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Genetic study in URD bean (*Vigna Mungo* (L.) Hepper) for inheritance of mungbean yellow mosaic virus resistance

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Abstract

Goodness of fit test pertaining to MYMV resistance confirmed that all the F_1cross combinations viz., MDU 1 x Mash-114, MDU 1 x VBN (Bg) 6, MDU x PU 31, MDU 1 x Uttara, LPG- 752 x Mash-114, LPG – 752 x VBN (Bg) 6 and CO 6 x VBN (Bg) 6 and BC2 were resistance to MYMV, showed that YMV resistance were controlled by dominant gene. Resistance nature of F_1 of all the crosses indicated clearly the resistance was dominant over susceptibility. Goodness of fit test pertaining to test the deviation of observed ratio to Mendelian segregation ratio for MYMV (resistance: susceptible) in the segregating population shows that, except 'MDU 1 x PU 31', F_2 of all crosses fitted well with 15: 1 (resistance: susceptible), exhibited the presence of duplicate dominant gene interaction. Whereas 'MDU 1 x PU 31; was confined well with 9:7 (resistance: susceptible), showed that the presence of complementary or duplicate recessive type of epistatic gene interaction. The inheritance ratio of 3:1(resistance: susceptible) in BC1 and all resistance in BC2 showed that the male parents taken for crossing were resistance, while female parents susceptible. The putative gene symbol for MYMV resistance assigned for female parents are r1r1r2r2, whereas for male parents viz., Uttara, VBN (Bg) 6 Mash-114 and PU 31 the symbol is R1R1R2R2. Hence, presence of complex nature of inheritance, it may appropriate to suggest the recombination breeding accompanied with one or two cycles of recurrent selection should be effective to enhance the YMV resistance in blackgram.

Highlights

- YMV resistance was governed by dominant gene action under digenic nature of epistatic interaction.
- Complex nature of inheritance necessitates the breeding programme should accompany with crossing followed by one or two recurrent cycle of selection may effective to get desirable recombinant with MYMV resistance.

Keywords: Putative gene symbol, goodness of fit, inheritance, complex nature and gene interaction

URD bean is an important grain legume occupies third position among the important pulse crops and being cultivated in various agro climatic conditions in India. Black gram is mainly cultivated in the marginal land and as well as a subsidiary crop prone to several biotic (viral, fungal, bacterial pathogens and insects) and abiotic (salinity, drought, temperature, water logging etc) stresses are the major constrains to production. Among the destructive yield liming factors, 'yellow mosaic disease (YMD)' caused by '*Mungbean yellow mosaic virus* (MYMV)' is a major cause for huge economical losses in the Indian subcontinent (Nene, 1973). Infection of MYMV may cause up to 85–100% yield loss in urdbean have been reported by Singh *et al*., 2011. Main pathogens causing YMD in India are *Mungbean yellow mosaic virus* (MYMV) and *Mungbean yellow mosaic India virus* (MYMIV) (Varma and Malathi (2003); Malathi and John (2008). The disease is caused by geminivirus with bipartite genomes transmitted by different species of whitefly belongs to the genus begomovirus and family geminiviridae. Nariani (1960) was the first person ever to report the mungbean yellow mosaic virus disease from the fields of IARI, New Delhi. The disease is characterized by the presence of bright yellow patches on leaves interspersed with green areas, complete yellowing and stunting of the plants. The knowledge on mode of inheritance of YMV resistance is important to formulate appropriate breeding strategy targeted to incorporation useful gene conferring resistance to MYMIV, otherwise agronomically poor cultivar. There are only few contrasting reports were published on mode of inheritance and gene governing the resistance. In blackgram, monogenic dominant nature of resistance was reported by Dahiya *et al*. (1977), Kaushal and Singh (1988) and Gupta *et al*. (2005) while it was reported to be digenic recessive by Singh (1980), Dwivedi and Singh (1985) and Verma and Singh (1986). However, digenic dominant natures of inheritance were also reported by Murugan and Nadarajan (2012). The prime objective of this present study is to decipher gene action involved in the inheritance of YMV resistance in black gram by using six generations.

