American Journal of Plant Sciences, 2013, 4, 1924-1927
http://dx.doi.org/10.4236/ajps.2013.410236 Published Online October 2013 (http://www.scirp.org/journal/ajps)

Inheritance of Resistance to Mungbean Yellow Mosaic Virus (MYMV) in Inter and Intra Specific Crosses of Mungbean (*Vigna radiata*)*

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Received July 10th, 2013; revised August 10th, 2013; accepted September 1st, 2013

ABSTRACT

The objective of this research was to study the mode of inheritance of resistance to mungbean yellow mosaic virus (MYMV) in inter TNAU RED × VRM (Gg) 1 and intra KMG 189 × VBN (Gg) 2 specific crosses of mungbean. An infector row technique was used for evaluating parents, F_1, F_2 and F_3 plants for MYMV resistance. No insecticide was sprayed in order to maintain the natural whitefly population in experimental field. In the field condition, only after 80% of plants showed *MYMV* incidence, and the scoring of the test materials was done by MYMV disease rating scale. According to the mean disease score, the mungbean genotypes were categorized into five groups resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS). 3 (Susceptible): 1 (Resistance) was observed in all two crosses of all F_2 population and it showed that the dominance of susceptibility over the resistance and the results of the F_3 segregation (1:2:1) confirm the segregation pattern of the F_2 segregation. Collectively all the two crosses F_2 and F_3 generations results suggested that a single recessive gene is involved in resistance against the MYMV disease.

Keywords: Inheritance; Mungbean Yellow Mosaic Virus; *Vigna spp.*

1. Introduction

Mungbean [*Vigna radiata* (L.) Wilczek], also known as greengram, green bean, mash bean, golden gram and green soy is an important source of dietary protein across Asia.It is widely grown in tropical and sub-tropical regions as a monoculture and as a component in cropping systems. Almost 90% of world's mungbean production comes from Asia, and India is the world's largest mungbean producer cultivated on 2.84 million ha area with a production of 1.04 million tones and productivity of 386 kg/ha [1]. However the standard yield of mungbean worldwide is very low (384 kg/ha) and the mungbean production has not considerably increased yet. The main cause for the low yield is the susceptibility of the crop to insects, weeds and diseases caused by fungus, virus or bacterium, of which Mungbean yellow mosaic virus (MYMV) is one of the most prevalent and destructive viral pathogens in mungbean. It causes severe yield loss and a reduction in seed quality. In India, MYMV affects all mungbean-producing regions in the country. MYMV produces typical yellow mosaic symptoms. The symptoms appear in the form of small irregular yellow specs and spots along the veins, which enlarge until leaves were completely yellowed. Diseased plants were stunted, with fewer flowers and pods that bear smaller, occasionally shriveled seeds in severe cases, and other plant parts also become completely yellow. Depending on the severity of the MYMV infection, the yield penalty may reach up to 85% [2]. MYMV transmitted in a circulative persistent manner by white fly *Bemisia tabaci*. MYMV control is often based on limiting the vector population with insecticides, which are ineffective under severe whitefly infestations [3]. The use of resistant varieties is the most desirable strategy to manage the disease in an economical and environmentally-friendly way. Information on in-

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heritance 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. Inheritance of MYMV resistance studies revealed that the resistance is controlled by a single recessive gene [4-9], dominant gene [10], two recessive genes [11-13] and complementary recessive genes [14]. Thus a more extensive study is needed in order to finalize the mode of inheritance of the resistance. Meanwhile understanding the inheritance of resistance to MYMV is of prime importance in mungbean breeding programmes. However sources of resistance to MYMV are very rare in the germplasm of mungbean, whereas a high proportion of Ricebean (*Vigna umbellata*) and urdbean (*Vigna mungo*) lines resistant to MYMV are available. Monika *et al*. and Pandiyan *et al.* [15,16] reported that Ricebean (*Vigna umbellata*) contains desirable genes for MYMV resistance. Therefore, the present study was undertaken to investigate the inheritance of resistance to MYMV in inter and intra specific crosses of mungbean.

