



Estimates of Gene Effects of Yield and Mosaic Resistance in Yard Long bean [*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt]

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ABSTRACT

Background: The incidence of viral diseases in yard long bean is becoming a severe threat in tropical regions, limiting the yield considerably. Host plant resistance is the most efficient and ecologically friendly method of managing viral infections. Resistance sources of major viruses viz; CABMV and BICMV causing mosaic disease have been identified in many cowpea breeding programmes. However, little is known about the gene action imparting virus resistance. Understanding the genetics of host resistance and genetic variability, can aid in developing breeding programs that will use genetic resistance to manage viral diseases reliably and efficiently. The current study used generation mean analysis to examine the gene action and inheritance of yield and mosaic resistance.

Methods: The six populations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) of three exceptional crosses, Githika × Manjari, KAU Deepika × Manjari and KAU Mithra × Manjari, which displayed heterosis and mosaic resistance in previous field trials were assessed in a replicated field experiment in Summer 2023. All the generations were screened for mosaic resistance in the field and the inheritance and gene action of mosaic resistance and yield parameters were investigated using the generation mean analysis.

Result: Epistasis interactions were discovered in the majority of the characters in the different crosses. The scaling tests for mosaic resistance were not statistically significant, suggesting that the additive-dominance model was sufficient for Cross I and II. However, dominance×dominance epistasis was evident in Cross III. For plant yield, Crosses II and III showed the prevalence of dominant gene action, but cross I revealed dominance×dominance (I) action. The results suggested the utilization of hybridization and selection, heterosis breeding and recurrent selection for improving different traits in yard long bean.

Key words: Gene action, Generation mean analysis, Mosaic resistance, Yard long bean.

INTRODUCTION

Yard long bean or trailing type of vegetable cowpea [*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt] is a subspecies of cowpea [*Vigna unguiculata* (L.) Walp.] distinguished by its trailing nature and long pods. It is a warm season vegetable crop widely cultivated in the tropical and sub-tropical areas of the world. It is a rich and cheap source of vegetable protein, vitamins A and C, fibre and other minerals (Suma *et al.*, 2021). Yard long bean has emerged as a remunerative vegetable crop in India, cultivated for its tender pods. High productivity, high nutritive value, suitability in different cropping systems, high nitrogen fixation ability and drought tolerant features make it a cost-effective and preferred crop in the tropics. In Kerala, yard long bean known as “Valli payar” is one of the most preferred vegetable crops.

Among different biotic stresses that limit the yard long bean production, aphid-transmitted potyvirus- *Black eye cowpea mosaic virus* (BICMV) has been reported as a significant threat in many parts of India (Radhika *et al.*, 2006; Shilpashree, 2006 and Pavithra *et al.*, 2014). Several studies have confirmed that the major virus that causes mosaic disease of cowpea in Kerala is Black eye cowpea mosaic virus (BICMV) (Radhika, 1999; Krishnapriya, 2015 and Chandran *et al.*, 2021). Symptoms include vein clearing, vein banding, leaf deformation, reduced leaf size,

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stunting with reduced flowering and fruiting. Resistance breeding is the most reliable and effective method of

managing viral diseases. Many researchers have identified sources of resistance to BICMV and CABMV. But, improved cultivars resistant to mosaic virus are lacking in yard long bean, despite the availability of several high yielding types. Understanding the genetics of host resistance and genetic variability can aid in developing breeding programmes that ensure stable and successful disease control.

Generation mean analysis, developed by Hayman (1958), is a standard method to study the inheritance of quantitative traits. Understanding the nature and magnitude of resistant genotypes is a prerequisite in a resistant breeding programme. Generation mean analysis estimates the main gene effects and their interactions controlling the traits. Here, an attempt was made to use generation mean analysis to quantify the effects of different genes and determine their relative significance in genetic control of yield and mosaic resistance in yard long bean.

