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Genetics of fruit yield and yield attributing traits in bitter gourd

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Abstract
The present study revealed the gene action and inheritance of yield and different yield attributing characters in bitter gourd. Six generations including P_1 (DBGS-2) and P_2 (Pusa Purvi), F_1, F_2, back cross 1 and back cross 2, were subjected to the generation mean analysis, scaling and joint scaling test. The results showed the presence of positive and significant additive effect (d) for the traits like days taken to first lateral, leaf length and width, peduncle length, pericarp thickness, seed number per fruit and yield. Among the two parents, DBGS-2 was observed as the higher yielding (25.86 tonne/ ha). Among the three inter-allelic interactions, the additive × additive [i] was observed significant for the traits like number of primary branches (2.71±1.21), leaf width (2.48±0.30), peduncle length (2.72±0.33), seed number per fruit (12.20±1.20) and yield (38.75±3.82). The duplicate type of epistasis was the observed as the predominant type for various traits studied. The correlation analysis revealed that yield was having significant, positive correlation with peduncle length (0.295) and seed number per fruit (0.269). It was observed that yield is a polygenic and complex trait, governed by many genes in a cumulative manner showing both additive and non-additive gene interaction.

Keywords: Correlation, duplicate epistasis, epistasis, *Momordica charantia* L., scaling test

Introduction

Momordica charantia L. (commonly known as bitter gourd, bitter melon, Karela or balsam pear) is the most widely cultivated species of *Momordica*. It belongs to Cucurbitaceae family, having a chromosome number, 2n=2x=22. It is commercially grown in India, Sri Lanka, Philippines, Thailand, Malaysia, China, Japan, Australia, tropical Africa, South America, and the Caribbean. Apart from being consumed regularly as a part of several Asian cuisines, it has been also used for centuries in ancient traditional Indian, Chinese, and African pharmacopoeia (Behera *et al.*, 2011) [2]. The consumer preference also varies for various fruit types or colour. There is a preference for the long and slender fruits by the both Indian people whereas less bitter, white coloured fruits by the south Indian people. Small fruited oval types are having higher demand in eastern India. It is not only a good source of vitamins and minerals but also rich in the charantin and saponin, which imparts the hypoglycaemic and dechlosterizing activity to the fruits (Tan *et al.*, 2016) [15]. All these factors driving the demand of bitter gourd higher. There is also a requirement to breed high yielding genotypes according to the consumer preferences based on fruit shape or colour. However, bitter gourd being a monoecious crop is highly cross pollinated. However, it expresses very little inbreeding depression. So, from breeders' point of view exploitation of heterosis in terms of yield, uniformity and earliness is a chief concern for improvement of crop. Available reports showed that the India is having a rich diversity of bitter gourd with respect to yield and various yield attributing characters including fruit size, shape, sex expression, maturity, growth habit, colour, surface texture *etc* (Behera *et al.*, 2006) [1]. Yield is a polygenic character, being governed by many genes acting in a cumulative manner. For breeding a variety for higher yield, there is a need to understand the genetics and inheritance of various yield attributing characters. Genetic improvement of bitter gourd depends primarily on the effectiveness of selection among progenies that differ in breeding value. The understanding of the genetics and inheritance of the characters can also help in the assessment of genetic gain. There is also a need to adopt an appropriate breeding and selection strategies which relies on the gene action and gene dosage effects in a breeding population. In this regard, generation mean analysis (GMA), scaling and joint scaling test not only provides information about the presence or absence of heterosis or inbreeding depression but also provides information on the additive, dominance and epistasis effect of a gene for any type of complex trait.

These information can be used by a breeder to adopt an appropriate breeding or selection method for the genetic improvement of bitter gourd. Only a few preliminary studies have been reported in bitter gourd for understanding the genetics of yield and yield attributing characters (Kumari *et al.*, 2015; Rathod *et al.*, 2021) [10, 14]. Report showed that there is predominance of additive and dominance gene action along with presence of epistasis effect in inheritance of many quantitative characters (Dey *et al.*, 2010) [10]. The present study, have revealed the various gene action and inheritance of different yield attributing characters using the generation mean analysis, scaling and joint scaling test in bitter gourd.

