



Genetic Variability, Heritability and Genetic Advance for Yield and Yield Contributing Characters in Bitter Gourd (*Momordica charantia* L.) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Twenty diverse genotypes were evaluated at Horticulture research centre of SVP university of Agriculture & Technology, Meerut during spring season, 2022. The experiment was laid out in Randomized block design with three replications. The analysis of variance revealed significant among all the genotypes for all the characters under study. The high percentage of Genotypic coefficient of variation and phenotypic coefficient of variation for fruit diameter, fruit yield per plot, number of fruits per plant, fruit yield per hectare, node number to first male flower, average fruit weight while, moderate were found for node number to first female flower and TSS and lowest in days to germination, number of leaves per plant, vine length, number of primary branches per plant, days to first male flower, days to first female flower and days to first fruit harvest which estimated that high degree of variability in these traits. The highest heritability recorded for fruit diameter 99.45% followed by number of fruits per plant, fruit yield per plot, fruit length, node number to first female flower, average fruit weight, number of leaves per plant, node number to first male flower, days to first male flower, fruit yield per hectare, days to first fruit harvest, TSS, days to germination, vine length, days to first female flower and number of primary branches per plant. Genetic advance as percent of mean was highest for fruit diameter, fruit length, fruit yield per plot, number of fruits per plant, fruit yield per hectare, node number to first male flower, average fruit weight, node number to first female flower. Which indicate that above characters may be most potential for further improvement.

Keywords: Bitter gourd; variability; heritability and genetic advance.

1. INTRODUCTION

Bitter gourd, scientifically known as *Momordica charantia* L., belongs to the Cucurbitaceae family and is commonly referred to as bitter melon, balsam pear, pare, or karela. It has a long history of consumption and medicinal use and is native to tropical Asia, particularly the Indo Burma region. Bitter gourd is extensively cultivated in countries such as India, Indonesia, Malaysia, China, and tropical Africa. In India alone, it covers an estimated area of 101 thousand hectares, with a production of approximately 1174 million tonnes and an average yield of 11.90 tonnes per hectare for bitter gourd (NHB 2020-21).

The *Momordica* genus comprises around 60 species, with *Momordica charantia* L. being the most widely grown. This monoecious crop is prone to cross-pollination, resulting in significant diversity in commercially relevant traits. Notably, the fruit's shape, size, and color exhibit noticeable variations [1]. Bitter gourd stands out due to its rich nutritional composition and the presence of various beneficial substances. It is a powerhouse of phytochemicals, vitamins, minerals, and antioxidants, which contribute to its

remarkable versatility in treating various diseases. The fruit is particularly abundant in folate (vitamin B9), vitamins B1, B2, and B3, vitamin C, vitamin A, and vitamin E. Bitter melon owes its high antioxidant capabilities, partly, to phenols, flavonoids, isoflavones, terpenes, anthraquinones, and glucosinolates, which also account for its bitter taste.

The consumption of vegetables has been on the rise due to their high content of bioactive compounds such as ascorbic acid, phenolic acids, carotenoids, flavonoids, proteins, minerals, and dietary fibers, while being low in sugar. Among various vegetables, bitter gourd stands out as one of the most nutritionally rich and medicinally beneficial vegetables worldwide [2]. Bitter gourd has been traditionally utilized in the form of fruits, seeds, leaves, vines, and roots for both culinary and medicinal purposes, offering a wide range of health benefits [2]. It plays an important role in maintaining sound health as part of the human diet. Additionally, the seeds of bitter gourd are a valuable source of protein and oil. The consumption of bitter gourd has been increasing significantly, not only due to its nutritional value but also due to its therapeutic properties. Bitter gourd is known to contain

beneficial compounds such as catechin, gallic acid, gentisic acid, chlorogenic acid, and saponins. Moreover, research by Horax et al. [3] has shown that bitter melon is a promising source of antioxidants that can be utilized in the food industry.