MATERIALS AND METHODS

The research was carried out at the Pepper Research Station, Panniyur, Kannur (10°32'N latitude and 75°16' longitude), between 2022 and 2023. Three superior hybrids (Githika × Manjari, KAU Deepika × Manjari and KAU Mithra × Manjari), their F_2 population and the back cross generations (BC_1 and BC_2) made up the materials for the generation mean analysis. Based on their high heterotic potential, high yield, mosaic resistance and good general combining ability for yield traits, the hybrids were selected from earlier research conducted at the Department of Vegetable Science, College of Agriculture, Vellayani. In a replicated field experiment conducted in the summer of 2023, the 18 treatments were assessed using a randomised block design with three replications at 1 m × 1 m spacing. One replication comprised two rows of the backcross generations BC_1 and BC_2 , seven rows of F_2 and one row of the parents and F_1 . There were ten plants in each row. During the cropping period, cultivation measures were adopted as per Package of Practices (KAU, 2016).

Pod length, pod weight, pods per plant, yield per plant and days to harvest were the yield parameters studied. The populations were tested for mosaic resistance in the field by a 0-5 scale scoring method proposed by Bos (1982). Based on the numerical scoring, the disease index or vulnerability index was also calculated using suitable formula. The information on additive, dominance and digenic epistatic interactions was obtained by applying the generation mean analysis (Hayman, 1958) and scaling test (Mather, 1949) to the mean VI values, variances and standard errors. The scaling tests, A, B, C and D were conducted to examine the adequacy of additive-dominance model combining weighted least square method of Hayman (1958). The significance of the scales and gene effects were tested by using the t-test (Singh and Chaudhary, 1999).

RESULTS AND DISCUSSION

The means, variances and vulnerability index for mosaic disease in six populations of three crosses are furnished

in Table 1. The mean vulnerability index among populations of cross I varied from 13.33 (Manjari) to 37.76 (Githika). The lowest vulnerability index was observed in resistant parent Manjari, followed by F_2 (17.42). The hybrid and the segregating populations gave a moderately resistant reaction. The mean VI values varied widely among cross II populations, which ranged from 13.33 (Manjari) to 52.50 (KAU Deepika). All the generations except parents exhibited moderate resistance to mosaic disease. The mean values in cross III, varied between 13.33 (Manjari) and 45.00 (KAU Mithra). F_1 recorded lowest VI value (16.67) besides Manjari. The disease reaction of F_1 was medium resistant while all the segregating populations recorded a moderately susceptible reaction. Existence of transgressive segregants was identified for mosaic resistance in all the crosses. The parent Manjari gave a consistent resistance reaction against mosaic virus in the field which is in accordance with Krishnan *et al.* (2021).

A highly positive and significant "m" value was found for every character studied in the crosses, indicating substantial variation within the generations for all characters. This suggests that these traits can be improved by adopting suitable breeding strategies. Similar results have been reported for various traits in cowpea by Lovely (2005), Sobda *et al.* (2018), Merin and Sarada (2019) and Jain *et al.* (2024). In terms of plant yield, the F_1 means of each cross outperformed the parents (Fig 1). The highest yield per plant was recorded in F_1 (1530.80 g) of cross II, followed by F_1 (1320.65) of cross III. Breeding approaches for improving different attributes are determined by the type of gene action. For the estimation of additive, dominance and epistasis effects, generation mean analysis was performed. The outcomes of the scaling tests and estimation of genetic components of the above three crosses for various characters are presented in Table 2 and 3.

Scaling tests for pod length indicated that Scale A was significant in cross III, whereas Scale B was non-significant in all crosses. Scale C was significant for all crosses, but in a negative direction, for cross II. Scale D was positively significant in cross I but negatively significant in crosses II and III. The significance of different scales for the trait indicates inadequacy of additive dominance model and presence of epistasis. The dominance gene action was found to be positive and substantial in crosses II and III, but negative in cross I. All the crosses showed a significant additive × additive (i) effect, but in an undesirable direction for cross I. Cross II and III were negatively significant for dominance × dominance (I) interaction. Inter-allelic interactions have a significant role in improving the phenotype, as indicated by the negative estimations of the various genetic components. Cross II and III have opposing values for the dominance effect (h) and the dominance × dominance (I) interaction, implying a duplicate form of epistasis. Biparental mating in the early generations may be used to enhance these traits by exploiting duplicate epistasis. Pedigree selection or recurrent selection will be beneficial. Non-additive gene action has been documented

