Electronic Journal of Plant Breeding, 4(3): 1237-1241 (Sep 2013)
ISSN 0975-928X

Research Article

Study of gene effects for yield and its component traits in bitter gourd (*Momordica charantia* L.) by generation mean analysis

K. Radha Rani[1*], K. Ravinder Reddy[2] and Ch. Surrender Raju[3]
[1] College of Horticulture, Rajendranagar, Hyderabad
[2] College of Horticulture, Rajendranagar, Hyderabad
[3] Rice Section, ARI, Rajendranagar, Hyderabad
*Email: radha.aphu@gmail.com

(Received: 10 Sep 2013; Accepted: 17 Sep 2013)

Abstract
The experiment was carried out to study the nature and magnitude of gene effects for yield and yield attributing traits in bitter gourd by generation mean analysis involving six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) at Model orchard, College of Horticulture, Rajendranagar, Hyderabad during *summer* 2011. The results revealed the presence of additive, dominance gene effects and epistatic interactions for all the characters except for vine length in cross IC-470550 × IC-470558 indicating the importance of both additive and non-additive gene actions in the expression of the characters. The greater magnitude of dominance gene effect as compare to additive effect for most of the traits suggest that heterosis breeding may be more useful. Biparental mating which could exploit both additive and non-additive type of gene effects is also suggested for the improvement of the traits in bitter gourd.

Key words
Bitter gourd, generation mean analysis, gene effects, non-allelic interactions.

Introduction

Bitter gourd (*Momordica charantia* L.) is an important cucurbitaceous vegetable grown throughout India for its tender fruits. It is a prized vegetable because of its nutritive value and therapeutic properties. The estimation of gene effects involved in the inheritance of yield attributing traits is helpful in planning correct breeding programme for improvement of this crop. Determination of the most important suitable breeding method and selection strategy for improvement of a trait would depend on the knowledge of gene action operating in the breeding population, especially about the components of genetic variation *viz*., additive, dominance and epistasis. Generation mean analysis is an efficient tool to understand the nature of gene effects involved in the expression of the characters. Though gene effects for yield and its related characters have been estimated in bitter gourd, information on epistatic gene effects is limited. Thus, the present study was carried out to estimate different kinds of gene effects in the inheritance of yield and its related traits through generation mean analysis.

Material and Methods

The experimental material consist of six generations *i.e*., parents (P_1, P_2), F_1, F_2, BC_1 ($F_1 \times P_1$) and BC_2 ($F_1 \times P_2$) of two crosses *viz*., IC-033227 × IC-470550 and IC-470550 × IC-470558. The parents wre maintained by selfing for many seasons. The crosses were made during *kharif*, 2009 and their F_2, BC_1 and BC_2 were developed during *summer*, 2010. Six generations of the two crosses were evaluated at Model Orchard, College of Horticulture, Rajendranagar, Hyderabad during *summer*, 2011 in a randomized block design with three replications. The vines were spaced at 2.0 m between rows and 0.5 m within a row. All the recommended package of practices was adopted to raise healthy crop. Data were recorded on five randomly selected plants in each parental line and its F_1 cross, 20 plants in F_2 and 15 plants in each BC_1 and BC_2 from each replication. Observations were recorded on nine quantitative characters *viz*., vine length (m), number of laterals/vine, days to 1st female flower appearance, node number at 1st female flower appearance, number of fruits/vine, average fruit weight (g), fruit length (cm), fruit girth (cm) and yield/vine (kg). The data were subjected to A, B, C and D scaling tests of Mather (1949) for testing the adequacy of additive and dominance model. The gene effects (additive and dominance) and interactions (additive × additive, additive × dominance and dominance × dominance) for each character were estimated according to Hayman (1958) and Jinks and Jones (1958).

