



RESEARCH PAPER

Generation mean analysis to study the genetics of fruit yield and yield attributing traits in bitter gourd

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Abstract

Bitter gourd (*Momordica charantia* L.), is a prized cucurbitaceous vegetable of the tropics, having high present-day demand along with higher future potential. Keeping the need for high yielding genotype, the present study was performed using the observations from six generations [Parent-1 (CBM-12), Parent-2 (Pusa Purvi), F₁, F₂, Back Cross 1 (BC₁) and Back Cross 2 (BC₂)]. The Generation mean analysis revealed that F₁ showed intermediate performance of Parent 1 and Parent 2, while few traits showed incomplete dominance. There was lower occurrence of inbreeding depression. Using the scaling and joint scaling test, it was revealed that for fruit length, the additive [d] (6.08) effect was significant and higher than the dominance [h] effect. A significant additive [d] effect was also observed for the fruit shape index (1.75) and fruit weight (45.45). The magnitude of the dominance × dominance [l] effect was higher than the other two epistasis interactions (i.e. additive × additive [i] and additive × dominance [j]) in the majority (nine out of thirteen) of the traits. It was evident that yield is a complex and polygenic trait governed by many genes in a cumulative manner showing both additive (predominant) and non-additive gene interaction. The existence of epistasis with duplicate type predominant, as compared to complementary, in genetic control of all the traits studied, was also revealed.

Keywords: Additive effect, Gene interaction, Epistasis, *Momordica charantia*, Yield.

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Citation: Panigrahi, I., Behera, T.K., Munshi, A.D., Dey, S.S. Jat, G.S. and Singh, A.K. (2023). Generation mean analysis to study the genetics of fruit yield and yield attributing traits in bitter gourd. *Vegetable Science* 50(2): 295-301.

Source of support: Nil

Conflict of interest: None.

Received: 21/09/2023 **Revised:** 22/12/2023 **Accepted:** 27/12/2023

Introduction

Bitter gourd (*Momordica charantia* L.), $2n=2x=22$, an important cucurbit vegetable, of Indo Burma region origin. Among the various vegetables cultivated in India, bitter gourd holds an important position in Indian cuisine (Moharana *et al.*, 2022; Priyadarshi *et al.*, 2022). The annual production of bitter gourd in India is 1.214 million MT from only 0.101 million Ha (Anonymous 2019-20). Among the various cucurbits, it is considered a prized vegetable owing to its higher nutritive and medicinal values, primarily, its hypoglycemic properties due to the presence of charantin and saponin (Behera, 2004). Apart from this, the fruit can be used in a variety of consumable forms including soups, juice, stews, curries, and salads around the world. In India, there is a regional preference for various fruit types North India prefers long and slender whereas the Southern prefers to less bitter fruit mainly white type and eastern Indian people prefer small oval types of fruit. All these factors drive the demand of the bitter gourd, compared to which there is a lower supply. These necessities the need for high-yielding varieties having consumer-preferred qualities (based of fruit size, shape, color etc).

Bitter gourd being a monoecious crop, is highly cross-pollinated in nature but expresses very little inbreeding depression. So, for the breeders' point of view, exploitation

of heterosis in terms of yield, uniformity and earliness is a chief concern for the improvement of crops. India is bestowed with higher genetic diversity in terms of growth habit, sex expression, maturity and various fruit characteristics including size, shape, color, etc. (Behera *et al.*, 2006). The yield trait of a plant is a complex character and polygenic in nature which is governed by many genes acting in a cumulative manner. Previous reports showed that there would be no separate gene system for yield *per se* and yield is an end product of the multiplicative interaction between various components of yield. For breeding a genotype for higher yield there is a need to design the breeding method and selection strategy which requires the knowledge and understanding of the inheritance and interaction of various genes operating in the population especially the components of the genetic variation *i.e.* additive, dominance and epistasis. Dey *et al.* (2010) reported that in addition to additive and dominance variation, epistasis may also be involved in the inheritance of many quantitative characters in bitter gourd. Although the gene effects for yield and its related traits have been estimated in bitter gourd but there is a dearth of information pertaining to the epistasis or gene interactions in bitter gourd. Generation mean analysis is an effective tool to unveil and understand the nature of genes involved in the expression of a particular trait in interest. In the present study, we have studied the gene action and inheritance of various yield-attributing traits through the generation mean analysis.