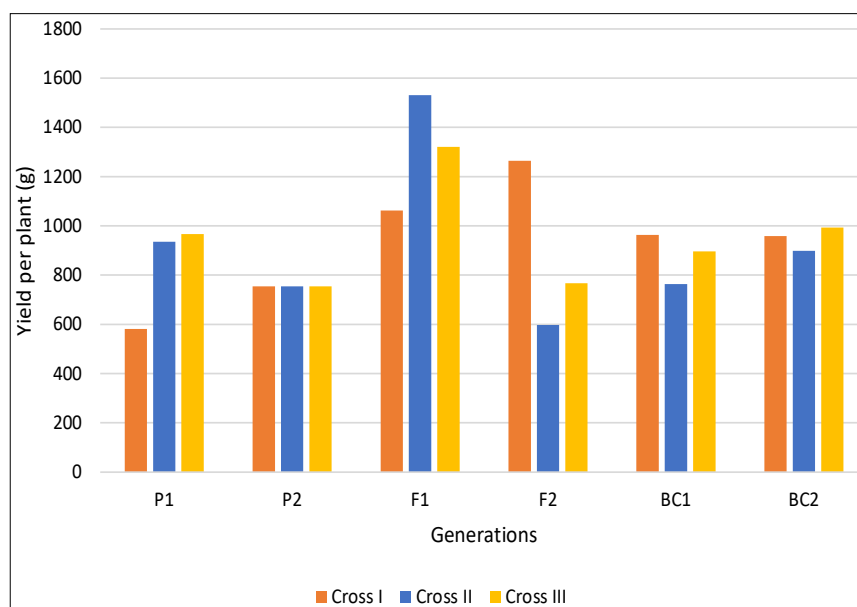


Fig 1: Generation means for yield per plant.

for pod length by Dinakar *et al.* (2018); Priya *et al.* (2018); Das *et al.* (2021); Edematie *et al.* (2021) and Owusu *et al.* (2022).

For pod weight, scale A was significant for cross III and scale B was positively significant for cross II and III. Scale C was positively significant for cross I and negatively significant for cross II. Significant D scale value was recorded for cross I in the positive and negative directions for cross II and III. Of the main gene effects, the additive effect (d) was substantial and positive only in cross III. The results of scaling tests indicated all types of digenic interactions. The dominance effect (h) were significant in all crosses but in negative direction for cross I. For all crosses, the additive $\times$ additive (i) interaction was significant; however, for cross I, it was negative. Cross III showed a strong additive $\times$ dominance (j) effect, while crosses II and III showed a significant dominance $\times$ dominance (l) interaction in the undesirable direction. The crosses II and III showed signs of duplicate epistasis. Cross I showed a substantial magnitude of both the additive interaction and the dominance effect, but in an undesired direction, indicating that these factors predominate in the inheritance of the trait. In crosses II and III dominance and additive $\times$ additive gene effects were relevant, along with duplicate epistasis. The character may be enhanced in biparental progenies through recurrent selection, facilitating the duplicate form of non-allelic interaction. The prevalence of non-additive gene action for pod weight in cowpea was observed by Lovely (2005); Rashwan (2010); Adeyanju *et al.* (2012), Merin and Sarada (2019).

The scale values, A, C and D, were positively significant in cross I and negatively significant in cross III for pods per plant. All the scales were negatively significant in Cross II.

High significance of more than one scale implies the existence of inter-allelic interactions. All the crosses had a significant positive mean (m), whereas all had a significant negative additive gene effect (d). The dominance (h) effect and additive $\times$ additive (i) interaction were negatively significant in cross I and positively significant in cross II and III. The predominance of inter-allelic interactions is indicated by a high magnitude of additive and dominance gene action in cross I, but in an undesired direction. In crosses II and III, dominant gene action had a major influence on the trait's inheritance. Hence, the trait can be improved by heterosis breeding in II and III. Involvement of both additive and non additive gene action in improvement of the trait has been reported by Uma and Kalubowila (2010); Ushakumari *et al.* (2010); Merin (2018); Shinde *et al.* (2021) and Owusu *et al.* (2022).