Results and Discussion

The two crosses involved with diverse parents were subjected to A, B, C and D scaling test to sort out interacting and non-interacting crosses (Table 1). The A and B scaling tests provide evidence for the presence of all three types of interactions *viz*., additive × additive (*i*), additive × dominance (*j*) and dominance × dominance (*l*) gene effects. The C scale test provides information about presence of dominance × dominance (*l*) type of interaction effect while D scaling test is evident about the presence of additive × additive (*i*) type of gene interaction. In the present study, the significance of scaling test revealed that out of four scaling tests, at least two were significant for all the characters studied except for vine length in cross IC-470550 × IC-470558 in which none of the scales was significant and for number of laterals/vine in the cross IC-033227 × IC-470550 in which only D scale was significant. These results indicated the presence of non-allelic interactions in inheritance of these characters (Dalamu *et al*., 2012).

Estimates of components of generation means for different characters in bitter gourd are presented in Table 2. The results showed that for vine length, only additive effect was significant in the two crosses. Regarding interaction effects, additive × dominance (j) was found to be significant in cross IC-033227 × IC-470550 while simple additive model was adequate in inheritance of vine length in cross IC-470550 × IC-470558. Therefore, improvement in this cross can be achieved through simple pedigree selection. The epistasis for vine length was observed to be duplicate type confirming the complex nature of inheritance of this character. Similar results were reported by Sirohi and Chaudhury (1980). For number of laterals/vine, additive and dominance gene effects were found to be important for the cross IC-033227 × IC-470550 where as dominance gene effect was predominant in cross IC-470550 × IC-470558. Among the interaction effects, additive × additive (*i*) type of gene effect was significant in desired direction in both the crosses. The predominant role of dominance gene action and additive × additive (*i*) interaction gene effects, suggests that simple selection procedures can be adopted for improvement of this trait. Both crosses showed duplicate epistasis as the signs of dominance [*h*] and dominance × dominance [*l*] effects were in opposite direction (Sirohi and Chaudhury 1979).

Additive and dominance gene effect was found to be relatively more important in cross IC-033227 × IC-470550 for earliness in terms of days to 1st female flower and node number at 1st female flower appearance whereas only additive gene effect was predominant in cross IC-470550 × IC-470558. Further, partitioning of genetic components indicated that additive × additive and additive × dominance type of interaction effects were in desired direction for these traits in IC-033227 × IC-470550. Preponderance of duplicate epistasis suggested that inheritance of these traits might pose problems in their genetic improvement but one can expect some progress in selection programme due to presence of substantial amount of non-allelic interactions. These results are in agreement with the earlier reports of (Tewari *et al*. 1998).

Both additive and dominance gene effects were highly significant in two crosses but the dominance gene effects were higher in magnitude for number of fruits/vine. Among interaction effects, additive × additive gene effect was in desired direction (Singh and Ram 2003). For average fruit weight, among the main effects, dominance gene effect was highly significant. Similarly additive × additive interaction effect was found to be highly significant in desired direction. The predominant role of dominance gene action and additive × additive interaction gene effects, suggests that simple selection procedures can be adopted for improvement of this trait.

Greater importance of dominance gene effect was observed for fruit length in both crosses. Among interaction effects, additive × additive gene effect was predominant in cross IC-033227 × IC-470550 while dominance × dominance has major role in inheritance of this trait in case of IC-047550 × IC-470558. The preponderance of dominance [*h*] and dominance × dominance [*l*] along with complimentary epistasis in cross IC-470550 × IC-470558 indicated that biparental mating would be a good approach for improvement of this trait (Patel *et al*. 2005). Additive [*d*] and dominance × dominance [*l*] gene effects were predominant in inheriting fruit girth. Duplicate type of gene action was exhibited for this trait (Akhtar *et al*. 2010).

Dominance gene effect played major role and it was higher in magnitude compared to additive gene effect for yield/vine in the present study. Among the interaction effects, additive × additive [*i*] and additive × dominance [*j*] were predominant. These results suggested that this character can be fixed through progeny selection by following proper selection methods as well as by hybridization (Celine and Sirohi 1998). The presence of duplicate epistasis would be detrimental for rapid progress, making it difficult to fix genotypes with increased level of character manifestation because the positive effect of one parameter would be cancelled out by the negative effect of another. Hence, early generation intermating besides accumulating the favourable genes and maintaining heterozygosity in the population are likely to throw out desirable recombinants.

