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Studies on allelic relationship for resistance to mungbean yellow mosaic virus disease in mungbean genotypes

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Abstract

The allelic relationship of resistant genes for resistance to Mungbean Yellow Mosaic Virus (MYMV) in mungbean has been studied in the present investigation at Research cum Instructional Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during *rabi* 2015-16 and *kharif* 2016. The objective of this study was to determine whether the genes for resistance to MYMV in the varieties are allelic. Resistant x resistant crosses were made, a total of 12 crosses (F₁s) were made during *rabi* 2015-16 viz, SML-1815 x Pusa Vishal, Malviya Jyoti x HUM 12, Pusa Vishal x CO 6, MH 934 x PUSA 9072, COGG 11-02 x MH 421, CO 6 x VGG 10-008, IPM 19 x COGG 11-02 (F₂ shown 61 resistant: 3 susceptible segregation ratio having three independent genes, two of them dominant and one are recessive for resistance), HUM-16 x SML 1815 (F₂ shown 63 resistant: 1 susceptible segregation ratio having three independent dominant genes for resistance), MH-421 x TM 96-2 (F₂ shown 57 resistant: 7 susceptible segregation ratio having three genes two of them dominant genes in complementation and one independent dominant gene for resistance), PKV AKM 4 x Pusa Vishal, VGG 10-008 x Malviya Jyoti (F₂ shown 13 resistant: 3 susceptible segregation ratio having two genes, one dominant genes and one recessive gene for resistance) and Samrat x VBN (Gg) 2 (allelic to each other) to build up F₂ generations for scored yellow mosaic disease during *kharif*, 2016. The only of cross Samrat x VBN (Gg) 2 was allelic and rest of 11 crosses were non-allelic.

Keywords: allelic, non-allelic, disease, mungbean, mymv, resistance, susceptible.

Introduction

Mungbean (*Vigna radiata* L. Wilczek) is the third most important short-duration pulse crop after chickpea and pigeonpea. It is widely grown in tropical and sub-tropical regions as a monoculture and as a component in cropping systems. It is also known as greengram, green bean, mash bean, golden gram and green soy is an important source of dietary protein across Asia. It plays an important role in human nutrition due to its richness in protein and it enormous agronomic, sanitary and economic potentialities. Mungbean is cultivated around the year in India leads to heavy disease and pest infestation, resulting in low productivity. 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. Among the diseases, Mungbean Yellow Mosaic Virus (MYMV) causes enormous yield losses ranged from 10 to 100% depending on the crop stage at which the plants becoming infected (Nene 1972 ^[6], Chenulu *et al.* 1979 ^[3], Marimuthu *et al.* 1981) ^[5].

One of the control measures for resistance to MYMV is the use of resistant varieties. However, the nature of the gene (s) controlling the resistance to MYMV is not well determined yet. Knowing the nature of this gene (s) is very important before undertaking a breeding scheme because it helps developing an appropriated breeding strategy. The allelic relationship study for the resistance to MYMV could eventually allow developing resistant varieties to MYMV and responding to farmers and consumer's needs. The objective of this study was to determine the allelic relationship of the resistance to this disease in mungbean.

Materials and Methods

The present investigation was conducted at Research cum Instructional Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. The 50 genotypes

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of mungbean were screened against MYMV disease under natural field condition during *kharif* 2015 and *rabi* 2015-16 (Fig-1 and 2). The F₁ generations were raised in the field in *rabi* season of 2015-16. The F₁s were advanced to F₂ in the *kharif* season of 2016 and the segregating generation (F₂) was score for MYMV resistance. The seed of these genotypes were procured from IIPR, Kanpur and MULLaRP, IGKV, Raipur. Each genotype was represented by single row of 4.0 m length with three replications at row spacing of 30 cm and 5-10 cm between plants. General cultural practices were followed to maintain the experiment except that no insecticides were sprayed to discourage whitefly population for spread of the disease. After emergence, the crop was regularly observed for development of yellow mosaic disease. Diseases severity was recorded at weekly intervals using 0-5 rating scoring Scale (Bashir 2005) [2] (Table-1). Plants were exposed to natural infection. Per cent disease incidence (PDI) of MYMV disease in each genotype/ variety was recorded by counting the number of infected plants out of the total number of plants.