For yield per plant, scale A was significant across all crosses. In cross II, scale B was negatively significant. Scales C and D were favourably significant in Cross I, but negatively significant in cross II and III. Hence, the presence of digenic interactions were confirmed for the character. In crosses II and III, the additive (d) effect was significant and negative. While the additive $\times$ additive (i) interaction and the dominance (h) effect were unfavourably significant in cross I, they were positively significant in cross II and III. Negative significance was noted for additive $\times$ dominance (j) component in cross II and III, whereas positive significance was noticed for dominance $\times$ dominance (l) component in cross I. The highest magnitude of dominance gene action was in crosses II and III, while the predominance of dominance $\times$ dominance effect was evident in cross I. Duplicate epistasis existed in crosses I and III based on the opposite directions of significance for the dominance

Table 1: Mean, variances and disease reaction of six generation for vulnerability index of mosaic disease in yard long bean

Crosses		P1	P2	F1	F2	BC1	BC2
Cross I (Githika × Manjari)	Mean (VI)	37.76	13.33	26.67	17.42	29.16	18.33
	Variance	14.96	233.32	33.34	22.87	39.58	2.78
	Disease score*	0-3	0-1	0-1	0-5	0-2	0-2
	Disease reaction	Moderately susceptible	Resistant	Moderately resistant	Moderately resistant	Moderately resistant	Moderately resistant
Cross II (KAU Deepika × Manjari)	Mean (VI)	52.50	13.33	26.67	19.36	36.39	25.83
	Variance	81.252	233.32	33.34	1.89	55.82	89.59
	Disease score	0-4	0-1	0-1	0-3	0-3	0-4
	Disease reaction	Susceptible	Resistant	Moderately resistant	Moderately resistant	Moderately susceptible	Moderately resistant
Cross III (KAU Mithra × Manjari)	Mean (VI)	45.00	13.33	16.67	31.47	38.75	31.11
	Variance	25	233.32	133.33	20.09	95.32	12.05
	Disease score	0-3	0-1	0-1	0-5	0-4	0-4
	Disease reaction	Moderately susceptible	Resistant	Moderately resistant	Moderately susceptible	Moderately susceptible	Moderately susceptible

Range of disease score.

Table 2: Generation means, scale values and genetic components for yield characters of three crosses in yard long bean

	Pod length (cm)			Pod weight (g)			Pods per plant		
	Cross I	Cross II	Cross III	Cross I	Cross II	Cross III	Cross I	Cross II	Cross III
Scale values									
A	-0.30	3.43	15.93**	22.35	1.35	18.95**	20.55*	-58.35**	-22.75*
B	-1.08	1.85	7.13	20.00	4.15*	4.85*	0.40	-41.50**	-20.95
C	6.26**	-16.64**	0.26*	18.25*	-11.38*	0.64	85.26**	-175.95**	-75.64**
D	3.82**	-10.96**	-11.39**	21.38*	-8.44**	-11.58**	32.16**	-38.05**	-15.97*
Genetic components									
m	45.25**	44.31**	47.73**	21.38**	20.58**	22.76**	90.29**	47.45**	62.54**
d	1.89	7.53**	10.91**	1.15	3.00	10.00**	-13.53*	-22.85**	-22.00**
h	-9.01*	19.63**	19.35**	-9.35**	14.93**	22.46**	-63.56**	103.43**	52.64**
i	-7.64*	21.92**	22.79**	-6.42*	16.88**	23.16**	-64.31**	76.10**	31.94*
j	0.39	0.79	4.40	-0.03	-1.40	7.05**	10.08	-8.43	-0.90
l	9.01	-27.19**	-45.85**	6.17	-22.38**	-46.96**	43.36	23.75	11.76
Gene action	D		D	D		D	D		

*Significant at 5% level; **Significant at 1% level; D- Duplicate epistasis.

(h) and dominance×dominance (l) genetic components. This may require complex breeding strategies to exploit the genetic variation. The greater magnitude of dominance and dominance × dominance (l) component indicates that heterosis breeding or pedigree method is suitable for enhancing this character, which is in agreement with the findings of Patel *et al.* (2009), Adeyanju (2012) and Merin (2018).

