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EVALUATION OF F_2 SEGREGATING POPULATIONS FOR YIELD AND YIELD ATTRIBUTES IN BITTER GOURD (*MOMORDICA CHARANTIA* L.)

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ABSTRACT:
The present investigation was undertaken to estimate the genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance as per cent of mean in the F_2 generation for twelve growth, flowering, yield and quality characters in two intraspecific crosses of bitter gourd, viz., IC85633 × IC50526 and IC599421 × IC50526. Each F_2 population comprising 250 plants was evaluated separately in an augmented block design along with the respective parents, F_1 and the check Phule Green Gold during *Kharif* 2025. Analysis of variance revealed significant differences among the F_2 plants for all the characters in both crosses. In the F_2 population of the cross IC85633 × IC50526, high (> 20 %) genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were detected for vine length at last harvest, number of branches per vine, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, flesh thickness and cavity size. In the F_2 population of the cross IC599421 × IC50526, high GCV and PCV were observed for the same eight characters and also for fruit length. Fruit yield per vine recorded the highest GCV and PCV in both the populations. High heritability (> 60 %) along with high genetic advance as per cent of mean (> 20 %) was recorded for all the twelve characters in the F_2 population of IC85633 × IC50526 and for all the characters except days to first harvest in IC599421 × IC50526, which showed high heritability with moderate genetic advance as per cent of mean. This indicated that these traits are governed largely by additive gene action and hence selection in the F_2 and subsequent generations would be effective for the improvement of fruit yield and its component traits in bitter gourd.

KEYWORDS: Bitter gourd, F_2 population, variability, GCV, PCV, heritability, genetic advance as per cent of mean, augmented block design.

INTRODUCTION

Bitter gourd (*Momordica charantia* L.), also known as balsam pear or bitter melon, is an important nutritive and commercial vegetable crop belonging to the family Cucurbitaceae. It is a diploid with chromosome number 2n = 2x = 22 and eastern India and southern China are considered the possible centres of its domestication (Behera *et al*., 2023). It is an annual, monoecious vine in which the sex ratio is highly skewed in favour of staminate flowers (Rasco and Castillo, 1990), which favours cross-pollination. The fruits are valued for their antidiabetic property attributed to charantin and polypeptide-p, while the characteristic bitterness is due to the alkaloid momordicin. The fruits are also a rich source of vitamin C, carotenoids and minerals.

Despite its commercial importance, the productivity of bitter gourd remains low, largely because of the shortage of high-yielding, genetically improved varieties and hence efforts to improve yield must begin with an understanding of the genetic variability available (Kumari *et al.,* 2018). Intraspecific hybridisation followed by selection in the segregating generations is an effective means of combining desirable traits. Segregation and recombination are maximum in the F_2 generation and therefore it is the ideal generation for imposing selection. However, the apparent variability in a population may be partly environmental in origin and hence greater emphasis should be placed on assessing the genetic, rather than merely the phenotypic, variability (Reddy *et al*., 2013). Heritability estimates are more meaningful for predicting the response to selection when considered together with genetic advance (Johnson *et al.,* 1955).

In the present study, the variability observed in the F_2 populations is due to segregation and recombination of genes, which might help the breeder to obtain desirable trait combinations for improving yield. Hence, the present study was conducted to know the extent of variability in two F_2 populations of bitter gourd through different genetic parameters, viz., PCV, GCV, heritability and genetic advance as per cent of mean.

MATERIAL AND METHODS

The study was carried out at the Experimental Block, Department of Vegetable Science, College of Horticulture, Bagalkot, University of Horticultural Sciences, Bagalkot, Karnataka, India, which lies in the Northern Dry Zone (Zone-3) of Karnataka at an altitude of 533 m above mean sea level, during *Kharif* 2025. Two high-yielding hybrids developed earlier at the Department, viz., H-55 (IC85633 × IC50526) and H-58 (IC599421 × IC50526), were selfed during *Rabi* 2024 to develop the F_2 populations. Population I was derived from IC85633 × IC50526 and Population II from IC599421 × IC50526.

Each population consisted of 250 F_2 plants and the two populations were evaluated separately in independent augmented block designs (Federer and Raghavarao, 1975). Each population was divided into five blocks with 50 F_2 plants per block. Four checks, viz., the two respective parents, the corresponding F_1 and the commercial variety Phule Green Gold, were included in each block, so that each block consisted of 54 plots. Seedlings were spaced at 1.20 m × 1.00 m on raised beds with drip irrigation and black polyethylene mulch. The crop was raised as per the recommended package of practices of the University of Horticultural Sciences, Bagalkot (Anonymous., 2013).