Materials and Methods
Planting Materials and Experimental Details
This study was have been carried out by growing the parents, P_1 (DBGS-2) and P_2 (Pusa Purvi) along with F_1 (DBGS-2 × Pusa Purvi), F_2 (selfed F_1), BC_1 [(DBGS-2 × Pusa Purvi) × DBGS-2] and BC_2 [(DBGS-2 × Pusa Purvi) × Pusa Purvi] in randomized block design (RBD) consisting of five replication. The F_1s were developed during spring season, 2019 in poly house condition, from which the F_2 and backcross progenies (BC_1 and BC_2) were developed during the *kharif* season of 2020-21. All these six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were grown and evaluated during subsequent *rabi* season at the Research Farm of Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi. Seed sowing and seedling raising was done in 50-cell plug trays containing artificial soil media (cocopeat, vermiculite and perlite) in the poly house. Transplanting in the open field of the Research Farm was done at the two true leaf stages. A spacing of 2.0 m between rows and 0.5 m within a row was maintained for the plants of all generation. Standard recommended package practices were adopted for growing of a healthy crop. Various data was recorded from 10 plants for each parent, 20 plants for F_1, and 40 plants for BC_1 and BC_2 generation and 120 plants for F_2 for estimation of the gene effect.

Statistical and Genetic Analysis
Generation Mean Analysis (GMA) was performed as per Hayman (1958) [7], while ABCD scaling test as per Hayman and Mather (1955) [6]. With addition to this scaling test, data were further used to analyse joint scaling test as scaling test always not able to depict the additive-dominance model. Joint scaling test was performed by checking the adequacy of simple additive-dominance model as per Mather and Jinks (1982) [11]. Joint scaling test revealed the mean effect [m], genetic effects including additive [d] and dominance [h], and epistasis effects comprising of additive × additive [i], additive × dominance [j] and dominance × dominance [l]. Students 't' test was used for testing the significance of the various scales. The type of epistasis effect was determined using the dominance (h) effect and dominance × dominance (l) effect. The same sign of these effects shows complementary epistasis, while different sign show duplicate epistasis (Kearsey and Pooni, 1996) [9]. Correlation among yield and various yield attributing parameters was calculated using the F_2 means using IBM® SPSS® 16.0 software.

Results and Discussion
Generation Mean Analysis (GMA) was done using the data recorded for the six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2).

The results of the mean performance (Table 1) of six generations derived from cross DBGS-2 × Pusa Purvi signified that among the two parents, the first parent (P_1) DBGS-2 was superior for days taken to first lateral (32.00), intermodal length (10.22 cm), leaf length (6.42 cm), leaf width (5.19 cm), peduncle length (6.31 cm), pericarp thickness (14.60 mm) and seed number per fruit (31.80). However, the number of primary branches (22.00), leaf length width ratio (1.23), peduncle length (6.31 cm) was higher in the parent Pusa Purvi. DBGS-2 was observed as the higher yielding (25.86 tonne/ ha) among the two parents. All the characters studied show the intermediated F_1 value as compared to the P_1 and P_2. This intermediate value indicated that these traits are governed by the incomplete dominance. Similar findings were also reported by Kumari *et al.* (2015) [10] who also observed intermediate performance for most of the yield attributing traits like fruit length, weight *etc* in bitter gourd F_1. However, in the present study, for every character the mid parent (MP) value was in between the two parents, which indicates the absence of over-dominance for these traits. But, Dey *et al.* (2012) [5] reported the presence of heterosis in bitter gourd hybrids for the traits like earliness and vine length. Therefore, it implied that, different characters/ traits in bitter gourd have different genetics. In our study it was observed that the means of F_2 generation were higher than the F_1 for characters like days taken to first lateral (34.86), intermodal length (9.28 cm), leaf length width ratio (1.44), yield (24.28 tonne/ ha), while the F_2 mean was lower than the F_1 for number of primary branches (11.55), leaf length (3.86 cm), leaf width (2.99 cm), peduncle length (2.89 cm), pericarp thickness (8.93 mm) and seed number per fruit (12.03). This lower F_2 mean value of the traits indicates the presence of inbreeding depression for these traits. The means of various traits in the back cross generations BC_1 [(DBGS-2 × Pusa Purvi) × DBGS-2] and BC_2 [(DBGS-2 × Pusa Purvi) × Pusa Purvi] resembled to the recurrent parent. In BC_1, various traits like number of primary branches (9.12), days taken to first lateral (34.15), intermodal length (6.98 cm), leaf length (4.82 cm), leaf width (4.71 cm), leaf length width ratio (1.07), peduncle length (4.54 cm), pericarp thickness (10.39 mm), seed number per fruit (21.81) and yield (57.92 tonne/ ha) were observed to resemble to the recurrent parent DBGS-2. Similarly, in BC_2, various traits like number of primary branches (15.34), days taken to first lateral (27.24), intermodal length (7.18 cm), leaf length (3.16 cm), leaf width (2.52 cm), leaf length width ratio (1.40), peduncle length (2.59 cm), pericarp thickness (5.02 mm), seed number per fruit (8.34) and yield (16.02 tonne/ ha) were observed to resemble to the recurrent parent Pusa Purvi. Similar observations were made by Kumari *et al.* (2015) [10] and Mishra *et al.* (2015) [12] that the means of back cross progeny resembles to the mean of the recurrent parent used in the cross.