Materials and Methods

Two parents namely CBM-12 (P_1) and Pusa Rasdar (P_2) were crossed during the *rabi* season (Oct-Feb), 2019-20, for the development of F_1 hybrids under net house. Further, the F_1 seeds were sown to raise the plants from which other generations *viz.* F_2 , back cross 1 (BC_1) [(CBM-12 \times Pusa Rasdar) \times CBM-12] and back cross 2 (BC_2) [(CBM-12 \times Pusa Rasdar) \times Pusa Rasdar] were developed during the *khari*f season (May-Sept), 2020 under net house. The experimental materials consisting of all six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) were grown under the open field condition at the Research Farm of the Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi, during the *rabi* season (Oct-Feb), 2020-21, in a randomized block design with five replications. Seedlings of all these six generations were raised under a poly house by sowing the seeds in 50-cell plug trays containing artificial soil media composed of cocopeat, vermiculite, and perlite. Seedlings were transplanted in the main field at the two true leaf stages with a spacing of 2.0 m between rows and 0.5 m within a row. All the recommended package practices were adopted for the growing of a healthy crop. The 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

various economical traits to estimate the gene effect. Various quantitative traits were recorded at proper vegetative and reproductive growth stages in the bitter gourd plants of all six generations. The quantitative traits recorded were: (i) days to first female flower, (ii) days to first male flower, (iii) node to first female flower, (iv) node to first male flower, (v) vine length (m) at 45 days after transplanting (DAT), (vi) vine length (m) at 90 DAT (vii) days to first fruit harvest (viii) fruit length (cm), (ix) fruit diameter (cm), (x) fruit length/ diameter, (xi) fruit weight (g), (xii) Fruit number per plant, and (xiii) yield per plant (kg). Fruits were harvested at marketable stage to note various fruit-related parameters.

Generation Mean Analysis (GMA) was estimated as per Hayman (1958) for performing the scaling and joint scaling test. These data were used for A, B, C, D scaling test as per Mather (1949), for testing the adequacy of the additive and dominance model. In addition to this scaling test, data were further used to analyze joint scaling test (Hayman 1958). Using the joint scaling test, the mean effect [m], genetic effects including additive [d] and dominance [h], and epistatic effects comprising of additive \times additive [i], additive \times dominance [j] and dominance \times dominance [l] were estimated for every traits. Statistical analysis for generation mean analysis was carried out using OP Stat software (Sheoran *et al.* 1998). The type of epistasis effect was estimated using the dominance (h) effect and dominance \times dominance (l) effects (when these effects had the same sign, it shows complementary gene action, while different signs show duplicate epistasis) (Kearsey and Pooni 1996). The frequency distribution graph and the normal distribution curve were prepared using the IBM® SPSS® 16.0 software.

Results and Discussion

Generation mean analysis

To devise the magnitude of gene action for yield and its attributing traits, computation of Generation Mean Analysis (GMA) was done using recorded data of six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) of the cross CBM-12 and Pusa Rasdar. The results of the mean performance (Table 1) of six generations derived from cross CBM-12 \times Pusa Rasdar signified that the second parent (P_2) Pusa Rasdar was superior to CBM-12 for days to first female flower opening (23.20), a node at first female flower opening (7.00), vine length at 45 DAT (1.04 m) and vine length at 90 DAT (2.81 m), fruit length (9.60 cm), fruit diameter (4.84 cm), fruit length/diameter (1.98), fruit weight (73.39 g) and yield per vine (5.68 kg) (Figure 1). However, CBM-12 showed better performance for number of fruits per vine (22.20). The flowering behavior suggested that the female flower comes earlier in Pusa Rasdar as compared to the CBM-12, however, the days to the first fruit harvest was earlier in CBM-12, which is due to the fact that the fruits of CBM-12 are smaller in size (Figure 1) which took 7-8 days to