Materials and methods

The present investigation was conducted at Agricultural College and Research Institute, Madurai, Plant Breeding and Genetics Department research farm. To study the inheritance pattern of mungbean yellow mosaic disease (MYMV) resistance three susceptible blackgram genotypes *viz*., MDU 1, CO6 and LPG-752 were crossed with four resistant genotypes *viz*., VBN (Bg) 6, PU 31, Mash-114 and Uttara during *Rabi*, 2015. Seven cross combinations *viz*., MDU 1 x Mash-114, MDU 1 x VBN (Bg) 6, MDU x PU 31, MDU 1 x Uttara, LPG-752 x Mash-114, LPG – 752 x VBN (Bg) 6 and CO 6 x VBN (Bg) 6 were raised along with parents to build up $F_{2,}$ BC_1 and BC_2 generations during *Kharif*, 2015..

Evaluation of MYMV reaction

For evaluation of the test material against MYMV, the infector row method of sowing two test rows alternating with spreader rows of highly susceptible check 'CO 5' was adopted at the test location which is hot spot for MYMV. Seeds of six generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2 were raised at National Pulses Research Centre, Vamban during June-July, 2015 and evaluated for inheritance pattern of MYMV resistance. Infector row was pulled out when the disease incidence was reached up to 80% and percent disease incidence calculated as Percent disease incidence = [(Number of plantsinfected in a row) / (Total number of plants in a row)] × 100. The genotypes were later grouped into different categories based on 0 to 9 scales adapted Mayee and Datar, 1986 (Table 1). To confirm goodness of fit of each cross Mendelian segregation ratio for MYMV (resistance: susceptible) in the segregating population was tested through Chi-square test.

Table 1: Grouping of genotypes into different categories based on 0 to 9 scale

Scale	Description	Category
0	No plants showing any symptom	Immune
1	1% or less plants that exhibiting symptom	Resistant
3	1~10% plants exhibiting symptom	Moderately resistant
5	11~20% plants exhibiting symptom	Moderately susceptible
7	21~50% plants exhibiting symptom	Susceptible
9	>51% plants exhibiting symptom	Highly susceptible

Results and discussion

To decipher the inheritance pattern of MYMV resistance seven blackgram cross combinations were evaluated and Chi-square test was worked out to ascertain the expected deviation from the Mendelian segregation ratio of segregating generation *viz*., F_2, BC_1 and BC_2 and the results are presented in Table 2.

All the available information pertaining to MYMV resistance confirmed that the F_1 of all the crosses *viz*., MDU 1 x Mash-114, MDU 1 x VBN (Bg) 6, MDU x PU 31, MDU 1 x Uttara, LPG- 752 x Mash-114, LPG – 752 x VBN (Bg) 6 and CO 6 x VBN (Bg) 6 were resistance to MYMV. Resistance nature of all the F_1 of each cross combination indicated clearly that the resistance was dominant over susceptibility. With respect to observed: expected F_2 segregation ratio for resistance: susceptible out of seven cross combinations six crosses " MDU 1 x Mash-114, MDU 1 x VBN (Bg) 6, MDU 1 x Uttara, LPG- 752 x Mash-114, LPG – 752 x VBN (Bg) 6 and CO 6 x VBN (Bg) 6" recorded the chi-square test was non-significant and the expected ratio fitted well with 15:1 (resistant: susceptible) in F_2 and 1:3 in BC_1 (resistant: susceptible), whereas all the BC_2 plants were resistant. However in "MDU 1 x PU 31" the available evidence supported the presence of complementary gene action, in which the chi-square test showed non-significance chi-square value with chi-square table value between the probability of 0.80 - 0.70 confirmed of the expected ratio, fitted well with 9:7 in F_2 and 1:3 in BC_1. While, all the plants in BC_2 were resistance. Mode of inheritance of resistance to mungbean yellow mosaic virus (MYMV) in urdbean appeared to each of the six out of seven cross combinations segregation ratio for resistance: susceptibility was homogeneously fitted with a15:1 in F_2 and 3:1 in BC_1, except cross combination 'MDU 1 x PU-31' where the inheritance ratio fitted with 9:7, clearly indicated the presence of complementary gene action. The frequency of resistant to susceptible plants did not deviate significantly from15:1 ratio suggesting that existence of true inheritance of two dominant genes controlling resistance nature to MYMIV in blackgram with duplicate dominant type of non allelic interactions. The present result was also in accordance with earlier report of Murugan and Nadarajan, 2012 and Durga Prasad *et al*. 2015. In all the seven crosses the F_1 was found to be resistant, where the female parents MDU 1, LPG-752 and CO 6 were susceptible which demonstrated clearly that resistance was dominant over susceptible. In blackgram dominant nature of resistance was reported by Patel *et al*. (2009) and Gupta *et al*. (2005). The inheritance of MYMV resistance in six crosses appeared to be under the control of digenic dominant gene with duplicate dominant type of intra-genic or non allelic intraction. Whereas in cross 'MDU 1 x PU 31' inheritance in F_2 was confirmed with the ratio of 9:7 showed that the dominant and recessive gene interact in dominant and recessive type of interaction. Shukla *et al.* (1978) and Singh (1980) reported the presence of duplicate dominant genes for YMV in black gram. From the above discussion it was found that, though in four crosses same female parent 'MDU 1' was involved there exist two types of interactions duplicate dominant interaction in 'MDU 1 x Mash-114, MDU 1 x Uttara and MDU 1 x VBN (Bg) 6 and duplicate recessive type of epistatic interaction in 'MDU 1 x PU-31'. The difference in gene interaction may be attributed to the presence of set of non-allelic genes in male parents. The putative gene symbol (Table 3) for MYMV in female parent assigned as $r_1r_1r_2r_2$, whereas for male parents viz., Uttara, VBN (Bg) 6 Mash-114 and PU 31 the symbol are $R_1R_1R_2R_2$, which act in duplicate manner in combination with recessive allele of the female parent. From the above results it has been concluded that the complicate nature of digenic dominant interaction restricts the understanding on nature of inheritance and steps forwards to improve the crop to sustain MYMV resistance. Therefore because of the complex nature of inheritance the breeding programme should be accompany with crossing followed by recurrent selection may effective to get desirable recombinant with MYMV resistance.

