Research article

Diallel analysis for different horticultural traits in bitter gourd (*Momordica charantia* L.) using Hayman's numerical and graphical approach

K. Radha Rani

College of Horticulture, Rajendranagar, Hyderabad, India
*Corresponding Author: radha.aphu@gmail.com   [Accepted: 24 August 2014]

Abstract: Twenty eight F_1 hybrids developed during summer, 2010 by crossing 8 diverse parents in all possible combinations without reciprocals were evaluated for diallel analysis for genetic parameters and graphic representation for yield and yield attributing traits during summer 2011 at College of Horticulture, Rajendranagar, Hyderabad, India. The validity of the assumptions of diallel analysis was confirmed for all the traits studied except number of fruits/vine other traits such as average fruit weight, pulp thickness and yield/vine as t^2 values for these traits were found to be significant. The dominance variance was found to be greater in magnitude than additive variance for all the traits indicating the presence of over dominance controlling the traits which was further confirmed from the regression line of Wr-Vr graph was found to cut the ordinate below origin. The distribution of array points along and around the regression line for yield/vine indicated that the parents IC-470560, IC-470550 and IC-033227 had an excess of dominant genes whereas IC-045339 being farthest from the origin carrying maximum recessive genes. The predominance of dominant gene action coupled with low heritability observed for all the traits except average fruit weight suggesting the importance of heterosis breeding for improvement of yield and yield attributing traits in bitter gourd.

Keywords: Hayman's graphical approach - Genetic parameters - Wr-Vr graph - Gene action.

[**Cite as:** Radha Rani K (2014) Diallel analysis for different horticultural traits in bitter gourd (*Momordica charantia* L.) using Hayman's numerical and graphical approach. *Tropical Plant Research* 1(2): 60–64]

INTRODUCTION

The procedure of quantitative genetic analysis to estimate genetic parameters from the component of genetic variation, essentially involves calculating variance and covariances of arrays of diallel table and regression of variance of parent upon covariances of hybrids to ascertain dominance, additive and non-additive gene action and finally inheritance pattern of particular character leading to the targeted selection of entries for further utilization/developing commercial cultivars. Bitter gourd is an important commercial crop rich in nutrients and therapeutic properties. Though a wide range of genetic variability is present in this crop for yield and other related characters, a very little attempt has been done on inheritance of characters. Hence, the present investigation was undertaken to supplement the genetic parameters interpretations with diallel graphs and to pinpoint which parents contain preponderance of dominance/recessive genes with increasing/decreasing character attributes for utilizing them judiciously in future breeding programmes.

MATERIAL AND METHODS

Eight genetically diverse inbreds of bitter gourd *viz.*, IC-033227, IC-044417, IC-044438, IC-045339, IC-085622, IC-470550, IC-470558 and IC-470560 were crossed in dialle mating design without reciprocals to get 28 F_1 hybrids during summer 2010. The hybrids along with parents were evaluated at college of Horticulture, Rajendranagar, Hyderabad in a randomized block design with three replications during summer 2011. The seeds were sown in rows at spacing of 2 m between rows and 0.5 m between plants. The crop was raised by following the recommended package of practices. Data recorded on fifteen characters *viz.*, vine length (m), number of laterals/vine, internodal length (cm), days to 1st male flower appearance, days to 1st female flower appeared, node number at which 1st male flower appeared, node number at which 1st female flower appearance, sex ratio (male to female), number of fruits/vine, average fruit weight (g), fruit length (cm), fruit girth (cm), pulp

thickness (cm), number of seeds/fruit and yield/vine (kg) from five randomly selected plants in each replication. Gene action was elucidated by adopting genetical and graphical analysis as suggested by Hayman (1954a,b).