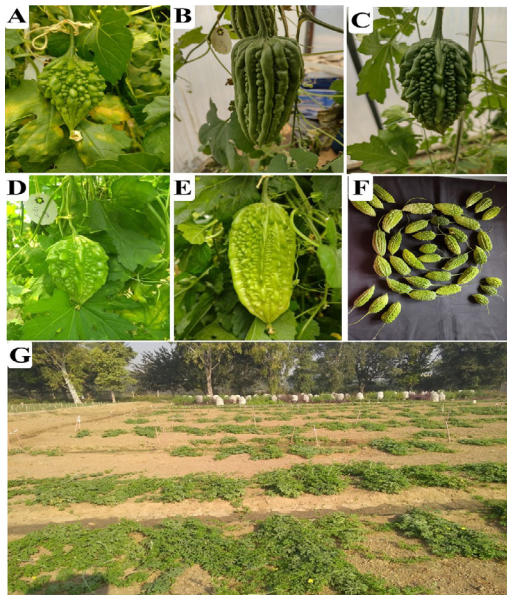


Figure 1: Fruits of CBM-12 (A), Pusa Rasdar (B), F₁ (C), BC₁ (D) and BC₂ (E); Variations for fruit shape, size, colour in F₂ population (F)

harvest after pollination but the fruits of Pusa Rasdar being larger in size (almost double in length and diameter), which took 12-15 days to harvest after pollination.

Most of the traits in F₁ showed intermediate performance (Table 1; Figure 1), except the traits days to first female flower opening (31.20 kg), vine length at 45 DAT (1.17), and days to first fruit harvest (53.47). This indicated that these traits follow incomplete dominance. Kumari *et al.* (2015) also observed the intermediate performance for most of the traits including fruit length, fruit weight *etc* in bitter gourd F₁ involving parents S-2 and Pusa Purvi. Various fruit-related

traits like fruit length, fruit diameter, fruit shape index (fruit length/ diameter), fruit weight and other traits including days to the first female flower, vine length at 45DAT and at 90 DAT were observed as superior to the mid parent (MP) value, which indicates the over-dominance of these traits and thus, it is advisable to improve these through heterosis breeding. Dey *et al.* (2012) also reported the presence of heterosis in bitter gourd hybrids for earliness and vine length. The presence of morphological variations for fruit shape, size and color in F₂ population was observed (Figure 1). The means of F₂ generation were higher than the F₁ almost all the traits like days to first female flower opening (31.97), days to first male flower opening (36.04), node to first female flower (13.19), node to first male flower (19.50), vine length at 45 DAT (1.21 m), vine length at 90 DAT (2.74 m), days to first fruit harvest (53.47), fruit length (9.07 cm), fruit length/ diameter (3.19), number of fruit per plant (18.58) and yield per plant (5.39 kg). Whereas lower value of F₂ was obtained for fruit diameter (3.36 cm) and fruit weight (62.89 g) signifying the inbreeding depression effect. This showed that there was lower occurrence of inbreeding depression in bitter gourd.

Back cross generations, BC₁ [(CBM-12 × Pusa Rasdar) × CBM-12] and BC₂ [(CBM-12 × Pusa Rasdar) × Pusa Rasdar] resembled to their recurrent parent for most of the traits (Table 1, Figure 1). In BC₁ generation, traits like fruit length (4.63), fruit diameter (2.51), fruit length/diameter (2.13), fruit weight (33.33), fruit number per plant (26.35) and yield per plant (2.34) have resemblance with their recurrent parent (Pusa Rasdar). Similarly in the BC₁ traits like days to first female flower (31.63), days to first male flower (33.87), node to first female flower (19.97), node to first male flower (16.38), vine length at 45DAT (0.95), vine length at 90DAT (1.64) and

Table 1: Generation mean for different traits in the cross CBM-12 × Pusa Rasdar of bitter gourd

