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Gene Action and Heterosis of Resistance to Distortion Mosaic Virus in Bittergourd (*Momordica charantia* L.)

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ABSTRACT. *The damage from a new viral disease caused by bittergourd distortion mosaic virus (BDMV) has resulted in yield losses recently in many bittergourd growing areas of India. Since available varieties are susceptible to this disease, a preliminary study was conducted to identify the source of resistance from germplasm collection. Then the resistant lines and high yielding varieties were crossed in 8 x 8 half-diallel design. The result showed non-additive gene action for BDMV resistance and additive as well as non-additive gene action for fruit yield. Parent IC 68275 was identified as the best general combiner for BDMV resistance and fruit yield. The other resistant parents viz., IC 68335 and IC 68263B which produced low fruit yield can be used to diversify the source of resistance in hybridization programme. Hybrids exhibited either high yield or high resistance but seldom both except IC 68263B x IC 68275 and IC 68275 x IC 68342B. Hybrids derived from resistant verses susceptible parents exhibited low coefficient of infection to BDMV with moderately high yield.*

INTRODUCTION

Bittergourd (*Momordica charantia* L.) is one of the nutritious medicinal vegetables grown in India and Southern Asia. Recently in India, a new viral disease with distortion mosaic symptoms was reported (Giri and Mishra, 1986; Mathew *et al.*, 1991; Pandey *et al.*, 1998). It has been identified as bittergourd distortion mosaic virus (BDMV) which causes even 100% yield loss in severe cases. Majority of high yielding and locally adapted bittergourd varieties in India were susceptible to BDMV diseases; resulting in uneconomical and low productive cultivation. Therefore, a search for in built resistance in the germplasm is an essential research area in bittergourd cultivation. Accessions of Bittergourd germplasm collected in Kerala shown resistance to BDMV diseases (Arunachalam *et al.*, 2002). However, little is known on the ability to incorporate the resistant gene into high yielding cultivars through a suitable mating design. Therefore the overall objectives of this study were to identify general combining ability, heterosis and nature of gene actions of various F_1 hybrids of bittergourd.

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MATERIALS AND METHODS

This study was conducted during 2000 to 2002 at College of Horticulture, Kerala Agricultural University, Trichur, India. The climate of the experimental area is warm humid tropical with an annual rainfall of 3400 mm.

Experimental material

A total of 86 diverse bittergourd germplasm collected from different regions of India were field screened for BDMV resistance under natural epiphytotic condition during September to December 2000 and again field tested for confirmation of BDMV resistance from March to June 2001. The germplasm were maintained by selfing. From the above experiments four resistant genotypes and four susceptible genotypes were chosen for further study (Table 1). These genotypes were crossed in 8 x 8 half-diallel mating design (Griffing, 1956).

Table 1.   Origin, source and reaction to bittergourd distortion mosaic virus (BDMV) of parental genotypes.

Genotypes	District	State	Source*	BDMV reaction
IC 68335	Palakkad	Kerala	NBPGR	Highly resistant
IC 68263B	Wayanad	Kerala	NBPGR	Highly resistant
IC 68275	Wayanad	Kerala	NBPGR	Highly resistant
IC 68250A	Kannur	Kerala	NBPGR	Highly resistant
Preethi	Trichur	Kerala	KAU	Moderately susceptible
VKV 134	Trichur	Kerala	KAU	Susceptible
IC 45341	Madurai	Tamil Nadu	NBPGR	Susceptible
IC 68342B	Palakkad	Kerala	NBPGR	Highly susceptible

*NBPGR - Natural Bureau of Plant Genetic Resources, New Delhi; KAU - Kerala Agricultural University, Trichur.

Evaluation of F₁ hybrids

The 28 F_1 hybrids generated by diallel cross were sown along with their parents during October 2001 to January 2002 in a randomized complete block design (RCBD) with two replications. BDMV susceptible variety 'Priyanka' was grown as infector rows at one row per five rows of test genotypes and also all around the field border. The plants were raised in pits of size 60×60×30 cm with the spacing of 2×2 m. All crop husbandary measures as recommended by Kerala Agricultural University (KAU, 1996) were followed to establish good crop stand except the application of plant protection chemicals.

Observations on fruit yield per plant (grams) and symptom development on weekly intervals were recorded. Reaction of hybrids and parents against BDMV was scored by using a 0 to 5 scale (Arunachalam *et al.*, 2002). Then the coefficient of infection (CI) was calculated (Datar and Mayee, 1981) and these values were subjected to combining ability analysis described by Griffing (1956).