RESULTS

The validity of the assumptions of diallel analysis was confirmed for all the traits studied except number of fruits/vine, average fruit weight, pulp thickness and yield/vine as t^2 values for these traits were found to be significant (Table 1). The regression line of Wr-Vr graph was found to be deviate from unit slope for all the characters in the present study. However, the 'b' values were exceeding 0.5 for 8 characters *viz*., vine length, number of laterals/vine, intermodal length, days to 1st male & female flower appeared, node number at 1st male and female flower appeared and sex ratio indicating the absence of epistasis (Table 1). Components of variance due to genetic and environmental factors were presented in table 2. Both additive and dominance component of variation for inheritance was significant for all the traits studied except average fruit weight, fruit length, pulp thickness, number of seeds/fruit and yield/vine for which dominance component only was significant (Table 2). The dominance variance was found to be greater in magnitude than additive variance for all the traits indicating the presence of over dominance controlling the traits which was further confirmed from the regression line of Wr-Vr graph was found to cut the ordinate below origin.

Table 1. Estimates of t^2, a, b, SEb, b-0/SEb and 1-b/SEb.

Character	t^2	a	b	SEb	b-0/SEb	1-b/SEb
Vine length	0.529	-0.034	0.875	0.111	7.882	1.126
No. of laterals/vine	2.035	-0.069	0.696	0.140	4.971	2.174
Intermodal length	0.013	-0.156	0.732	0.260	2.815*	1.030
Days to 1st male flower	1.048	0.256	0.820	0.119	6.890**	1.512
Days to 1st female flower	0.024	1.587	0.608	0.351	1.732*	1.116
Node No. at 1st male flower	0.368	-0.363	0.843	0.343	2.457	0.457
Node No. at 1st female flower	0.688	-0.038	0.576	0.223	2.583*	1.901
Sex ratio	0.603	-0.205	1.035	0.198	5.227**	-0.176
No. of fruits/vine	8.481**	2.167	0.416	0.126	3.301*	4.634*
Ave. fruit weight	6.355**	6.618**	0.163	0.162	1.006*	5.166**
Fruit length	1.001	-0.193	0.303	0.257	1.179	2.712*
Fruit girth	1.697	-0.110	0.386	0.218	1,771*	2.816**
Pulp thickness	2.800*	0.010	-0.059	0.215	-0.274*	4.925**
No. of seeds/fruit	3.626*	0.026	0.292	0.186	1.569	3.806*
Yield/vine	8.460**	0.019	0.198	0.144	1.375	5.569**

*Significant at 0.05% probability   ** Significant at 0.01% probability

The dominant and recessive genes contributed by parental arrays for different traits were depicted in from fig. 1 and fig. 2. For vine length, the distribution of array points showed (Fig. 1A) the concentration of dominant genes in the parent IC-085622 (array 5) followed by IC-470550 (array 6) as they were located close to origin while the parent IC-470558 (array 7) contributed most recessive genes as its position was far away from origin. Similarly for number of laterals/vine, IC-044438 had most dominant genes (Fig. 1B) while IC-045339 had most recessive genes. Based on their position of arrays, IC-470558 showed (Fig. 1C) most dominant genes while IC-044417 contributed recessive genes for intermodal length. The results of graphic analysis (Fig. 1D&E) indicated that the parent IC-470558 had most dominant genes both for days to 1st male and female flower whereas IC-045339 and IC-033227 had most recessive genes for days to 1st male and female flower respectively. For node number at 1st male and female flowers (Fig. 1F&G), the parent IC-470558 contributed dominant genes while IC-045339 contributed recessive genes. The parent IC-045339 had recessive genes while IC-044438 contained most dominant genes for sex ratio (Fig. 1H).

Maximum frequency of dominant alleles for number of fruits/vine was observed in IC-033227 followed by IC-470550 and IC-470560 (Fig. 1I), for average fruit weight (Fig. 2A) in array, IC-470560 followed by IC-033227, for fruit length (Fig. 2B) in IC-470550 and IC-470560, for fruit girth (Fig. 2C) in IC-470560, for pulp thickness and number of seeds/fruit (Fig. 2D&E) in IC-085622.while parent IC-045339 had maximum recessive genes for all these traits except for number of fruits/vine (IC-044417) and number of seeds/fruit (IC-470550). The distribution of array points along and around the regression line for yield/vine (Fig. 2F) indicated that the

Table 2. Estimates of genetic parameters for different traits in bitter gourd.