Parameter	P ₁	P ₂	MP	F ₁	F ₂	BC ₁	BC ₂
Days to first female flower	29.60 ± 2.70	23.20 ± 3.34	26.4	31.20 ± 1.92	31.97 ± 0.32	31.63 ± 1.05	28.27 ± 0.91
Days to first male flower	27.20 ± 4.23	34.20 ± 2.86	30.70	29.40 ± 3.51	36.04 ± 0.44	33.87 ± 1.16	36.50 ± 0.92
Node to first female flower	13.40 ± 1.82	7.00 ± 1.00	10.20	8.80 ± 1.30	13.19 ± 0.27	19.97 ± 0.65	11.52 ± 0.55
Node to first male flower	9.20 ± 1.78	16.80 ± 3.03	13.00	11.00 ± 2.00	19.50 ± 0.38	16.38 ± 0.75	20.10 ± 0.85
Vine length at 45 DAT (m)	0.75 ± 0.22	1.04 ± 0.34	0.90	1.17 ± 0.33	1.21 ± 0.04	0.95 ± 0.06	1.01 ± 0.09
Vine length at 90 DAT (m)	1.82 ± 0.49	2.81 ± 0.73	2.31	2.31 ± 0.24	2.74 ± 0.06	1.64 ± 0.09	2.35 ± 0.11
Days to first fruit harvest	40.80 ± 2.28	48.40 ± 3.57	44.60	40.40 ± 3.36	53.47 ± 0.54	49.21 ± 1.01	53.65 ± 1.18
Fruit length (cm)	4.22 ± 1.23	9.60 ± 1.71	6.91	8.05 ± 0.67	9.07 ± 0.21	4.63 ± 0.33	10.71 ± 0.41
Fruit diameter (cm)	1.88 ± 0.55	4.84 ± 0.29	3.36	3.58 ± 0.51	3.36 ± 0.11	2.51 ± 0.22	4.21 ± 0.29
Fruit shape index	1.98 ± 0.30	2.37 ± 0.71	2.18	2.29 ± 0.40	3.19 ± 0.16	2.13 ± 0.24	2.87 ± 0.29
Fruit weight (g)	27.01 ± 7.23	73.39 ± 22.91	50.20	65.11 ± 8.75	62.89 ± 2.26	33.33 ± 2.02	78.77 ± 3.44
Fruit No. per plant	22.20 ± 2.58	14.40 ± 2.30	18.30	16.00 ± 2.91	18.58 ± 0.39	26.35 ± 0.97	19.15 ± 0.73
Yield per plant (kg)	2.31 ± 0.78	5.68 ± 0.97	4.00	3.37 ± 0.49	5.39 ± 0.20	2.34 ± 0.18	3.65 ± 0.27

P₁, CBM-12; P₂, Pusa Rasdar; MP, Mid-parent; F₁, Hybrid of CBM-12 × Pusa Rasdar; F₂, Second generation of CBM-12 × Pusa Rasdar; BC₁, Back Cross 1; BC₂, Back Cross 2; DAT, Days after transplanting

days to first fruit harvest (49.21) have resemblance with the recurrent parent (Pusa Rasdar). In BC₂ generation, various fruit-related traits like fruit length (10.71 cm), fruit diameter (4.21 cm), fruit length/diameter (2.87), fruit weight (78.77 g), fruit number per plant (19.15) and yield per plant (3.65 kg) showed resemblance with the recurrent parent (CBM-12). Other yield attributing traits like days to first female flower (28.27), days to first male flower (36.50), node to first female flower (11.52), node to first male flower (20.10), vine length at 45 DAT (1.01 m), vine length at 90 DAT (2.35 m) and days to first fruit harvest (53.65) have resemblance to the recurrent parent (CBM-12). Our study is in confirmation with Kumari *et al.* (2015), who also reported that the resemblance of the backcrosses {BC₁ [(Sel-2 × Pusa Purvi) × Sel-2] and BC₂ [(Sel-2 × Pusa Purvi) × Pusa Purvi]} to their respective recurrent parents.