Observations were recorded on individual F_2 plants for twelve characters, viz., vine length at last harvest (m), number of branches per vine, node to first female flower, days to first female flowering, days to first harvest, fruit length (cm), fruit diameter (mm), average fruit weight (g), number of fruits per vine, fruit yield per vine (kg), flesh thickness (mm) and cavity size (mm). The analysis of variance for augmented block design was carried out as per Federer and Raghavarao (1975) and Peterson (1985) in R software (v4.3.1) using the augmentedRCBD and variability packages. The data recorded were statistically analysed for genotypic coefficient of variation and phenotypic coefficient of variation according to Burton and DeVane (1953) and classified as low (0–10 %), moderate (10.1–20 %) and high (> 20 %) as suggested by Sivasubramanian and Menon (1973). Heritability in broad sense was estimated as per the formula suggested by Lush (1940) and classified as low (0–30 %), moderate (30.1–60 %) and high (> 60 %) according to Robinson *et al*. (1949). Genetic advance at 5 per cent selection intensity (k = 2.06) was estimated as per Allard (1960) and genetic advance as per cent of mean was computed and classified as low (0–10 %), moderate (10.1–20 %) and high (> 20 %) as proposed by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the checks and F_2 plants for all twelve characters in both crosses. In IC599421 × IC50526, all the sources of variation were highly significant ($P \leq 0.01$) for every character, while in IC85633 × IC50526, all the characters were highly significant except node to first female flower and fruit length, which were significant at the 5 per cent level. This indicated the presence of sufficient variability among the F_2 plants to warrant the estimation of genetic parameters.

The extent of variability present in the two crosses of bitter gourd in F_2 generation was measured in terms of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as per cent of mean, which are given in Table 1 and Table 2. A considerable amount of variability was observed for all the characters under study, which proves that there is ample scope for selection in the subsequent generations. The PCV was higher than the GCV for all the characters in both the populations, but the difference between them was narrow for most of the characters, indicating a relatively low influence of environment on their expression. The outcomes of variability and genetic components of variation are discussed below with regard to growth, flowering, yield and quality parameters in F_2 population of the cross IC85633 × IC50526 (Table 1).

For vine length at last harvest, high GCV (43.14 %) and PCV (44.63 %) values were observed in the F_2 population of the cross IC85633 × IC50526. The difference between GCV and PCV was narrow, indicating that the variability observed was largely genetic in nature with little influence of the environment. These results are in conformity with the findings of Maurya *et al*. (2018), Tyagi *et al.* (2018) and Mehta *et al.* (2021) in bitter gourd. High heritability (93.44 %) coupled with high genetic advance as per cent over mean (86.29 %) was noted for this character, which revealed the predominance of additive gene action and hence direct selection would be effective for improving vine length. These findings are in accordance with Rahman *et al.* (2019), Bhati *et al.* (2023) and Singh *et al.* (2025) in bitter gourd, whereas Sahana *et al*. (2025) recorded low to moderate heritability for vine length in F_2 populations of bitter gourd.

Number of branches per vine also showed high GCV (33.35 %) and PCV (33.71 %) with a minor difference between them, indicating the existence of considerable genetic variability and less influence of non-genetic factors. High heritability (97.88 %) along with high genetic advance as per cent over mean (68.17 %) was observed, indicating that the trait was governed by additive genes and offers good scope for improvement through selection. Similar results were reported by Talukder *et al.* (2018), Chaudhary *et al*. (2019) and Sowmya *et al.* (2021) in bitter gourd. However, Sahana *et al.* (2025) observed low heritability with moderate genetic advance as per cent over mean for number of primary branches, which suggests that heritability estimates for this trait vary with the genetic material and the growing environment.

Moderate GCV (13.80 %) and PCV (16.65 %) values were recorded for node to first female flower and the comparatively wider difference between them indicated an appreciable influence of environment on its expression. Similar observations were made by Tyagi *et al.* (2018) and Mehta *et al.* (2021) in bitter gourd. High heritability (68.70 %) coupled with high genetic advance as per cent over mean (23.60 %) was noted, indicating that a considerable proportion of the variability was heritable and governed by additive gene action; hence, selection for a lower node to first female flower would be rewarding in the subsequent generations. These results are in accordance with the findings of Sowmya (2018), Bhati *et al.* (2023) and Sahana *et al.* (2025) in bitter gourd and Varalakshmi *et al.* (2015) in ridge gourd.