The mean data of the six generations of various traits were used to estimate the ABCD scaling test (Table 2). Among the four scales, A scale was observed significant for the traits number of primary branches (9.56±1.41), intermodal length (1.60±0.75), pericarp thickness (4.23±1.35) and seed number per fruit (5.98±2.12), while the B scale was significant for number of primary branches (10.52±2.12), leaf width (1.27±0.42), pericarp thickness (6.96±0.97) and seed number per fruit (10.92±1.68). However, C scale was significant for primary branches (22.79±2.91), leaf width (3.65±0.65),

peduncle length (3.75±0.46), pericarp thickness (6.27±1.79) and seed number per fruit (29.10±3.38) while the D scale was significant for days taken to first lateral (8.33±0.58), intermodal length (4.39±0.22), leaf length width ratio (0.41±0.09) and pericarp thickness (2.46±0.32). The results of scaling test, either both or C and D alone revealed significant values indicates that the additive-dominance model was not found adequate for all traits in this cross. This failure of additive-dominance model can be attributed to the epistasis. Thus, joint scaling test was used to detect non-allelic interaction component of the mean of the phenotypic distribution (Jinks and Jones, 1958) [8].

These six parameters *viz*., mean [m], gene effects such as additive [d], dominance [h] and their inter-allelic interaction *i.e.* additive × additive [i], additive × dominance [j] and dominance × dominance [1] were presented in Table 2. It was observed that the mean effect (m) was significant for all the 10 traits studied. This signified that all these traits followed quantitative inheritance. Rathod *et al*. (2021) [14], also reported that similar findings in bitter gourd in which various traits like vine length, fruit weight, days to first female flower appearance, yield per vine were quantitatively inherited. For the traits number of primary branches (6.61±1.86), days taken to first lateral (-19.17±2.20), intermodal length (-10.77±0.68), leaf width (2.92±0.44), leaf length width ratio (-1.18±0.27), the absolute magnitude of dominance [h] effect was higher the additive [d] effect. While for the rest other traits (leaf length, peduncle length (cm), pericarp thickness (mm), seed number per fruit, yield tonne per ha) the additive [d] effect was higher than the dominance [h] effect. The sign of the additive effect (d) and dominance effect (h) indicated the parents who possess the highest number of positive alleles for increasing the characters. In the present study there was presence of positive and significant additive effect (d) for the majority of the traits like days taken to first lateral, leaf length and width, peduncle length (cm), pericarp thickness (mm), seed number per fruit and yield (tonne per ha). This showed the predominance of the additive effects of the genes for these traits. However, dominance [h] effect was positive and significant for the traits like number of primary branches, leaf width, peduncle length, seed number per fruit and yield, which signified the predominance of dominant gene for these traits. Therefore, selection for these traits can be delayed until the homozygosity is achieved in the population. The traits which showed additive gene action can be improved through pedigree breeding approach, while the traits showing dominance effect can be improved through heterosis breeding approach.