Table 2: Chi-square test for inheritance of MYMV resistance in urdbean

Generation	Observed values		Expected ratio	χ^2 values	Probability between
	Resistant	Susceptible			
MDU1 x Uttara	Resistant	-	--	0.44	0.50
F_1	268	15	15:1	0.016	0.90
F_2	64	22			
BC_1	Resistant	----			
BC_2					
MDU1 x MASH-114	Resistant	-	--	0.50	0.50 - 0.40
F_1	272	15	15:1	0.11	0.70 – 0.60
F_2	62	19	3:1		
BC_1	Resistant	----			
BC_2					
MDU1 x VBN (BG)6	Resistant	-	--	0.83	0.40 - 0.30
F_1	269	14	15:1	0.19	0.70 – 0.60
F_2	89	27	3:1		
BC_1	Resistant	----			
BC_2					
MDU1 x PU 31	Resistant	--	--	0.06	0.80 - 0.70
F_1	292	134	9:7	0.85	0.40 – 0.30
F_2	21	73	1:3		
BC_1	Resistant	----			
BC_2					
LPG-752 x VBN(Bg) 6	Resistant	-	--	0.56	0.50 - 0.40
F_1	272	14	15:1	1.2	0.30 – 0.20
F_2	58	14	3:1		
BC_1	Resistant	----			
BC_2					
LPG-752 x MASH-114	Resistant	-	--	0.51	0.50 - 0.50
F_1	200	16	15:1	0.34	0.60 – 0.50
F_2	76	22	3:1		
BC_1	Resistant	----			
BC_2					
CO6 x VBN (Bg) 6	Resistant	-	--	0.90	0.40 - 0.30
F_1	255	13	15:1	0.63	0.50 – 0.40
F_2	60	16	3:1		
BC_1	Resistant	----			
BC_2					

Table 3: Mean MYMV score, disease reaction category and putative gene symbols of parents

Genotypes	Mean MYMV score (%)	Reaction to MYMV	Putative gene symbo1
VBN (Bg) 6	0.95	Resistant	R_1R_1 R_2R_2
PU 31	1.0	Resistant	R_1R_1 R_2R_2
Uttara	0.6	Resistant	R_1R_1 R_2R_2
Mash – 114	0.7	Resistant	R_1R R_2R_2

CO 6	35	Susceptible	$r_1r_1r_2r_2$
MDU 1	33	Susceptible	$r_1r_1r_2r_2$
LPG-752	32	Susceptible	$r_1r_1r_2r_2$

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