Days to first female flowering exhibited moderate GCV (13.39 %) and PCV (13.58 %) with negligible difference between them, indicating a relatively narrow genetic base with minimal environmental influence. High heritability (97.26 %)

together with high genetic advance as per cent over mean (27.25 %) indicated the role of additive gene action and there is reasonable scope for selection of early flowering segregants. Similar results were reported by Maurya *et al.* (2018), Sowmya (2018) and Bhati *et al.* (2023) in bitter gourd. Contrary to this, Talukder *et al.* (2018) recorded high heritability with low genetic advance for this trait, which might be due to differences in the genetic material studied.

Days to first harvest showed moderate GCV (10.51 %) and PCV (11.13 %) values, indicating an intermediate level of variability for this character. High heritability (89.10 %) accompanied by high genetic advance as per cent over mean (20.46 %) suggested the involvement of additive gene action and that selection for earliness would be effective in this cross. Comparatively low estimates of GCV and PCV for this trait were also reported by Maurya *et al*. (2018), Chinthan *et al.* (2021), Mehta *et al. (*2021) and Bhati *et al.* (2023) in bitter gourd, while Sahana *et al.* (2025) recorded low GCV with moderate heritability and moderate genetic advance as per cent over mean for days to first fruit harvest.

In the cross IC85633 × IC50526, fruit length showed moderate GCV (16.00 %) and high PCV (20.60 %) values. The difference between them was the widest among the characters studied in this cross, indicating that environmental factors played a relatively greater role in the expression of this trait. High heritability (60.38 %) followed by high genetic advance as per cent over mean (25.59 %) was documented, indicating that the genetic component still predominated and the trait can be improved through selection in future generations. These results are in agreement with Sowmya (2018), Tyagi *et al*. (2018), Rahman *et al*. (2019), Chinthan *et al.* (2021) and Bhati *et al.* (2023) in bitter gourd and Varalakshmi *et al.* (2015) in ridge gourd. As the heritability estimate was close to the lower limit of the high category, selection for fruit length in this cross would be more reliable when practised over successive generations.

With respect to fruit diameter, high GCV (27.79 %) and PCV (28.15 %) were recorded with a narrow difference between them, indicating considerable genetic variability and less influence of non-genetic factors. High heritability (97.45 %) coupled with high genetic advance as per cent over mean (56.58 %) indicated the preponderance of additive gene action and hence, this character offers considerable scope for improvement through simple selection. These results are in accordance with the findings of Adarsh (2018), Tyagi *et al.* (2018), Chaudhary *et al.* (2019) and Bhati *et al.* (2023) in bitter gourd and Farheen *et al.* (2022) in ridge gourd.

High GCV (39.58 %) and PCV (40.07 %) were noticed for average fruit weight, indicating wider variation in the population and less environmental influence on the expression of this trait. High heritability (97.56 %) along with high genetic advance as per cent over mean (80.65 %) indicated that the high heritability was mainly due to additive gene effects and hence selection would be highly effective for this character. Similar results were obtained by Sowmya (2018), Talukder *et al.* (2018), Tyagi *et al.* (2018), Rahman *et al.* (2019), Bhati *et al.* (2023) and Sahana *et al.* (2025) in bitter gourd.

High estimates of both GCV (45.47 %) and PCV (45.71 %) were observed for number of fruits per vine, indicating the existence of high variability which will be amenable for further improvement through selection in the existing population. High heritability (98.98 %) accompanied with high genetic advance as per cent over mean (93.30 %) indicated the dominance of additive gene action in the genetic control of this trait and selection is enough for improving it. Similar results were upheld by Vitthal (2012), Pathak *et al.* (2014), Sowmya (2018), Chinthan *et al.* (2021), Bhati *et al.* (2023) and Singh *et al.* (2025) in bitter gourd and Varalakshmi *et al.* (2015) in ridge gourd.