Among the three inter-allelic interaction *i.e.* additive × additive [i], additive × dominance [j] and dominance × dominance [1], the additive × additive [i] was observed significant for the traits like number of primary branches (2.71±1.21), leaf width (2.48±0.30), peduncle length (2.72±0.33), seed number per fruit (12.20±1.20) and yield (38.75±3.82). However, the additive × dominance [j] interaction was significant for the days taken to first lateral (7.22±2.44), leaf width (1.38±0.49), seed number per fruit (4.94±1.69) and yield (57.65±5.05). The dominance ×

dominance [1] interaction was observed significant for number of primary branches (17.37±3.53), intermodal length (5.84±1.27) and pericarp thickness (16.11±2.05). In our study most of the scales in the scaling and joint scaling tests were observed significant. This is due to the presence of inter-allelic interactions, which affected the trait expression. Thus, the additive-dominance alone is not sufficient to deal with these traits, which necessitate the six-parameter (m, d, h, i, j and l) model (Jinks and Jones, 1958) [8]. Various other reports also showed that non-allelic gene interactions were involved in expression of quantitative characters in bitter gourd (Rani *et al*., 2013 [13]; Kumari *et al*., 2015 [10]). In this study, among the three interactions, the magnitude of the dominance × dominance [I] effect was higher than other two epistasis interactions (*i.e.* additive × additive [i], additive × dominance [j]), for the traits like number of primary branches, leaf length, pericarp thickness and yield. This showed that the dominance × dominance [I] interaction was the major interaction. Our findings are also in congruence with that of the Dalamu *et al.* (2012) [3], who also observed that dominance × dominance [I] interaction effect was predominated in majority of the yield attributing traits in bitter gourd.

Previous reports showed that epistasis was also involved in the inheritance of various quantitative traits in bitter gourd (Dey *et al*., 2010) [4]. In our study, duplicate type of epistasis was the observed as the predominant type (eight out of the ten traits *i.e.* days taken to first lateral, intermodal length, leaf length, leaf width, leaf length width ratio, peduncle length, pericarp thickness and yield), while the complementary epistasis was operating only in two traits *i.e.* number of primary branches and seed number per fruit. This predominance of duplicate epistasis showed that there are high chances of getting transgressive segregant in later generations. This occurrence of higher duplicate epistasis in various traits was also reported Kumari *et al*. (2015) [10] and Rathod *et al*. (2021) [14].

The correlation of yield with various other yield attributing traits revealed that yield is positively correlated with days taken to first lateral, leaf length (cm), leaf width (cm), leaf length width ratio, peduncle length (cm), pericarp thickness (mm) and seed number per fruit (Table 3). Among these seven parameters, peduncle length (cm) (0.295) and seed number per fruit (0.269) were observed as statistically significant. However, yield was negative correlated with number of primary branches (-0.258) and intermodal length (-0.178), among which the number of primary branches was statistically significant. This signified that, higher number of primary branches and intermodal length shall reduce the yield of the bitter gourd. Among the other combinations, the significant correlation coefficients were observed for number of primary branches with leaf weight (-0.219); days taken to first lateral with leaf length (0.212) and leaf weight (0.254); leaf length with leaf weight (0.242), leaf length width ratio (0.478) and peduncle length (0.290); leaf weight with leaf length width ratio (-0.647), peduncle length (0.324) and pericarp thickness (0.210); pericarp thickness with seed number per fruit (0.330).

Table 1: Generation mean for different traits in the cross DBGS-2 × Pusa Purvi of bitter gourd

Parameter	P_1	P_2	MP	F_1	F_2	BC_1	BC_2
Number of primary branches	8.60±1.673	22.00±3.54	15.30	19.20±2.49	11.55±0.39	9.12±0.51	15.34±0.99
Days taken to first lateral	32.00±1.87	25.40±4.62	28.70	26.20±3.35	34.86±0.35	34.15±0.78	27.24±0.81
Intermodal length (cm)	10.22±1.41	4.44±1.14	7.33	5.35±0.71	9.28±0.16	6.98±0.30	7.18±0.24
Leaf length (cm)	6.42±1.66	2.90±0.44	4.66	3.99±0.69	3.86±0.10	4.82±0.29	3.16±0.23
Leaf width (cm)	5.19±0.61	2.18±0.71	3.69	4.12±0.53	2.99±0.08	4.71±0.22	2.52±0.18
Leaf length width ratio	1.23±0.21	1.46±0.59	1.34	0.99±0.28	1.44±0.07	1.07±0.08	1.40±0.15
Peduncle length (cm)	6.31±0.36	2.38±0.33	4.34	3.31±0.42	2.89±0.09	4.54±0.24	2.59±0.22
Pericarp thickness (mm)	14.60±2.70	6.60±1.67	10.60	10.40±1.14	8.93±0.23	10.39±0.38	5.02±0.40
Seed number per fruit	31.80±2.77	9.80±1.48	20.80	17.80±3.34	12.03±0.41	21.81±0.96	8.34±0.45
Yield (tonne/ ha)	25.86±7.02	11.70±4.62	18.78	11.44±2.35	24.28±1.01	51.92±3.21	16.02±1.99

P_1, DBGS-2; P_2, Pusa Purvi; MP, Mid-parent; F_1, Hybrid of DBGS-2 × Pusa Purvi; F_2, Second generation of DBGS-2 × Pusa Purvi; BC_1, Back Cross 1; BC_2, Back Cross 2.

