reduce the yield losses of farmers and also prevent the spread of virus. The knowledge of inheritance of resistance genes and role of each gene in the development of resistance or susceptibility will be very useful for the mungbean breeding programme to breed MYMIV resistant varieties. Inheritance of resistance to MYMV in mungbean has been studied extensively using different resistant sources but results were contradictory. Inheritance of MYMV resistance studies revealed that the resistance is controlled by a single recessive gene (Singh and Patel 1977, Thakur *et al.* 1977, Malik *et al.* 1986, Reddy and Singh 1995, Saleem *et al.* 1998, Basak *et al.* 2004, Reddy 2009 and Rashmi *et al.* 2013) dominant gene (Sandhu *et al.* 1985), two recessive genes (Verma and Singh 1988, Pal *et al.* 1991, Amavasai *et al.* 2004, Dhole and Reddy 2012 and Gajaraj *et al.* 2013) and complementary recessive genes (Shukla and Pandya 1985). In the present study, susceptibility of F<sub>1</sub>s of all four crosses involving resistant and susceptible parents suggested the recessive nature of MYMIV resistance. The involvement of two recessive genes in controlling resistance with segregation ratio of 15: 1 in F<sub>2</sub> was also different because of the different rating scale (Table 1) used by them (Verma and Singh 1988, Pal *et al.* 1991, Amavasai *et al.* 2004). This is the first report on the inheritance of resistance of MYMIV in mungbean which

Table 2 Reaction to Mungbean Yellow Mosaic India Virus (MYMIV) in six generations of four mungbean crosses

Generation	Disease reaction				Total no. of plants	Expected genetic ratio S:R, S:MS:MR:R	X <sup>2</sup> value	P
	S	MS	MR	R				
UPM 99-03 (P <sub>1</sub> )	0	0	0	45	45			
Pusa 9531 (P <sub>2</sub> )	45	0	0	0	45			
F <sub>1</sub>	50	0	0	0	50			
BC <sub>1</sub>	66	0	0	0	66	All susceptible		
BC <sub>2</sub>	11	12	14	12	49	1:1:1:1	0.4	0.95
F <sub>2</sub>	78	34	32	10	154	9:3:3:1	2.1	0.55
PM 4 ( P <sub>1</sub> )	0	0	0	48	48			
K 851 ( P <sub>2</sub> )	59	0	0	0	59			
F <sub>1</sub>	54	0	0	0	54			
BC <sub>1</sub>	67	0	0	0	67	All susceptible		
BC <sub>2</sub>	16	14	9	10	49	1:1:1:1	2.7	0.46
F <sub>2</sub>	73	27	35	8	143	9:3:3:1	3.6	0.31
PDM 139 ( P <sub>1</sub> )	0	0	0	49	49			
EC 398885 ( P <sub>2</sub> )	45	0	0	0	45			
F <sub>1</sub>	56	0	0	0	56			
BC <sub>1</sub>	67	0	0	0	67	All susceptible		
BC <sub>2</sub>	11	10	14	14	49	1:1:1:1	1.0	0.79
F <sub>2</sub>	83	30	26	14	153	9:3:3:1	2.5	0.47
IPM 99-125 ( P <sub>1</sub> )	0	0	0	49	49			
EC 398885 ( P <sub>2</sub> )	59	0	0	0	59			
F <sub>1</sub>	56	0	0	0	56			
BC <sub>1</sub>	68	0	0	0	68	All susceptible		
BC <sub>2</sub>	14	15	11	9	49	1:1:1:1	1.9	0.61
F <sub>2</sub>	71	27	30	8	136	9:3:3:1	1.3	0.73

is common in northern Indian sub continent. But our study is unique as that of Dhole and Reddy (2012) with respect to MYMIV but not MYMV. So segregation ratio of 9 S: 3 MS: 3 MR: 1 R in F<sub>2</sub> populations of all four crosses revealed that two recessive genes were controlling resistance of MYMIV disease. In all four test crosses we could see that in BC<sub>1</sub> all plants are susceptible to MYMIV. But in case of all BC<sub>2</sub> test cross segregation ratio of 1 S: 1 MS: 1 MR: 1R was observed on the basis of phenotypic expression and development of disease symptoms (Table 2). The F<sub>2</sub> populations were grouped into four classes on the basis of a modified disease rating scale and with the help of critical phenotypic observation of infected plants (Table 1). On the basis of these experimental observations, MYMIV resistance is governed by two recessive genes, viz. r1 and r2 segregating independently.

Reason for these contradictory results can possibly be due to the differences in genotypes of the host, strains of virus and the interaction between them. The weather parameters in relation of vector activities are other important factors responsible for the differences in the inheritance. This may be due to differences in the source (s) of resistance used and/or variation in the virus strain. The possibility of environmental modification of disease occurrence also

cannot be ruled out. Since two recessive genes are responsible for the inheritance of resistance of this disease, it is essential to grow large segregating populations to recover resistant plant, coupled with other useful traits for success of breeding programme. The weather condition during the cropping season in relation of vector activities are other important factors responsible for the differences in the inheritance patterns. However the present study will be useful for developing DNA markers linked with MYMV resistance gene.

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