In cross I, scales A and B were significant for days to harvest, with the latter in a negative direction. Scales A, C and D were significant and positive in cross II, but scale B was negative. All the scales were negatively significant, except the positive D scale in cross III. Among the main gene effects, there was a significant positive mean (m) and additive (d) effect in all crosses. The dominance (h)

effect and additive × additive (i) were negatively significant for cross II and III and non-significant for cross I. The additive × dominance (j) interaction was positively significant for cross I and II, whereas the dominance×dominance (l) effect was significant only in cross III. In cross I, the additive × dominance epistasis predominated, whereas in cross III, the dominance×dominance effect was prevalent. There was an additive×dominance interaction in cross II and the dominance components showed the highest amplitude in a desirable negative direction. The presence of duplicate epistasis was also observed in cross III. The findings imply the relevance of dominance action, dominance epistasis and additive × dominance action in the trait's inheritance. Hybridisation and selection would be appropriate breeding methods for the character enhancement. Non-allelic

Table 3: Generation means, scale values and genetic components for yield characters of three crosses in yard long bean

	Days to harvest			Yield per plant (g)			Incidence of mosaic virus		
	Cross I	Cross II	Cross III	Cross I	Cross II	Cross III	Cross I	Cross II	Cross III
Scale values									
A	9.20**	18.00**	-12.85**	281.73*	-938.40**	-494.95**	-6.11	-6.39	15.83
B	-7.50**	-7.70**	-11.45**	101.48	-487.5*	-87.30	-3.34	11.66	32.22
C	-5.19	30.27**	-9.76**	1598.07**	-2360.5**	-1294.30**	-34.75	-41.7	34.21**
D	-3.45	9.99**	7.27**	607.43**	-467.31**	-356.03**	-12.65	-23.5	-6.92
Genetic components									
m	69.84**	80.28**	72.26**	1264.64**	597.57**	766.95**	73.57*	89.27*	31.47*
d	5.28**	12.98**	3.35*	4.15	-134.65*	-97.23	12.22	19.59*	7.64
h	3.22	-26.89**	-25.34**	-820.26**	1620.82**	1172.30**	-137.7*	-86.92	14.67
i	6.89	-19.97**	-14.54**	-1214.86**	934.62**	712.05**	-	-	13.84
j	8.35**	12.85**	-0.7	90.13	-225.45*	-203.83*	-	-	-8.20
l	-8.59	9.670	38.84**	831.66*	491.28	-129.80	-	-	186.99**
Gene action			D	D		D			

*Significant at 5% level; **Significant at 1% level; D- Duplicate epistasis.

interactions were reported by Pal *et al.* (2007); Jithesh (2009); Merin and Sarada (2019) and Santos *et al.* (2020) for the trait.

The results of the scaling tests for the incidence of mosaic disease in yard long bean revealed that in cross I and cross II, scales A, B, C and D were not significant, but in cross III, scale C alone was significant in the preferred direction for mosaic resistance. The findings indicated absence of non-allelic interactions in crosses I and II and that the additive-dominance model was adequate. Hence, they were subjected to three parameter tests to estimate the gene effects. While the additive (d) effect in cross I was not significant, the dominance (h) effect was in the direction of susceptibility. A highly significant mean effect in cross I suggest improving the trait through simple breeding methods. The mean (m) and additive (d) effects were significant and positive in cross II. The dominance effect (h) was non-significant. The preponderance of additive effects indicates that selection techniques should be used to enhance the trait. Scaling test results showed a non-allelic interaction in cross III and that the additive-dominance model was insufficient. The mean (m) effect was only significant among the main effects. Among the epistatic gene interactions, the dominance×dominance (l) interaction was significant and all others were non-significant. Hence, the mosaic resistance can be incorporated by the pedigree method of selection. Singh (2004) and Singh *et al.* (2016) have also identified epistasis for mosaic resistance in cowpea.

CONCLUSION

In the first cross (Githika × Manjari), epistatic interactions were noted for each character, with both additive and dominant interactions being prominent in most of the traits. The dominant gene or dominance×dominance (l)

interaction was observed in the majority of traits in cross II (KAU Deepika × Manjari). In cross III (KAU Mithra × Manjari), both the additive × additive (i) component and the dominance × dominance (l) component, or one of them, were found to be significant for the inheritance of yield traits. Duplicate epistasis was identified for four traits: pod length, pod weight, yield per plant and days to harvest, all of which were present in cross III. Thus, utilizing both fixable and non-fixable gene effects will result in the enhancement of these attributes. The prevalence of dominant gene effects or dominance×dominance was observed for yield per plant and mosaic disease incidence. Therefore, breeding techniques such as heterosis breeding, pedigree selection and recurrent selection can be adopted to improve these qualities in yard long bean.

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Disclaimers

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Conflict of interest

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