Table 2: Scaling test, gene effects and standard error for different traits in the cross DBGS-2 × Pusa Purvi of bitter gourd

Parameter	A	B	C	D	m	d	h	i	j	l	Epistasis
Number of primary branches	9.56±1.41**	10.52±2.12**	22.79±2.91**	-1.36±0.60	11.55±0.17**	-6.22±0.49	6.61±1.86**	2.71±1.21*	0.96±2.01	17.37±3.53**	C
Days taken to first lateral	-10.10±1.85	-2.88±2.64	-29.65±3.78	8.33±0.58**	34.86±0.15**	6.91±0.49**	-19.17±2.20	-16.67±1.17	7.22±2.44**	3.69±4.27	D
Intermodal length (cm)	1.60±0.75*	-4.56±0.64	-11.75±1.07	4.39±0.22**	9.27±0.07**	-0.19±0.17	-10.77±0.68	-8.79±0.45	-6.16±0.88	5.84±1.27**	D
Leaf length (cm)	0.78±0.84	0.57±0.42	1.87±1.00	-0.26±0.19	3.86±0.04**	1.66±0.16**	-0.14±0.62	0.52±0.38	-0.21±0.83	0.83±1.21	D
Leaf width (cm)	-0.11±0.41	1.27±0.42**	3.65±0.65**	-1.24±0.15	2.99±0.03**	2.19±0.12**	2.92±0.44**	2.48±0.30**	1.38±0.49**	-1.32±0.83	D
Leaf length width ratio	0.08±0.17	-0.35±0.32	-1.09±0.39	0.41±0.09**	1.44±0.02**	-0.33±0.07	-1.18±0.27	-0.83±0.19	-0.43±0.32	0.55±0.49	D
Peduncle length (cm)	0.54±0.32	0.51±0.30	3.75±0.46**	-1.36±0.16	2.88±0.04**	1.95±0.14**	1.67±0.39**	2.72±0.33**	-0.03±0.36	-1.67±0.74	D
Pericarp thickness (mm)	4.23±1.35**	6.96±0.97**	6.27±1.79**	2.46±0.32**	8.94±0.10**	5.37±0.24**	-5.12±1.09	-4.92±0.65	2.74±1.51	16.11±2.05**	D
Seed number per fruit	5.98±2.12**	10.92±1.68**	29.10±3.38**	-6.10±0.60	12.03±0.18**	13.47±0.47**	9.20±2.04**	12.20±1.20**	4.94±1.69**	4.70±3.88	C
Yield (tonne per ha)	-66.54±4.38	-8.89±2.92	-36.68±4.66	-19.37±1.91	24.28±0.44**	35.90±1.68**	31.41±4.38**	38.75±3.82**	57.65±5.05**	-114.17±8.21	D

C, Complementary epistasis; D, Duplicate epistasis. ** Significant at P ≤ .01%; * Significant at P ≤ .05%.

Table 3: Correlation coefficient of yield (tonne per ha) with various yield attributing parameters

	NAPB	DTFL	IL	LL	LW	LLWR	PL	PT	SNPF	YTPH
NAPB	1.000									
DTFL	-0.068[NS]	1.000								
IL	0.157[NS]	-0.121[NS]	1.000							
LL	-0.048[NS]	0.212*	-0.060[NS]	1.000						
LW	-0.219*	0.254**	-0.082[NS]	0.242**	1.000					
LLWR	0.122[NS]	-0.059[NS]	0.022[NS]	0.478**	-0.647**	1.000				
PL	-0.284**	0.148[NS]	-0.007[NS]	0.290**	0.324**	-0.041[NS]	1.000			
PT	0.031[NS]	0.119[NS]	0.092[NS]	-0.013[NS]	0.210*	-0.104[NS]	0.158[NS]	1.000		
SNPF	-0.078[NS]	0.116[NS]	-0.116[NS]	0.065[NS]	0.149[NS]	0.083[NS]	0.133[NS]	0.330**	1.000	
YTPH	-0.258**	0.108[NS]	-0.178[NS]	0.008[NS]	0.088[NS]	0.020[NS]	0.295**	0.004[NS]	0.269**	1.000