During *rabi* 2015-16 study was planned to determine the allelic relationship of resistance in 12 selected genotypes *viz.* SML-1815, PKV AKM 4, HUM-16, Pusa Visal, Malviya Jyoti, MH-421, MH 934, VGG 10-008, COGG 11-02, CO 6, IPM 19 and Samrat. These 12 resistant genotypes were crossed with also resistant genotypes *viz.* Pusa Visal, SML 1815, CO 6, HUM 12, TM 96-2, PUSA 9072, Malviya Jyoti, MH 421, VGG 10-008, COGG 11-02 and VBN (Gg) 2 respectively. A total of 12 crosses (F₁s) were made during *rabi* 2015-16 *viz.* SML-1815 x Pusa Visal, PKV AKM 4xPusa Visal, VGG 10-008xMalviya Jyoti, HUM-16xSML 1815, Malviya Jyoti x HUM 12, Pusa Visal x CO 6, MH-421xTM 96-2, MH 934xPUSA 9072, COGG 11-02xMH 421, CO 6xVGG 10-008, IPM 19xCOGG 11-02 and Samrat x VBN (Gg) 2 to build up F₂ generations for scored yellow mosaic disease during *kharif* 2016. The plants showing yellow in mosaic symptoms were considered 'susceptible' failing which were considered 'resistant'. The goodness of fit to Mendelian segregation ratio has been tested in the F₂ segregating population by Chi-square test (Harnett 1970) [3].

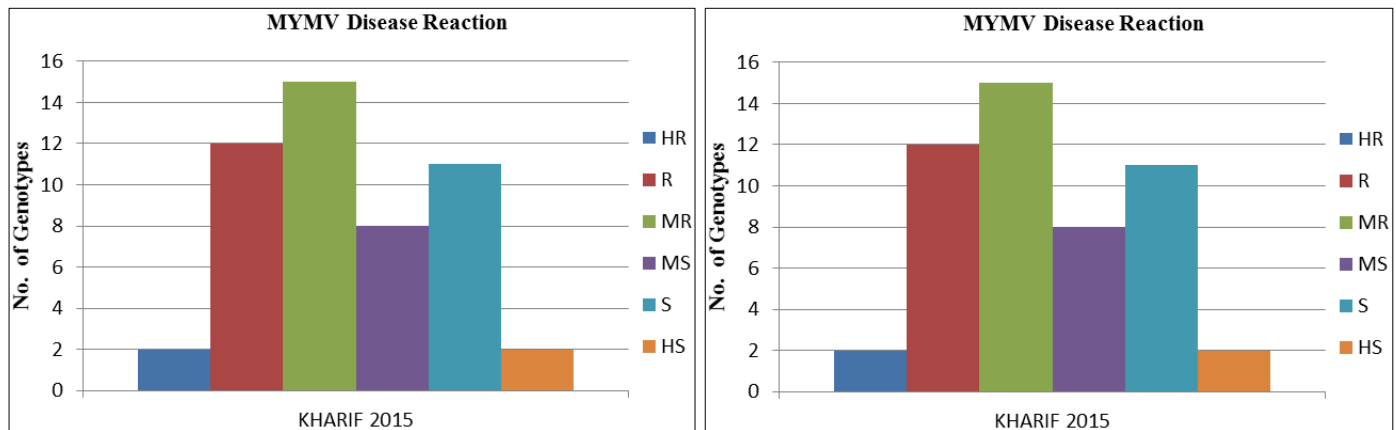


Fig 1 and 2: 50 genotypes of mungbean categorized in six classes for their reaction to MYMV under natural conditions during *kharif* 2015 and *rabi* 2015-16

Table 1: Mungbean yellow mosaic disease scoring (0 to 5 scale) (Bashir 2005) [2]

Score	Disease infection	Reaction
0	0	Highly Resistant (HR)
1	1-10	Resistant (R)
2	11-20	Moderately Resistant (MR)
3	21-30	Moderately Susceptible (MS)
4	31-50	Susceptible (S)
5	> 50	Highly Susceptible (HS)