RESULTS AND DISCUSSION

Symptom development

The disease appeared at all stages of crop growth irrespective of crop season. The symptom first appeared in the newly formed leaves and rapidly spreads to other leaves on the same vine. Severely infected young plants failed to produce flowers. The infected leaves showed chlorotic spots which coalesced to form large chlorotic patches and then developed into a typical mosaic pattern. At this stage, the leaf margin started to curl upward, leaf size became reduced due to severe puckering and finally distorted. The flowers on infected vines failed to open and already formed young fruits were deformed. Generally the vines showed clustered appearance with distorted leaves and the main vine showed increased thickness and more hairiness.

Combining ability

Significance of the differences among the means of parents and crosses, revealed by the preliminary analysis, provided evidence for variability with respect to fruit yield, resistance to infection and heterosis of these traits. The mean performance of parents and general combining ability effects are presented in Table 2.

Table 2. **Mean and general combining ability (gca) effects of the eight parental genotypes.**

Parents	Genotype	Fruit yield per plant		Coefficient of infection	
		Mean	*gca* effect	Mean	*gca* effect
P_1	IC 68335	338.75	-95.81**	4.25	-6.53**
P_2	IC 68263 B	336.25	-20.01	2.45	-8.82**
P_3	IC 68275	800.00	80.32**	0.55	-11.62**
P_4	IC 68250 A	590.00	80.27**	7.50	4.57*
P_5	Preethi	473.75	0.44	39.00	-1.72
P_6	VKV 134	776.25	64.59**	46.03	5.47**
P_7	IC 45341	402.50	-95.28**	67.70	8.51**
P_8	IC 68342 B	255.00	-17.53	87.00	9.53**
SE gi			13.58		1.80
SE (gi-gj)			20.52		2.72

The parents P_1, P_4 and P_6 expressed high *gca* effect with better mean performance for fruit yield per plant. Ram *et al.* (1999) reported that performance of parents bears direct relation with *gca* effects for yield per plant. Since plants exhibiting low coefficient of infection (CI) are grouped under resistant category, a low CI and negative *gca* effects are desirable. The parents P_1, P_2 and P_3 recorded low mean values of CI with significant negative *gca* effects. Therefore, these three parents may be regarded as best general combiners for BDMV resistance. Among the parents, only P_3 showed good general combining ability effects for both the characters *viz.*, fruit yield per plant and resistance to BDMV.

The hybrid combinations *viz.*, P_6 x P_8, P_4 x P_5 and P_2 x P_3 were found to be the best combiners in terms of high *sca* effects and *per se* performance for yield per plant (Table 3). It was interesting to note that parents involved as best general combiner (P_3, P_4 and P_6) when crossed with low general combiners resulted in high heterotic crosses. This was mainly due to the fact that crossing of genetically diverse parents tend to result in better heterotic combinations. However, Ram *et al.* (1999) reported that crosses which performed better, were mostly from high x high and high x medium combinations. But in this study it was not revealed specially with high x high combination for fruit yield per plant.

The hybrid combinations like P_4 x P_8, P_3 x P_8, P_2 x P_7, P_3 x P_7 and P_1 x P_8 recorded low BDMV infection with significant negative *sca* effects. In these cases, combining the resistant parents (P_1, P_2, P_3 and P_4) with susceptible parents (P_7 and P_8) resulted in better performance with low CI and negative *sca* effects, which indicated high x low cross combinations perform better when both diverse genetic backgrounds combined together.

Heterosis

The mid parent heterosis ranged from -31.76 (P_6 x P_7) to 121.89 (P_1 x P_8) per cent and better parent heterosis from -49.0 (P_6 x P_7) to 95.96 (P_2 x P_7) per cent for yield per plant (Table 3). The cross combinations *viz.*, P_2 x P_7, P_1 x P_8 and P_4 x P_5 exhibited high heterosis for this trait. The high heterosis values for fruit yield were also reported by Choudhury and Kale (1991); Lawande *et al.* (1991) and Celine and Sirohi (1996). The top performing specific combiners also showed desired negative heterosis for coefficient of infection (BDMV resistance) *viz.*, P_4 x P_8, P_3 x P_8, P_4 x P_8, P_2 x P_7 and P_1 x P_8

Gene action

Additive and non-additive gene action was significant (σ^2_{gca} = 1126.59±803.13 and σ^2_{sca} = 37293.71±755.54) for yield per plant. Importance of additive and non-additive gene action for fruit yield was reported by Gopalakrishnan (1986). With regard to coefficient of infection additive variance was found to be non-significant (σ^2_{gca} = 28.09±34.52) and only SCA variance was found to be significant (σ^2_{sca} = 341.89±101.71). Hence, non-additive gene action was shown to be more important for mosaic resistance.

Table 3. Mean performance, specific combining ability (*sca*) effects, mid-parent heterosis (MPH) and better parent heterosis (BPH) of 28 hybrids.