Scaling test and Joint scaling test

The mean data of various traits were recorded for different generations were subjected to scaling test (A, B, C, and D). Among the four scales, A and C scale were observed non-significant for the traits studied (Table 2). However, the B scale was observed significant for the traits vine length at 90 DAT (1.83), fruit length (8.39), fruit weight (71.48) and yield per plant (4.38). However, scale D was observed as significant for most of the traits *viz.* node to first male flower (2.52), vine length at 45 DAT (0.47), vine length at 90 DAT (1.48), days to first fruit harvest (4.07), fruit length (2.81), fruit diameter (-0.01), fruit shape index (Fruit length/ diameter) (1.38), fruit weight (13.67) and yield per plant (4.78). In addition to this scaling test, data were further used to analyze joint scaling test as scaling test are always not able to depict the additive-dominance model. The data of 13 quantitative traits recorded for the six generations (P₁, P₂, F₁, F₂, BC₁ and BC₂) involving the parents CBM-12 (P₁) and Pusa Rasdar (P₂) were used to analyze six parameter model (Jinks and Jones, 1958).

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 [l] were presented in Table 3. The mean effect (m) was observed significant for all the 13 traits studied. It signified that all these traits followed quantitative inheritance. Our study are in congruence with Rathod *et al.* (2021), who also observed the quantitative inheritance of various traits like vine length, days to first female flower appearance, fruit weight, number of fruits per vine, yield per vine in bitter gourd.

For the trait “days to first female flower appearance”, the absolute magnitude of the dominance [h] effect was higher than additive [d], with h being significant (Table 3). Among the epistatic interaction effects, a positive significant value (23.93) was observed for additive × additive [i] interaction. However, a non-significant negative value (-57.53) was observed for dominance × dominance [l] interaction. The

absolute magnitude of the additive [d] effect was higher than the dominant [d] for the trait days to the first male flower. Among all epistatic interaction effects, only the additive × dominance effect [j] was significant. Although the dominance × dominance [l] was observed as negative but the absolute value was higher than the remaining two interactions (i and j). The additive [d] effect was negative (-8.45), while the dominance [h] was positive and significant (8.83) for a node to first female flower appearance however, among the epistatic interactions, additive × additive [i] effect was positively significant (10.33). But for node to first male flower appearance, the additive [d] effect (3.72) and the additive × dominance interaction effect [j] were positive and significant. The additive [d] (1.07) and dominance [h] (-0.66) effects were not significant for vine length at 45 DAT however the magnitude of the additive effect was higher than dominance. All three epistatic interactions *i.e.* additive × additive [i] (0.93), additive × dominance [j] (0.43) and dominance × dominance [l] (1.15) were statistically significant for vine length at 45 DAT. For vine length at 90 DAT also, these three interactions were significant. The additive [d] effect was significant and positive (4.44), while the absolute magnitude of the dominance [h] effect was higher for the days to first fruit harvest. Among all epistatic interactions, only the additive × dominance [i] effect showed positive and significant value (16.48), while both the additive × dominance [i] and additive × dominance [j] were non-significant and negative. In fruit length, the additive [d] (6.08) was significant and higher than the dominance [h] effect. Among the epistatic interactions for fruit length, the additive × additive [i] effect (5.63) was positive (non-significant), whereas additive × dominance [j] (significant) and dominance × dominance [l] (non-significant) effect were negative. Among the gene effects for fruit diameter, both the additive [d] (1.70) and dominance [h] (2.23) were significant, and the later was higher than the former. The interaction additive × dominance [j] (6.37) and dominance × dominance [l] (3.42) were also significant and positive. A significant additive [d] effect was observed for the fruit shape index (1.75) and fruit weight (45.45). Among the interactions only interaction additive × dominance [j] (1.09) was significant for the fruit shape index but both the additive × dominance [j] (132.27) and dominance × dominance [l] (33.78) were significant for the fruit weight. Both the additive [d] and dominance [h] effect were observed as significant for the traits fruit number per plant and yield per plant. However, among the epistasis interactions, for fruit number per plant only the additive × additive [i] effect (16.68) was significant but for the yield per plant both the additive × dominance [j] (6.01) and dominance × dominance [l] (12.32) were significant.