Results and Discussion

The objective of this study is to determine whether the genes for resistance to MYMV in the varieties are allelic. The resistant x resistant crosses were made among Pusa Vishal with SML -1815 and PKV AKM 4; Malviya Jyoti with VGG 10-008. Similarly other crosses attempted were HUM-16xSML-1815, Malviya Jyoti x HUM-12, Pusa Vishal x CO 6, MH-421xTM 96-2, MH-934xPUSA 9072, COGG 11-2xMH-421, CO 6xVGG 10-008, Samrat x VBN (Gg) 2 and IPM-19xCOGG 11-02 (Table 2).

Study of allelic reaction of resistant genes shown that F₁ of cross Samrat x VBN (Gg) 2 was resistant and in F₂ generation

only resistant individuals were present, suggesting that genes present in Samrat are allelic to that present in VBN (Gg) 2.

F₁s of SML-1815xPusa Vishal, Malviya Jyoti x HUM-12, Pusa Vishal x CO 6, MH-934xPUSA 9072, and COGG 11-02xMH 421, CO 6xVGG 10-008 and IPM 19xCOGG 11-02 were resistant. The F₂ shown segregation ratio of 61 resistant: 3 susceptible indicating the presence of three independent genes, two of them dominant and one are recessive confirming resistance to MYMV. One dominant and a recessive gene present in HUM-12 & COGG 11-02 and another non-allelic dominant gene is present in Malviya Jyoti, MH-421 and IPM-19 which confirms the finding of inheritance of resistance in these two genotypes as shown in Table 3. Similarly two dominant genes for resistance are present in SML-1815, CO 6 and either of PUSA 9072 or MH-934 and another independent recessive gene for resistance in Pusa Vishal, VGG 10-08 and either of PUSA 9072 or MH-934.

The F₁ of cross HUM-16xSML-1815 was resistant and F₂ shown segregation ratio of 63 resistant: 1 susceptible indicated the presence of three independent dominant genes for resistance. Two dominant genes present in SML-1815 and

another dominant gene present in HUM-16 which confirm the inheritance of resistance to MYMV.

The F₁ of MH-421xTM 96-2 has shown resistant reaction. F₂ has shown segregation ratio of 57 resistant: 7 susceptible indicating the presence of three genes. Two of the dominant genes in complementation and one independent dominant gene confirm resistance to MYMV. Two complimentary dominant genes present in TM 96-2 and another dominant gene is present in MH-421.

The F₁ of cross PKV AKM 4 x Pusa Vishal and VGG 10-008xMalviya Jyoti are showing dominance nature and F₂ segregated in ratio of 13 resistant: 3 susceptible reveal digenic nature. Resistance is governed in Pusa Vishal and VGG 10-008 by independent recessive gene and in PKV AKM 4 & Malviya Jyoti is governed by single dominant gene.

Similar type of allelic relationship had been previously reported by Thakur *et al.* (1977)^[8], Verma and Singh (1986)^[9], Srinivas *et al.* (1997)^[7] and Antoine *et al.* (2016)^[11].

Table 2: Details of the parents used in the study

S. N.	Genotypes	Parentage	Place of origin	MYMV Reaction
1	SML-1815	-	PAU, Ludhiana	R
2	HUM-16	Pusa bold-1 x HUM 8	BHU, Varansi	MR
3	Malviya Jyoti	BHUM 1 x Pant U 30	BHU, Varansi	MR
4	Pusa Vishal	Selection from NM 92	IARI, New Delhi	MR
5	HUM-12	HUM 5 x DPM 90-1	BHU, Varansi	R
6	MH-421	Muskan x BDYR 2	CCS HAU, Hisar	R
7	TM 96-2	Kopergaon x TARM-2	BARC, Mumbai	MR
8	MH-934	MH 96-1 x 2 KM 117	CCS HAU, Hisar	MR
9	PKV AKM 4	BM 4 x PS 7	PDKV, Akola	MR
10	VBN (Gg) 2	VGG 4 x MH 309	NPRC, Vamban	R
11	COGG 11-02	COGG 912 x IPM 02-3	Coimbatore	MR
12	VGG 10-008	PDM 139 x BB 2664	NPRC, Vamban	R
13	PUSA 9072	PUSA 106 x 10-215	IARI, New Delhi	MR
14	CO 6	VGG 37 x CO 5	Coimbatore	R
15	IPM-19	(PM-3 x AMP-36) x EC 398897	IIPR, Kanpur	MR
16	Samrat	ML 20/19 x ML 5	PAU, Ludhiana	HR