Characters	D + SE (D)	F + SE (F)	H_1 + SE (H_1)	H_2 + SE (H_2)	h^2 + SE (h^2)	E + SE (E)
Vine length	0.05**+0.008	0.02+0.02	0.22**+0.12	0.18**+0.02	0.60**+0.01	0.003+0.003
No. lateral/vine	0.24**+0.04	-0.06+0.08	0.84**+0.08	0.77**+0.07	0.46**+0.05	0.02+0.01
Intermodal length	0.18**+0.07	0.22+0.16	0.91**+0.15	0.70**+0.13	1.84**+0.09	0.10**+0.02
Days to 1st male flower	6.98**+0.51	4.07**+1.20	6.69**+1.17	5.40**+1.02	-0.10+0.68	0.74**+0.17
Days to 1st female flower	15.49**+2.84	7.95+6.71	18.98**+6.53	14.64**+5.68	0.69+3.81	0.65+0.95
Node No. at 1st male flower	1.57**+0.34	1.87*+0.90	3.25**+0.87	2.61**+0.76	0.14+0.51	0.17+0.13
Node No. at 1st female flower	2.73**+0.65	1.15+1.54	5.82**+1.50	5.29**+1.30	1.23+0.87	0.24+0.22
Sex ratio	0.52**+0.09	0.44*+0.21	1.13**+0.21	0.80**+0.18	1.03**+0.12	0.09**+0.03
No. of fruits/vine	8.03**+1.18	-4.36+2.78	15.59**+2.71	12.25**+2.35	14.08**+1.58	0.25+0.39
Ave. fruit weight	37.02+38.61	14.36+91.22	185.48*+88.75	163.48*+77.21	101.31+51.78	4.96+12.87
Fruit length	1.93+1.25	1.70+2.95	9.41**+2.87	7.26**+2.50	2.94+1.67	0.05+0.42
Fruit girth	1.14*+0.45	1.69+1.07	3.18**+1.04	2.24*+0.91	2.01**+0.61	0.05+0.15
Puplp thickness	0.03+0.03	0.04+0.08	0.23**+0.08	0.20**+0.07	0.14**+0.04	0.003+0.01
No. of seeds/fruit	0.98+0.89	0.50+2.09	3.67+2.04	3.49*+1.77	0.10+1.19	0.86**+0.30
Yield/vine	0.07+0.04	-0.02+0.10	0.28**+0.09	0.23**+0.08	0.22**+0.05	0.002+0.01

*Significant at 0.05% probability   ** Significant at 0.01% probability

parents IC-470560, IC-470550 and IC-033227 had an excess of dominant genes whereas IC-045339 being farthest from the origin carrying maximum recessive genes.
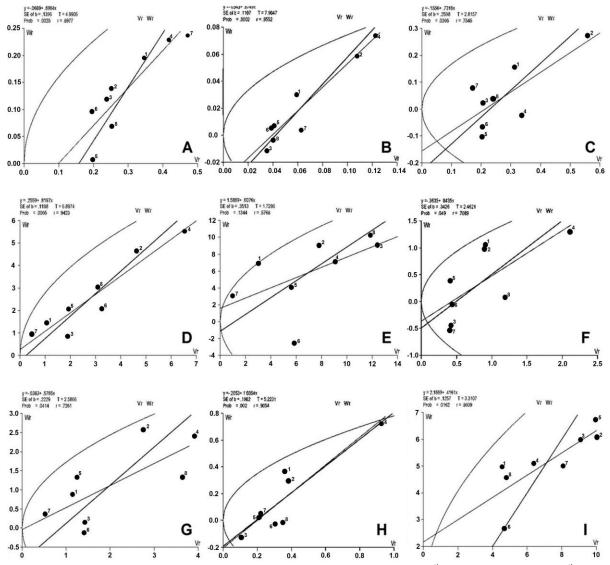