In the present study, the scaling (Table 2) and the joint scaling (Table 3) traits were observed as significant for most

Table 2: Test of significance of A, B, C, D scaling test and standard error for different traits in the cross CBM-12 × Pusa Rasdar of bitter gourd

Parameter	A	B	C	D
Days to first female flower	-7.74 ± 1.69	-25.86 ± 1.97	-9.67 ± 2.64	-11.97 ± 0.68
Days to first male flower	-22.40 ± 2.62	-2.14 ± 2.27	-23.96 ± 3.98	-0.29 ± 0.77
Node to first female flower	-0.84 ± 1.11	-24.14 ± 0.94	-14.75 ± 1.56	-5.11 ± 0.45
Node to first male flower	-20.00 ± 1.42	-4.96 ± 1.75	-30.01 ± 2.48	2.52** ± 0.61
Vine length at 45 DAT	-0.11 ± 0.19	0.32 ± 0.21	-0.72 ± 0.35	0.47** ± 0.06
Vine length at 90 DAT	-0.58 ± 0.26	1.83** ± 0.35	-1.72 ± 0.46	1.48** ± 0.08
Days to first fruit harvest	-26.10 ± 2.10	-9.62 ± 2.37	-43.87 ± 3.68	4.07** ± 0.85
Fruit length	-9.14 ± 0.73	8.39** ± 0.87	-6.38 ± 1.18	2.81** ± 0.30
Fruit diameter	-2.97 ± 0.42	3.40 ± 0.33	0.45 ± 0.57	-0.01** ± 0.19
Fruit shape index	-1.08 ± 0.45	0.01 ± 0.31	-3.83 ± 0.58	1.38** ± 0.22
Fruit weight	-65.42 ± 5.94	71.84** ± 11.11	-20.94 ± 13.89	13.67** ± 2.69
Fruit number per plant	-0.10 ± 1.86	-22.30 ± 1.87	-5.72 ± 3.11	-8.34 ± 0.65
Yield per plant	-1.63 ± 0.48	4.38** ± 0.51	-6.82 ± 0.80	4.78** ± 0.23

DAT, Days after transplanting. Value after ' ± ' signifies the standard error. ** Significant at $P \leq .01\%$;

* Significant at $P \leq .05\%$

of the traits. This can be attributed to the presence of inter-allelic interaction, affecting the expression of a trait, and thus, additive dominance alone shall not be sufficient to deal with such traits, and the improvement of such traits may become cumbersome. Hence, the six-parameter model (Jinks and Jones 1958) was also used to estimate the six components of genetic variation (*i.e.* m, d, h, i, j and l). Rani *et al.* (2013) and Kumari *et al.* (2015) also reported that non-allelic gene interactions were involved in the expression of quantitative characters in bitter gourd. The sign of the additive effect (d) and dominance effect (h) indicates the parents who possess the highest number of positive alleles for increasing the characters. In the present study the additive effects of the genes is predominant which is as evident by the presence of positive and significant additive effect (d) for the most of

the traits. However, the traits like days to first female flower, node to first female flower, fruit diameter, fruit number per plant had positive and significant values of h, which indicated the predominance of dominant gene effects and thus, it is advisable to delay the selection for these traits until heterozygosity is reduced and homozygosity is achieved in the population.

The magnitude of dominance × dominance [I] effect was higher than other two epistatic interactions (*i.e.* i and j) in majority (nine out of thirteen) of the traits *viz.* days to first female flower, days to first male flower, node to first female flower, node to first male flower, vine length at 45 DAT, vine length at 90 DAT, days to first fruit harvest, fruit number per plant and yield per plant, indicating that dominance × dominance [I] effect was the predominant interaction. Dalamu *et al.* (2012) also reported that dominance × dominance [I] interaction effect in majority of the traits including fruit weight, length and number of fruits per plant in bitter gourd.

Epistasis

Dey *et al.* (2010) reported that in addition to additive and dominance variation, epistasis may also be involved in the inheritance of many quantitative characters in bitter gourd. In the present study, the majority of the traits (nine out of thirteen) *viz.* days to first female flower, node to first female flower, vine length at 45 DAT, vine length at 90 DAT, fruit length, fruit shape index (fruit length/ diameter), fruit weight, fruit number per plant and yield per plant, the duplicate epistasis was observed (Table 3). This occurrence of higher duplicate epistasis signifies the chances of getting transgressive segregant in later generations. Kumari *et al.*