With respect to fruit yield per vine, the highest magnitude of GCV (53.87 %) and PCV (57.93 %) among all the characters was recorded in this population, indicating wider variation for this trait. High heritability (86.48 %) and the highest genetic advance as per cent over mean (103.81 %) in this population displayed that this trait was less affected by environmental factors and was under the control of additive gene action; thus, pedigree selection would be the best breeding approach for the improvement of this trait. Similar outcomes were observed by Vitthal (2012), Gowda (2017), Sowmya (2018), Tyagi *et al. (*2018) and Sahana *et al.* (2025) in bitter gourd and Farheen *et al.* (2022) in ridge gourd.

Flesh thickness exhibited high GCV (25.74 %) and PCV (25.87 %) with a negligible difference between them, pointing to limited environmental influence. High heritability (98.95 %) coupled with high genetic advance as per cent over mean (52.84 %) indicated additive gene action, offering good scope for improving flesh thickness through selection. These results are in line with Chakraborty *et al.* (2013) and Sowmya (2018) in bitter gourd and Farheen *et al.* (2022) in ridge gourd.

Cavity size, for which a smaller value is desirable, exhibited high GCV (24.01 %) and PCV (24.23 %) with a narrow gap between them. High heritability (98.22 %) with high genetic advance as per cent over mean (49.10 %) was noted, indicating that the trait was governed by additive genes and selection against a large seed cavity would be effective. Similar findings were reported by Chakraborty *et al.* (2013) and Nithinkumar (2018) in bitter gourd and Arizoo *et al.* (2024) in ridge gourd.

The outcomes of variability and genetic components of variation are briefly discussed below with regard to growth, flowering, yield and quality parameters in F_2 population of the cross IC599421 × IC50526 (Table 2).

High GCV (43.26 %) and PCV (43.96 %) values were noted for vine length at last harvest and the minute disparity between them indicated that the environment had little influence on this trait. High heritability (96.88 %) coupled with high genetic advance as per cent over mean (87.36 %) indicated that the trait was governed by additive gene action and selection would be effective. These results are in agreement with the findings of Maurya *et al.* (2018), Tyagi *et al.* (2018), Chaudhary *et al.* (2019), Bannatti *et al.* (2023), Sagar *et al.* (2024) and Singh *et al.* (2025) in bitter gourd.

Number of branches per vine showed high GCV (21.43 %) and PCV (24.25 %) and the moderate difference between them indicated some influence of environment on the expression of this trait. High heritability (78.01 %) coupled with high genetic advance as per cent over mean (39.02 %) was observed, indicating the importance of additive genes and that selection would be rewarding. These results are in conformity with Gupta *et al.* (2016) and Sowmya (2018) in bitter gourd and Varalakshmi *et al.* (2015) in ridge gourd, who reported high heritability and genetic advance for this trait.

Node to first female flower recorded moderate GCV (19.12 %) and PCV (19.61 %) with a narrow gap between them, indicating limited environmental influence. High heritability (95.00 %) as well as high genetic advance as per cent over mean (38.46 %) was noted, which showed strong genetic control and additive gene action for this trait; hence, there is scope for selecting segregants bearing the first female flower at lower nodes. These results are in accordance with the findings of Sowmya (2018) and Sahana *et al.* (2025) in bitter gourd and Varalakshmi *et al.* (2015) in ridge gourd, who reported high heritability and genetic advance for this trait.

Days to first female flowering showed moderate GCV (12.78 %) and PCV (13.16 %) values along with high heritability (94.41 %) and high genetic advance as per cent over mean (25.63 %), suggesting additive control of flowering time in spite of the moderate variability. This agrees with Sowmya (2018) and Rahman *et al.* (2019) in bitter gourd, while Talukder *et al.* (2018) reported high heritability but low genetic advance for this trait.

Days to first harvest was the only character in this population that recorded low GCV (7.68 %) and PCV (8.10 %), indicating a narrow genetic base for this trait. High heritability (89.94 %) was accompanied by only moderate genetic advance as per cent over mean (15.02 %), the only instance in the present study where high heritability did not result in high genetic advance as per cent over mean. This could be attributed to the limited genotypic variance available for this trait and the high heritability may be partly due to non-additive gene effects; hence, selection for earlier harvest in this cross would result in comparatively modest gains. Low variability for days to first fruit harvest was also reported by Sahana *et al*. (2025) and Singh *et al.* (2025) in bitter gourd.