In the present study, greater magnitude of dominance gene effect as compare to additive gene effect for most of the traits studied suggest that heterosis breeding may be more useful. At the same time significant additive effects will be beneficial for the improvement through selection procedures.

References

Akhtar, M., Singh, J. N., Shahi, J. P. and Srivastava, K. 2010. Generation mean analysis for yield traits in okra. *Indian J. Hort.*, **67** (Special): 203-207.

Celine, V. A. and Sirohi, P. S. 1998. Generation mean analysis for earliness and yield in bitter gourd (*Momordica charantia* L.). *Veg. Sci.***, 25**(1): 51-54.

Dalamu, Behera, T. K., Satyavati, C. and Pal, A. 2012. Generation mean analysis of yield related traits and inheritance of fruit colour and surface in bitter gourd. *Indian J. Hort.*, **69**(1):65-69

Hayman, B. I. 1958. The separation of epistasis from additive and dominance variation in generation means. *Heridity*, **12**: 371-390.

Jinks, J. L. and Jones, R. M. 1958. Estimation of the components of heterosis. *Genet.*, **43**: 223-234.

Mather, K. 1949. *Biometrical genetics.* First edition Dover publication Inc, New York.

Patel, N. B., Patel, J. B., Solanki, S. D. and Patel, J. J. 2005. Gene action study in bitter gourd (*Momordica charantia* L.) through generation mean analysis. *Internat. J. Biosci., Reporter,* **3**(2): 260 - 264.

Singh, D. K. and Ram, H. H. 2003. Genetics of quantitative traits in bitter gourd (*Momordica charantia* L.). *Prog. Horti.*, **35**(2): 189-191.

Sirohi, P. S. and Chaudhury, B.1979. Gene effects in bitter gourd (*Momordica charantia* L.). *Veg. Sci*., 7(2):102-107.

Sirohi, P. S. and Chaudhury, B. 1980. Inheritance of quantities fruit characters in bitter gourd (*Momordica charantia* L.). *Veg. Sci.*, 7:102-106.

Tewari, D., Ram, H. H. and Jaiswal, H. R. 1998. Gene effects for various horticultural traits in bitter gourd (*Momordica charantia* L.). *Veg. Sci*., **25**(2): 159-161.

Table 1. Test of significance of A, B, C, and D scales for different characters in bitter gourd

Cross	Scales	Vine length (m)	No. of laterals/vine	Days to 1st female flower	Node at 1st female flower	No. of fruits/vine	Average fruit weight (g)	Fruit length (cm)	Fruit girth (cm)	Yield/vine (kg)
IC-033227 × IC-470550	A	0.47** ± 0.08	0.36 ±0.38	-11.07** ±1.27	-4.64**±0.61 2	6.11** ± 0.84	4.30**±2.26	2.81**±0.46	1.56**±0.28	0.52** ± 0.07
	B	-0.35** ± 0.09	0.05 ± 0.30	-11.31** ± 1.43	-2.16** ± 0.79	-3.04**±0.80	-6.20**±1.75	2.94**±0.45	-0.93**±0.26	-0.30**± 0.05
	C	0.14 ± 0.157	-1.07 ± 0.62	7.27** ± 2.47	10.67** ± 1.21	-2.67 ± 1.41	-15.17** ± 3.80	-0.12 ± 0.77	4.41** ± 0.59	-0.50** ± 0.08
	D	0.01 ± 0.08	-0.71** ± 0.27	14.82** ± 1.29	8.73** ± 0.61	-2.87** ± 0.69	-6.64** ± 1.60	-2.93** ± 0.36	1.89** ± 0.26	-0.36** ± 0.04
IC-470550 × IC-470558	A	-0.01 ± 0.10	1.56** ± 0.32	-5.73** ± 1.37	-3.18** ± 0.84	-2.04** ± 0.84	-3.40* ± 1.618	-3.99** ± 0.46	-2.34** ± 0.28	-0.18** ±0.05
	B	0.18 ± 0.12	1.22** ± 0.30	-6.87** ± 1.56	-5.00** ± 0.89	0.911 ± 0.70	7.43** ± 1.90	-2.59** ± 0.34	-2.54** ± 0.31	0.19** ± 0.05
	C	0.05 ± 0.22	-1.27** ± 0.51	-11.93** ± 2.70	-9.73** ± 1.60	-7.93** ± 1.38	7.10 ± 3.95	-8.15** ± 0.73	-2.14** ± 0.71	-0.45** ± 0.08
	D	-0.07 ± 0.10	-2.02** ± 0.22	0.33 ± 1.20	-0.78 ± 0.64	-3.40** ± 0.65	1.54 ± 1.88	-0.79* ± 0.33	1.37** ± 0.31	-0.23** ± 0.04