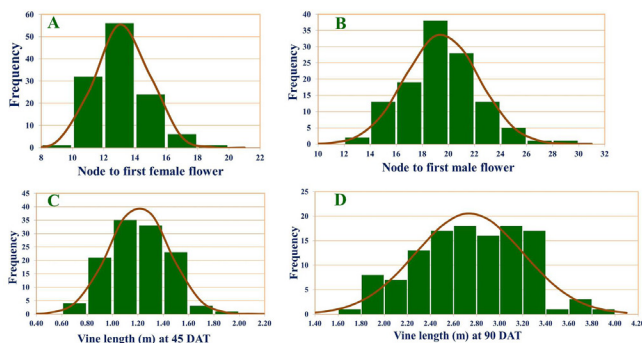


Figure 2: Normal distribution curve with histogram (bars representing frequency of each class) of various parameters in F_2 population of the CBM-12 × Pusa Rasdar. A. Node to first female flower (Range, 8,40), B. Node to first male flower (Range, 16,20), C. Vine length (m) at 45 DAT (Range, 1,13), D. Vine length (m) at 90 DAT (Range, 2,24). N=120 for all parameters)

Table 3: Components of generation means (Joint scaling test) and standard error for different traits in the cross CBM-12 × Pusa Rasdar of bitter gourd

Parameter	<i>m</i>	<i>d</i>	<i>h</i>	<i>i</i>	<i>j</i>	<i>l</i>	Epistasis
Days to first female flower	31.97** ± 0.14	-7.36 ± 0.62	27.23** ± 1.88	23.93** ± 1.37	28.12 ± 2.29	-57.53 ± 3.63	D
Days to first male flower	36.04** ± 0.20	6.63** ± 0.66	-0.72 ± 2.49	0.58 ± 1.55	20.26** ± 2.67	-25.12 ± 4.79	C
Node to first female flower	13.18** ± 0.12	-8.45 ± 0.38	8.83** ± 1.17	10.23** ± 0.90	-23.30 ± 1.20	35.21 ± 2.19	D
Node to first male flower	19.50** ± 0.17	3.72** ± 0.51	7.05 ± 1.71	-5.05 ± 1.22	15.04** ± 1.87	-19.91 ± 3.20	C
Vine length at 45 DAT	1.21** ± 0.01	1.07 ± 0.04	-0.66 ± 0.21	0.93** ± 0.12	0.43* ± 0.20	1.15** ± 0.40	D
Vine length at 90 DAT	2.73** ± 0.02	0.71** ± 0.06	-2.97 ± 0.28	1.97* ± 0.17	2.41** ± 0.41	4.22** ± 0.53	D
Days to first fruit harvest	53.47** ± 0.24	4.44** ± 0.69	-12.35 ± 2.46	-8.15 ± 1.70	16.48** ± 2.35	-27.57 ± 4.62	C
Fruit length	9.07** ± 0.09	6.08** ± 0.24	-4.49 ± 0.82	5.63 ± 0.61	-17.54** ± 1.05	-4.88 ± 1.51	D
Fruit diameter	3.36** ± 0.05	1.70** ± 0.16	2.23* ± 0.47	2.01 ± 0.38	6.37** ± 0.43	3.42* ± 0.87	C
Fruit shape index	3.19** ± 0.07	1.75** ± 0.17	2.65 ± 0.51	-2.76 ± 0.45	1.09* ± 0.48	-1.69 ± 0.89	D
Fruit weight	62.89** ± 1.01	45.45** ± 1.78	12.45 ± 8.56	27.36 ± 5.39	137.27** ± 11.32	33.78* ± 15.63	D
Fruit number per plant	18.58** ± 0.17	7.20** ± 0.54	14.38** ± 1.99	16.68** ± 1.29	-22.20 ± 1.89	-39.08 ± 3.80	D
Yield per plant	5.39** ± 0.09	1.32** ± 0.14	10.19* ± 0.58	-9.57 ± 0.46	6.01** ± 0.63	12.32** ± 0.99	D

DAT, Days after transplanting; C, Complementary epistasis; D, Duplicate epistasis

Value after ' ± ' signifies the standard error. **Significant at $P \leq .01\%$; * Significant at $P \leq .05\%$

(2015) also reported the presence of duplicate epistasis for the majority of the traits like No. of days to open the first female flower, node bearing first female flower, number of days to open first male flower, fruit length and yield per plant.