In the F_2 of the cross IC599421 × IC50526, fruit length recorded high GCV (21.15 %) and PCV (21.91 %) values with a narrow difference, indicating strong genetic control. High heritability (93.13 %) followed by high genetic advance as per cent over mean (42.16 %) was documented for this trait, indicating the predominance of additive gene action and good scope for selection. These results agree with Tyagi *et al.* (2018) and Sowmya (2018) in bitter gourd and Varalakshmi et *al*. (2015) in ridge gourd. Fruit length showed higher genetic variability and heritability in this cross than in IC85633 × IC50526, indicating that this population would be a better source for the selection of long-fruited segregants.

With respect to fruit diameter, high GCV (27.89 %) and PCV (28.07 %), high heritability (98.71 %) and high genetic advance as per cent over mean (57.17 %) were noticed, pointing to strong genetic control and additive gene action, which offer strong scope for selection. These results are in accordance with Adarsh (2018), Tyagi *et al.* (2018), Chaudhary *et al.* (2019), Singh and Kandasamy (2020) and Bhati *et al.* (2023) in bitter gourd and Farheen *et al.* (2022) in ridge gourd.

High GCV (50.98 %) and PCV (51.10 %) were noticed for average fruit weight, exceeded in magnitude only by fruit yield per vine, indicating wider variation in the population and less environmental influence on the expression of this trait. Near-complete heritability (99.51 %) coupled with very high genetic advance as per cent over mean (104.91 %) revealed that this trait was governed by additive gene action and is highly amenable to selection. These are in accordance with the earlier observations made by Tyagi *et al.* (2018), Sowmya (2018), Chinthan *et al.* (2021), Bannatti *et al.* (2023) and Sagar *et al.* (2024) in bitter gourd and Varalakshmi *et al.* (2015) in ridge gourd.

High GCV (37.98 %) and PCV (38.42 %) values were displayed for number of fruits per vine, indicating a high potential for genetic improvement of this trait. High heritability (97.70 %) coupled with high genetic advance as per cent over mean (77.45 %) was observed, indicating strong genetic control and additive gene action. Similar results were reported by Maurya *et al.* (2018), Sowmya (2018), Chinthan *et al.* (2021) and Singh *et al.* (2025) in bitter gourd and Varalakshmi *et al.* (2015) in ridge gourd.

With respect to fruit yield per vine, the highest magnitude of GCV (59.84 %) and PCV (62.85 %) were recorded, indicating wider variation in the population. High heritability (90.63 %) and the highest genetic advance as per cent over mean (116.67 %) recorded in the present study displayed that this trait was less affected by environmental factors and was under the control of additive gene action; pedigree selection would therefore be the best breeding approach for the advancement of this trait. Similar outcomes were observed by Tyagi *et al.* (2018), Sowmya (2018), Chinthan *et al.* (2021) and Sahana *et al.* (2025) in bitter gourd and Farheen *et al.* (2022) in ridge gourd.

Flesh thickness showed high GCV (24.62 %) and PCV (24.92 %), high heritability (97.59 %) and high genetic advance as per cent over mean (50.19 %), reflecting a strong genetic component and good scope for selection. This agrees with Chakraborty *et al*. (2013), Angadi and Mulge (2017) and Sowmya (2018) in bitter gourd and Farheen *et al.* (2022) in ridge gourd.

Cavity size showed high GCV (28.16 %) and PCV (28.65 %), high heritability (96.61 %) and high genetic advance as per cent over mean (57.12 %), indicating additive gene action and favouring selection against a large seed cavity. Similar findings were recorded by Arizoo *et al.* (2024) in ridge gourd.

On comparing the two crosses, the F_2 population of IC599421 × IC50526 recorded higher GCV for fruit yield per vine, average fruit weight, fruit length, node to first female flower and cavity size, whereas IC85633 × IC50526 recorded higher GCV for number of fruits per vine, number of branches per vine and days to first harvest. Fruit yield per vine and average fruit weight consistently emerged among the traits offering the greatest scope for genetic gain in both the populations. However, as the heritability estimated in the present study is in the broad sense and includes non-additive components, the effectiveness of selection for these traits needs to be confirmed in the advanced generations.