2. Materials and Methods

Materials for the present investigation comprised a MYMV resistant mungbean line KMG 189 and ricebean line TNAU RED, Two MYMV susceptible mungbean lines VBN (Gg) 2 and VRM (Gg) 1 (All the lines are originated from Tamilnadu, India), F_1, F_2 and F_3 generation plants (derived from crossing between resistant and susceptible parents were used in the present study. The field experiment was conducted during the period of 2006-2010 in every kharif and summer season of the year at the National Pulse Research Centre. The plants were maintained properly by providing row to row and plant to plant spacing at 50 cm and 10 cm, respectively. The infector row method, where in two test rows alternating with spreader rows of the susceptible variety (C0 5 mungbean) were sown, was adopted in the field condition, for the evaluation of *MYMV* infestation. No insecticide was sprayed in order to maintain the natural whitefly population in experimental field. Only after 80% of plants showed *MYMV* incidence, the scoring of the test materials was done. The rating scale suggested by Singh *et al.*, [17] was adopted. The mean disease score was calculated as disease rating and frequency per total number of plants was also calculated. Based upon the MYMY score, the mungbean plants were divided into five categories, resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS). Plants that are moderately susceptible (MS), susceptible (S) and highly susceptible (HS) were included in susceptible group and resistant (R), moderately resistant (MR) plants were included in resistant group. The chi-square test was performed to determine the goodness of fit of observed segregation for MYMV disease reaction in F_2 and F_3 generations.

3. Results and Discussion

Mungbean yellow mosaic virus (MYMV) is widespread in the major mungbean-growing areas in India. A severe outbreak of MYMV in the southern and northern states is currently causing serious concern to mungbean growers and to the mungbean industry in these regions. Resistance to MYMV was determined by visual symptomatology. Symptomless lines were assumed to be resistant. As mungbean lines can be infected without showing symptoms, it is possible that these are not resistant lines. Breeding for cultivars with resistance is a commonly accepted and effective strategy for controlling the MYMV disease and also prevent the multiplication 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 breeders to breed MYMV-resistant varieties. The objective of this study was to determine the inheritance of MYMV resistance in inter and intra specific crosses of mungbean. In the field condition, MYMV infection can be evaluated by MYMV disease rating scale suggested by Singh *et al*., [17]. The susceptible parents VBN (Gg) 2, VRM (Gg) 1 and F_1 plants of all two crosses showed susceptible reaction (S), that is, symptoms observed on both leaves and pods. No symptoms were observed in resistant parents KMG 189 and TNAU RED up to maturity, and hence, they were scored as resistant. Based on the rating scale in all the two F_2 and F_3 generations, five reactions were recorded, resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S) and highly susceptible (HS). F_2 generation disease screening results are presented in **Table 1**.

The X_2 tests of the two crosses showed a good fitness to 3 (Susceptible): 1 (Resistance) in F_2 population (**Table 2**) and it showed the dominance of susceptibility over the resistance which indicated a monogenic inheritance designated as MYMV. But the segregation for 3:1 in F_2 [10,11,13] is totally different from the present study. However the F_3 progenies from two crosses showed

Table 1. MYMV disease screening results in F_2 generation of crosses between resistant and susceptible plants.

Plant materials	Total plants	(HS)	(S)	(MS)	(MR)	(R)
TNAU RED × VRM(Gg)1	187	24	50	59	30	24
KMG 189 × VBN(Gg)2	203	19	56	57	41	30

Table 2. Segregation for mungbean yellow mosaic crosses between virus resistance in F_2 and F_3 generation of resistant and susceptible genotypes.

Plant materials	Total	Susceptible (MS-HS)	Segregation	Resistant (MR-R)	Expected ratio	X^2	P value
TNAU RED	30	0	-	30	-	-	-
VRM(Gg)1	30	30	-	0	-	-	-
F_1	20	20	-	0	-	-	-
F_2	187	133		54	3:1	1.72	0.40 - 0.30
F_3	56	16	30	10	1:2:1	0.30	0.50 - 0.60
KMG 189	30	0	-	30	-	-	-
VBN(Gg)2	30	30	-	0	-	-	-
F_1	30	20	-	0	-	-	-
F_2	203	132	-	71	3:1	1.02	0.40 - 0.30
F_3	54	13	28	15	1:2:1	0.20	0.65 - 0.75

a segregation pattern of 1 (none segregating susceptible): 2 (segregating): 1 (non segregating resistant) (**Table 2**). The results of the F_3 segregation clearly confirmed the segregation pattern of the F_2 segregation. Collectively all the results confirmed that single recessive gene was controlling resistance of MYMV disease. Similar results of single recessive genes inheritance of the mungbean have been reported by various workers [6,8,9]. There are, however, reports indicating the involvement of dominant gene [10], two recessive genes [13] and complementary recessive genes [14]. 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. However the present study will be useful for developing DNA markers linked with MYMV resistance gene. In addition we suggest that to improve the MYMV resistance in mungbean virus strain-based investigations will be needed in future.

4. Acknowledgements

We thank the Department of Bio-Technology, a division under the Department of Science and Technology, India, for the funding and supporting the research programme.

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