Frequency distribution

The frequency distribution graph and normal distribution curve (Figure 2) for the F_2 population, showed that the traits viz. node to first female flower (Figure 2A), node to first male flower (Figure 2B), vine length (m) at 45 DAT (Figure 2C) and vine length (m) at 90 DAT (Figure 2D) are governed quantitatively by polygenes. The data of the F_2 generation for these traits fit into the normal distribution as evident from the bell-shaped curve. The existence of many classes in a continuous manner in the frequency distribution graph, for the traits, proved the presence of higher variation in the population. Apart from this, the higher range for the traits (node to first female flower, 8.40; node to first male flower, 16.20; vine length (m) at 45 DAT, 1.13; vine length (m) at 90 DAT, 2.24), also proved the presence of immense variability in the F_2 population obtained by selfing the CBM-12 and Pusa Rasdar.

Conclusion

From the results of the present study, it can be concluded that yield is a complex and polygenic trait governed by many genes in a cumulative manner showing both additive and non-additive gene interaction, however, the additive (d) effects of the genes is predominant. The traits that show additive gene action can be improved through the pedigree

breeding approach. Further, the involvement of epistasis (involving higher duplicate as compared to complementary epistasis) in genetic control of all the traits studied was confirmed. These findings signified that, the breeding of high-yielding bitter gourd genotypes can be undertaken by combining the breeding approach based on hybridization followed by selection with moderate selection intensity.

Acknowledgments

Authors sincerely acknowledge the ICAR-IARI, New Delhi for providing the research facilities and the Department of Science & Technology, Ministry of Science and Technology, Government of India, for grant of DST-INSPIRE fellowship to the first author.

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सारांश

करेला (*मोमोर्डिका चारेण्टिया* एल.), उष्णकटिबंधीय क्षेत्र की एक बेशकीमती कद्दूवर्गीय सब्जी है, जिसकी वर्तमान समय में उच्च मांग के साथ-साथ भविष्य की संभावनाएं भी अधिक हैं। उच्च उपज देने वाले जीनोटाइप की आवश्यकता को ध्यान में रखते हुए, वर्तमान अध्ययन छह पीढ़ियों [पेरेंट-1 (सीबीएम-12), पेरेंट-2 (पूसा पूर्वी), एफ₁, एफ₂, बैक क्रॉस 1 (बीसी₁) और बैक क्रॉस 2 (बीसी₂)] के अवलोकनों का उपयोग करके, किया गया था। जनरेशन माध्य विश्लेषण से पता चला कि एफ₁, ने पेरेंट 1 और पेरेंट 2 का मध्यवर्ती प्रदर्शन दिखाया, जबकि कुछ लक्षणों ने अधूरा प्रभुत्व दिखाया। अंतःप्रजनन अवसाद की घटना कम थी। स्केलिंग और संयुक्त स्केलिंग-टेस्ट का उपयोग करते हुए, यह पता चला कि फल की लंबाई के लिए, योगात्मक प्रभाव [डी] (6.08) महत्वपूर्ण था एवं यह, प्रभुत्व [एच] प्रभाव से अधिक था। फल आकार सूचकांक (1.75) और फल वजन (45.45) के लिए भी योगात्मक प्रभाव [डी] महत्वपूर्ण देखा गया। प्रभुत्व × प्रभुत्व [आई] प्रभाव का परिमाण अन्य दो एपिस्टासिस इंटरैक्शन (अर्थात् योगात्मक × योगात्मक [i] और योगात्मक × प्रभुत्व [j]) की तुलना में अधिकांश गुणों (तेरह में से नौ) में अधिक था। यह स्पष्ट था कि, उपज एक जटिल और बहुजीनी गुण है, जो की संचयी तरीके से कई जीनों द्वारा शासित है। यह दोनों योगात्मक (प्रमुख) और गैर-योगात्मक जीन इंटरैक्शन को दर्शाता है। अध्ययन किए गए सभी लक्षणों के आनुवंशिक नियंत्रण में पूरक की तुलना में डुप्लिकेट प्रकार के प्रमुखता के साथ एपिस्टासिस का अस्तित्व भी सामने आया था।