Table 3: MYMV reaction in F₁ and F₂ generations derived from cross of resistant x resistant genotypes

S. N.	Crosses	Reaction of F ₁	Reaction of F ₂ population		Expected ratio	Calculated X ²	X ² table value at	
			Resistant	Susceptible			5%	1%
1	SML-1815 x Pusa Visal	R	305	13	61:3	0.256	3.841	6.634
2	PKV AKM 4 x Pusa Visal	R	268	58	13:3	0.205	3.841	6.634
3	VGG 10-008 x Malviya Jyoti	R	219	40	13:3	2.168	3.841	6.634
4	HUM-16 x SML 1815	R	378	8	63:1	0.495	3.841	6.634
5	Malviya Jyoti x HUM 12	R	389	20	61:3	0.036	3.841	6.634
6	Pusa Visal x CO 6	R	394	18	61:3	0.100	3.841	6.634
7	MH-421 x TM 96-2	R	329	40	57:7	1.383	3.841	6.634
8	MH 934 x PUSA 9072	R	403	18	61:3	0.175	3.841	6.634
9	COGG 11-02 x MH 421	R	353	19	61:3	0.135	3.841	6.634
10	CO 6 x VGG 10-008	R	370	20	61:3	0.156	3.841	6.634
11	Samrat x VBN (Gg) 2	R	398	0	-	-	-	-
12	IPM 19 x COGG 11-02	R	319	16	61:3	0.006	3.841	6.634

References

- Antoine B, De La Salle TJB, Zakaria D, Zakaria K, Leandre P, Mahamadou S. Inheritance and the Allelic Relationship of Resistance to Cowpea Aphid Borne Mosaic Virus (CABMV) in Two Cowpea Genotypes, KVV640 and KVV396-4-5-2D in Burkina Faso. *Int. J. Curr. Microbiol. App. Sci.* 2016; 5(8):285-292.
- Bashir M. Studies on viral diseases of major pulse crops and identification of resistant sources. Technical Annual Report (April, 2004 to June, 2005) of ALP Project. Crop Sciences Institute, National Agricultural Research Centre, Islamabad, 2005; 169.
- Chenulu V, Venkateshwarlu V, Rangaraju R. Studies on yellow mosaic disease of mungbean. *Indian Phytopathol.* 1979; 32:230-235.
- Harnett DL. Introduction to Statistical Methods. Addison Wesley Publishing Company Inc, California, 1970, 436.
- Marimuthu T, Subramanian CL, Mohan R. Assessment of yield losses due to yellow mosaic infection in mungbean. *Pulse Crop News Letter.* 1981; 1:104.
- Nene YL. A survey of viral diseases of pulse crop in Uttar Pradesh, Research Bulletin-4. G. B. Pant University of Agriculture and Technology, Pantnagar, U. P, India, 1972, 191.
- Srinivas T, Reddy MV, Jain KC, Reddy MSS. Studies on inheritance of resistance and allelic relationship for strain 2 of pigeonpea sterility mosaic pathogen. *Annals of Applied Biology.* 1997; 130:105-110.
- Thakur RP. Genetical relationships between reactions to bacterial leaf spot, yellow mosaic virus and *Cercospora* leaf spot diseases in mungbean (*Vigna radiata*). *Euphytica.* 1977; 26:765.
- Verma RPS, Singh DP. The allelic relationship of genes giving resistance to mung bean yellow mosaic virus in black gram. *Theor. Appl. Genet.* 1986; 72:737-738.