NAPB, Number of primary branches; DTFL, Days taken to first lateral; IL, Intermodal length (cm); LL, Leaf length (cm); LW, Leaf width (cm); LLWR, Leaf length width ratio; PL, Peduncle length (cm); PT, Pericarp thickness (mm); SNPF, Seed number per fruit; YTPH, Yield (tonne/ ha).

** Significant at P ≤ .01%
* Significant at P ≤ .05%
[NS] Non-significant.

Conclusion

Findings of the present study revealed that, both additive and non-additive gene interactions were playing roles in various yield attributing traits in bitter gourd. However, the additive effect was observed for majority of the traits. The traits with additive gene action can be improved using pedigree breeding approach, while for the dominance effect the improvement through heterosis breeding approach can be followed. Yield is a polygenic trait governed by many genes and complex in nature. Of the two types (duplicate and complementary) of epistasis, duplicate epistasis was observed in majority of the traits.

References

1. Behera TK, Dey SS, Sirohi PS. DBGy-201 and DBGy-202: two gynoecious lines in bitter gourd (*Momordica charantia* L.) isolated from indigenous source. Indian Journal of Genetics and Plant Breeding. 2006;66(1):61-62.
2. Behera TK, John KJ, Bharathi LK, Karuppaiyan R. Momordica. In: Wild crop relatives: genomic and breeding resources. Springer, Berlin, Heidelberg; c2011. p. 217-246.
3. Dalamu Behera TK, Satyavati CT, Pal A. Generation mean analysis of yield related traits and inheritance of fruit colour and surface in bitter gourd. Indian Journal of Horticulture. 2012;69(1):65-69.
4. Dey SS, Behera TK, Munshi AD, Pal A. Combing ability analysis in bitter gourd. Indian Journal of Horticulture. 2010;67(3):399-401.
5. Dey SS, Behera TK, Munshi AD, Rakshit S, Bhatia R. Utility of gynoecious sex form in heterosis breeding of bitter gourd and genetics of associated vegetative and flowering traits. Indian Journal of Horticulture. 2012;69(4):523-29.
6. Hayman BI, Mather K. The description of genetics of interaction in continuous variation. Biometrics. 1955;11(1):69-82.
7. Hayman BI. The separation of epistatic from additive and dominance variation in generation means. Heredity. 1958;12:371-390.
8. Jinks JL. Jones RM. Estimation of the components of heterosis. Genetics. 1958;43(2):223-234.
9. Kearsey MJ, Pooni HS. The genetic analysis of quantitative traits, Chapman and Hall, London; c1996.
10. Kumari M, Behera TK, Munshi AD, Talukadar A. Inheritance of fruit traits and generation mean analysis for estimation of horticultural traits in bitter gourd. Indian Journal of Horticulture. 2015;72(1):43-48.
11. Mather K, Jinks JL. Biometrical genetics: the study of continuous variation, 3rd Edn. London UK: Chapman Hall; c1982.
12. Mishra S, Behera TK, Munshi AD, Bharadwaj C, Rao AR. Inheritance of gynoecism and genetics of yield and yield contributing traits through generation mean analysis in bitter gourd. Indian Journal of Horticulture. 2015;72(2):218-222.
13. Rani KR, Reddy KR, Raju CS. Study of gene effects for yield and its component traits in bitter gourd (*Momordica charantia* L.) by generation mean analysis. Electronic Journal of Plant Breeding. 2013;4(3):1237-1241.
14. Rathod V, Behera TK, Munshi AD, Jat GS, Gaikwad AB. Genetic analysis for yield and its attributes in bitter gourd (*Momordica charantia*). Indian Journal of Agricultural Sciences. 2021;91:68-73.
15. Tan SP, Kha TC, Parks SE, Roach PD. Bitter melon (*Momordica charantia* L.) bioactive composition and health benefits: a review. Food Reviews International. 2016;32(2):181-201.