*,** Significant at 5 and 1 % probability respectively

Table 2. Estimates of components of generation means for different characters in bitter gourd

Character	Cross	Estimates of Gene effects						Epistasis
		[m]	*[d]*	*[h]*	*[i]*	*[j]*	*[l]*	
Vine length (m)	IC-033227 × IC-470550	2.08**	0.53**	0.32	-0.02	0.41**	-0.10	Duplicate
	IC-470550 × IC-470558	1.98**	-0.29**	0.16	0.13	-0.10	-0.31	Duplicate
No. of laterals/ vine	IC-033227 × IC-470550	4.93**	0.58**	1.69**	1.42**	0.18	-1.78	Duplicate
	IC-470550 × IC-470558	4.53**	-0.33**	3.41**	4.04**	0.17	-6.82**	Duplicate
Days to 1st female flower	IC-033227 × IC-470550	56.00**	-2.64**	-30.28**	-29.64**	0.12	52.02**	Duplicate
	IC-470550 × IC-470558	51.40**	2.47**	-2.63	-0.67	0.57	13.27**	Duplicate
Node no. at 1st female flower	IC-033227 × IC-470550	18.00**	-2.38**	-19.33**	-17.47**	-1.24**	24.27**	Duplicate
	IC-470550 × IC-470558	13.20**	2.24**	0.69	1.56	0.91	6.62**	Complimentary
No. of fruits/ vine	IC-033227 × IC-470550	16.6**	7.98**	7.07**	5.73**	4.58**	-8.80**	Duplicate
	IC-470550 × IC-470558	14.2**	-3.71**	8.30**	6.80**	-1.48**	-5.67**	Duplicate
Average fruit weight (g)	IC-033227 × IC-470550	61.33**	11.2**	16.94**	13.28**	5.25**	-11.38**	Duplicate
	IC-470550 × IC-470558	65.41**	-11.26**	-2.17	-3.08	-5.42**	-0.95	Complimentary
Fruit length (cm)	IC-033227 × IC-470550	14.3**	0.67**	4.10**	5.87**	-0.07	-11.61**	Duplicate
	IC-470550 × IC-470558	13.32**	-1.60**	1.51*	1.57*	-0.70**	5.00**	Complimentary
Fruit girth (cm)	IC-033227 × IC-470550	12.69**	2.18**	-4.52**	-3.78**	1.25**	3.16**	Duplicate
	IC-470550 × IC-470558	11.61**	-0.59**	-1.89**	-2.74**	0.10	7.62**	Duplicate
Yield/ vine (kg)	IC-033227 × IC-470550	1.01**	0.72**	0.85**	0.72**	0.41**	-0.95**	Duplicate
	IC-470550 × IC-470558	0.92**	-0.42**	0.55**	0.46**	-0.19**	-0.47**	Duplicate

*,** Significant at 5 and 1 % probability respectively