Hybrids	Fruit yield per plant				Coefficient of infection			
	Mean	*sca* effects	MPH	BPH	Mean	*sca* effects	MPH	BPH
$P_1 \times P_2$	400.00	-103.39*	18.52	18.08	16.00	6.64	381.20	276.47
$P_1 \times P_3$	690.00	86.29*	21.19	-13.75	23.95	17.99**	908.42	463.53
$P_1 \times P_4$	713.75	110.09*	53.70	20.97	25.66	3.51	336.68	242.07
$P_1 \times P_5$	478.50	-45.34	17.78	1.00	8.05	-7.85	-63.01	-79.49
$P_1 \times P_6$	528.75	-59.24	-8.24	-35.02	22.97	-0.07	-8.62	-50.09
$P_1 \times P_7$	467.50	36.39	26.14	16.15	39.90	13.82*	10.91	-41.06
$P_1 \times P_8$	658.75	157.89**	121.89	94.46	6.65	-20.44**	-85.40	-92.34
$P_2 \times P_3$	969.75	290.24**	70.69	21.22	4.55	0.23	210.34	87.50
$P_2 \times P_4$	655.00	-21.46	42.08	11.53	48.80	28.35**	885.86	550.67
$P_2 \times P_5$	770.00	170.36**	90.12	62.53	11.00	-3.16	-46.86	-71.79
$P_2 \times P_6$	665.00	1.21	15.65	-18.28	9.05	-12.35*	-62.83	-80.45
$P_2 \times P_7$	788.75	281.84**	113.54	95.96	3.05	-21.39**	-91.44	-95.57
$P_2 \times P_8$	408.75	-132.91**	51.80	33.46	37.63	12.21	-15.83	-56.75
$P_3 \times P_4$	740.00	-54.79	4.32	-9.38	35.30	18.25**	782.50	370.67
$P_3 \times P_5$	478.75	-221.21**	-24.83	-40.16	5.37	-5.44	-73.06	-86.36
$P_3 \times P_6$	575.00	-189.11**	-28.74	-29.34	30.65	12.70*	31.76	-33.41
$P_3 \times P_7$	460.00	-147.24**	-23.49	-42.50	0.00	-20.99**	-100.00	-100.00
$P_3 \times P_8$	877.50	195.51**	66.35	9.69	0.00	-22.01**	-100.00	-100.00
$P_4 \times P_5$	1120.00	420.09**	110.58	89.83	37.30	10.35	60.43	4.36
$P_4 \times P_6$	588.75	-175.31**	-16.12	-27.65	58.00	23.86**	116.72	26.02
$P_4 \times P_7$	676.25	69.06	36.27	14.62	39.10	1.92	3.99	-42.25
$P_4 \times P_8$	713.75	31.81	68.93	20.97	3.50	-34.75**	-92.70	-96.03
$P_5 \times P_6$	705.25	22.01	9.71	-13.21	11.96	15.89**	-71.87	-74.01
$P_5 \times P_7$	518.75	-8.61	18.40	9.50	23.95	-6.94	-55.11	-64.62
$P_5 \times P_8$	557.50	-44.61	53.00	17.68	24.15	-7.76	-61.67	-72.24
$P_6 \times P_7$	415.00	-176.51**	-31.76	-49.00	20.65	-17.43**	-63.68	-69.50
$P_6 \times P_8$	1112.50	446.24**	108.19	36.71	26.00	-12.00**	-60.46	-69.77
$P_7 \times P_8$	518.75	9.36	57.79	28.88	40.00	-2.14	-48.29	-54.02
SEsij		41.62				5.53		
SE(sij-sik)		61.58				8.18		
SE(sij-skl)		58.06				7.71		

CONCLUSIONS

The genotype IC 68275 (P₁) showed resistance to BDMV with high fruit yield. Two hybrid combinations (P₂ x P₃ and P₃ x P₈) of P₃ parent showed high fruit yield and good resistance to BDMV. The parents P₁, P₂ and P₄ showed resistance to BDMV but recorded low yield. All hybrid combinations involving P₁, P₂ and P₄ parents with P₃, P₅, P₆, P₇ and P₈ recorded either high yield or good resistance but seldom both except P₂ x P₃ and P₃ x P₈ crosses. Similarly hybrids P₆ x P₈ and P₄ x P₅ exhibited high yield but showed susceptibility to BDMV. These hybrids can be further tested with adequate plant protection measures to use as promising hybrids. The resistant parents IC 68335 (P₁) and IC 68263B (P₂) resulted in low yield per plant. These genotypes can be crossed further with high yielding varieties to increase genetic diversity of BDMV resistance. The gene actions suggest preponderance of non-additive gene action for both the traits. Therefore, recurrent selection would be the best option to improve both yield and resistance to BDMV. The cross (P₂ x P₃) which showed relatively low level of infection, was derived from two resistant sources has potential for selection of transgrassive segregants with combined resistance from both parents.

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