Table 1: Estimates of mean, range and genetic parameters for growth, flowering, yield and quality traits in F_2 population of IC85633 × IC50526 of bitter gourd

Sl. No.	Characters	Mean	Range		GCV (%)	PCV (%)	h^2bs (%)	GA	GAM (%)
			Min	Max					
1	Vine length at last harvest (m)	1.75	0.29	3.17	43.14	44.63	93.44	1.51	86.29

Sl. No.	Characters	Mean	Range		GCV (%)	PCV (%)	h^2bs (%)	GA	GAM (%)
			Min	Max					
2	Number of branches per vine	7.35	4.70	15.40	33.35	33.71	97.88	5.01	68.17
3	Node to first female flower	14.20	5.52	19.27	13.80	16.65	68.70	3.35	23.60
4	Days to first female flowering	46.46	29.09	56.24	13.39	13.58	97.26	12.66	27.25
5	Days to first harvest	61.38	41.04	74.09	10.51	11.13	89.10	12.56	20.46
6	Fruit length (cm)	13.56	7.51	22.84	16.00	20.60	60.38	3.47	25.59
7	Fruit diameter (mm)	26.53	11.26	54.04	27.79	28.15	97.45	15.01	56.58
8	Average fruit weight (g)	65.93	25.58	131.37	39.58	40.07	97.56	53.17	80.65
9	Number of fruits per vine	17.47	8.09	47.61	45.47	45.71	98.98	16.30	93.30
10	Fruit yield per vine (kg)	1.05	0.27	3.81	53.87	57.93	86.48	1.09	103.81
11	Flesh thickness (mm)	18.51	7.90	29.46	25.74	25.87	98.95	9.78	52.84
12	Cavity size (mm)	17.21	8.15	24.75	24.01	24.23	98.22	8.45	49.10

PCV - Phenotypic coefficient of variation; GCV - Genotypic coefficient of variation; h^2bs - Heritability (broad sense); GA - Genetic advance; GAM - Genetic advance as per cent of the mean

Table 2: Estimates of mean, range and genetic parameters for growth, flowering, yield and quality traits in F_2 population of IC599421 × IC50526 of bitter gourd

Sl. No.	Characters	Mean	Range		GCV (%)	PCV (%)	h^2bs (%)	GA	GAM (%)
			Min	Max					
1	Vine length at last harvest (m)	1.82	0.30	3.49	43.26	43.96	96.88	1.59	87.36
2	Number of branches per vine	8.97	4.78	16.00	21.43	24.25	78.01	3.50	39.02
3	Node to first female flower	15.13	6.49	20.39	19.12	19.61	95.00	5.82	38.46
4	Days to first female flowering	46.02	27.46	58.51	12.78	13.16	94.41	11.79	25.63
5	Days to first harvest	61.22	43.10	69.90	7.68	8.10	89.94	9.19	15.02
6	Fruit length (cm)	12.43	7.55	24.15	21.15	21.91	93.13	5.24	42.16
7	Fruit diameter (mm)	34.04	14.15	59.46	27.89	28.07	98.71	19.46	57.17
8	Average fruit weight (g)	56.84	9.25	129.52	50.98	51.10	99.51	59.63	104.91
9	Number of fruits per vine	15.74	8.51	40.40	37.98	38.42	97.70	12.19	77.45
10	Fruit yield per vine (kg)	0.90	0.15	3.19	59.84	62.85	90.63	1.05	116.67
11	Flesh thickness (mm)	19.85	8.20	31.26	24.62	24.92	97.59	9.96	50.19
12	Cavity size (mm)	16.51	7.63	25.10	28.16	28.65	96.61	9.43	57.12

PCV - Phenotypic coefficient of variation; GCV - Genotypic coefficient of variation; h^2bs - Heritability (broad sense); GA - Genetic advance; GAM - Genetic advance as per cent of the mean

CONCLUSION

In the F_2 population of the cross IC85633 × IC50526, high GCV and PCV were detected for vine length at last harvest, number of branches per vine, fruit diameter, average fruit weight, number of fruits per vine, fruit yield per vine, flesh thickness and cavity size. In the F_2 population of the cross IC599421 × IC50526, high GCV and PCV were observed for the same characters and also for fruit length, which indicates the existence of considerable variability for the traits recorded and ample scope for their improvement through selection. Fruit yield per vine recorded the highest GCV, PCV and genetic advance as per cent over mean in both the populations. High heritability along with high genetic advance as per cent over mean was reported for all the twelve characters in the F_2 population of IC85633 × IC50526 and for all the characters except days to first harvest in the F_2 population of IC599421 × IC50526. High heritability suggests that the observed variation in these traits is largely due to genetic factors, making them more predictable and responsive to selection. High genetic advance indicates that selecting individuals with desirable traits, particularly for fruit yield per vine, average fruit weight and number of fruits per vine, is expected to result in appreciable improvement will result in significant improvement in the next generation.

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