Figure 1. A, Vine length; **B,** Number of laterals/vine; **C,** Internode length; **D,** Days to 1st male flower; **E,** Days to 1st female flower; **F,** Node number at 1st male flower; **G,** Node number at 1st female flower; **H,** Sex ratio; **I,** Number of fruits/vine.
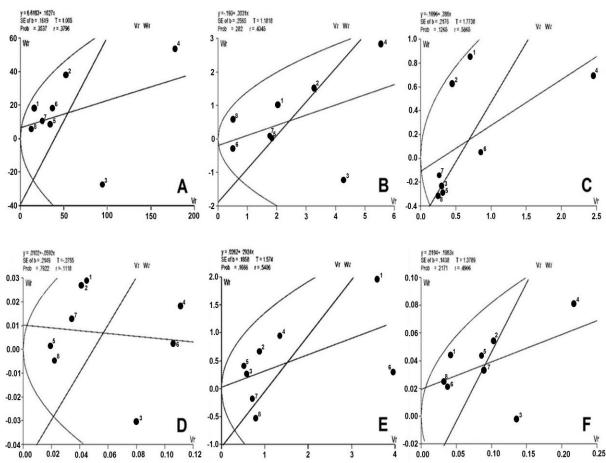
Figure 2. A, Average fruit weight; **B,** Fruit length; **C,** Fruit girth; **D,** Pulp thickness; **E,** Number of seeds/fruit; **F,** Yield/vine.

DISCUSSION AND CONCLUSION

Both additive and dominant genes in the inheritance of vine length, number of laterals/vine, days to 1st male and female flower, node number at 1st male & female flower, sex ratio, fruit girth had been reported earlier by Sundaram (2007). Similarly the involvement of additive and dominant genes in the inheritance of fruit girth and vine length in bitter gourd had been recorded by Devdass (1993) while Lawande & Patil (1991) found the involvement of both additive and dominant genes in the inheritance of number of fruits/vine. The presence of both additive and non-additive gene action along with high heritability was observed for majority of the traits indicating the possibility of isolating superior inbreds from segregating generations as suggested by Sundaram (2007). Reciprocal recurrent selection could be adopted to exploit both additive and non-additive gene effects. The predominance of dominant gene action coupled with low heritability observed for all the traits except average fruit weight suggesting the importance of heterosis breeding for improvement of yield and yield attributing traits in bitter gourd. Similar reports were mentioned by Sundaram (2007) in bitter gourd. The possibilities for commercial exploitation of heterosis had also been reported earlier by Chaubey & Ram (2004), Patel *et al.* (2005), Maurya *et al.* (2009) and Thangamani *et al.* (2011) in bitter gourd.

REFERENCES

Chaubey AK & Ram HH (2004) Heterosis for fruit yield and its components in bitter gourd (*Momordica charantia* L.). *Vegetable Science* 31(1): 51–53.

Devdass VS (1993) *Genetic studies on fruit and seed yield and quality in bitter gourd (Momordica charantia L.), Ph.D. (Hort) Thesis*. Tamil Nadu Agricultural University, Coimbatore. Chennai, India.

Hayman BI (1954a) The theory and analysis of diallel crosses. *Genetics* 39: 789–808.

Hayman BI (1954b) The analysis of variance of diallel tables. *Biometrics* 10: 235–244.

Lawande KE & Patil AV (1991) Studies on gene action in bitter gourd (*Momordica charantia* L.). *Vegetable science* 18(2): 192–199.

Maurya M, Mohan J & Kushwaha L (2009) Studies on heterobeltiosis and combining ability in bitter gourd (*Momordica charantia* L.). *Pantnagar Journal of Research* 7(2): 177–179.

Patel NB, Patel JB, Solanki SD & Patel JJ (2005) Heterosis, Inbreeding depression, heritability and genetic advance study in bitter gourd (*Momordica charantia* L.). *International Journal of Bioscience Reporter* 3 (2): 278–283.

Sundaram V (2007) Hayman's diallel analysis in bitter gourd (*Momordica charantia* L.) under salt stress. *The Asian Journal of Horticulture* 2(2): 80–86.

Thangamani C, Pugalendhi L, Sumathi T, Kavitha C & Rajashree V (2011) Estimation of combining ability and heterosis for yield and quality characters in bitter gourd (*Momordica charantia* L.). *Electronic Journal of Plant Breeding* 2(1): 62–66.