3. MATERIALS AND METHODS

In 2022, a research experiment titled "Studies on Genetic Variability for yield and its components traits in Bitter Melon (*Momordica charantia*)" was conducted at the Horticulture Research Centre of Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut (U.P.). The study involved 20 bitter melon genotypes obtained from NBPGR, New Delhi. These genotypes were collected from diverse sources, including indigenous and exotic origins. Table 1 provides a comprehensive overview of the collected genotypes and their respective sources of supply. The experiment was carried out with three replications to ensure robustness and reliability in the results.

2.1 Analysis of Variance

The mean values of genotypes in each replication were used for statistical analysis.

The data were analyzed for a randomized block design to test the significance of differences between the genotypes for various characters. The steps involved in the analysis of the randomized block design were as described by Panse and Sukhatme [4].

$$\text{Genotypic variance } (\sigma^2g) = (MSt/MSe)/r$$

$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + \sigma^2e$$

$$\text{Error variance } (\sigma^2e) = MSe$$

2.2 Heritability

Heritability in broad sense $h^2(b)$ was computed as a ratio of genotypic variance to phenotypic variance [5].

$$h^2(b) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where,

$h^2(b)$ = Heritability in broad sense

σ^2g =Genotypic Variance

σ^2p =Phenotypic Variance

Table 1. List of genotypes used in the experimental trial

S. No.	Number of Genotypes	Source
1	Pusa Aushadhi	NBPGR, New Delhi
2	Pusa-do-mausami	NBPGR, New Delhi
3	Pusa Rasdar	NBPGR, New Delhi
4	Pusa Poorvi	NBPGR, New Delhi
5	Pusa Vishesh	NBPGR, New Delhi
6	Pusa Hybrid-2	NBPGR, New Delhi
7	TCR-271 1C85647	NBPGR, New Delhi
8	TCR-290 1C66023	NBPGR, New Delhi
9	TCR-333 1C470535	NBPGR, New Delhi
10	TCR-331 1C505638	NBPGR, New Delhi
11	TCR-337 1C113876	NBPGR, New Delhi
12	TCR-358 1C505630	NBPGR, New Delhi
13	TCR-344 1C505640	NBPGR, New Delhi
14	TCR-289 1C65972	NBPGR, New Delhi
15	TCR-356 1C505621	NBPGR, New Delhi
16	TCR-336 1C505637	NBPGR, New Delhi
17	TCR-334 1C505629	NBPGR, New Delhi
18	TCR-349 1C470546	NBPGR, New Delhi
19	TCR-359 1C470553	NBPGR, New Delhi
20	TCR-276A 1C85649A	NBPGR, New Delhi

2.3 Genetic Advance

The expected genetic advanced under section for different character was estimated as suggested by Allard (1960).

$$G.A. = h^2 (b) \times \sigma_p \times k$$

Where,

G.A.= Expected genetic advance

(b) = Heritability in broad sense

σ_p = Phenotypic standard deviation ($\sqrt{\sigma^2 p}$)

K= Intensity of selection, the value of which is 2.06 when 5percent of the individuals are selected from the population

3. RESULTS

3.1 Genetic Variability Parameters

3.1.1 Coefficient of variation

The data was presented in Table 2 and Fig. 1 at genotypic and phenotypic coefficients of variation for sixteen characters of bitter gourd are presented. The estimates of coefficients of variation revealed that for all of the traits, phenotypic coefficients of variation (PCV) was found high magnitude of than the genotypic coefficient of variation (GCV), (PCV>GCV) indicating that the environment played a substantial impact.

3.1.1.1 Genotypic Coefficient of Variation (GCV)

It is revealed in Table 2 and Fig. 1 that, the genotypic coefficient of variation (GCV) value from 4.64% to 23.40%. The highest genotypic coefficient of variation was seen in fruit diameter (23.27%) followed by fruit yield per plot (22.77%), number of fruits per plant (22.60%), fruit yield per hectare (22.50%), node number to first male flower (20.5%), average fruit weight (20.14%) and the moderate genotypic coefficient of variation was seen in node number to first female flower (17.32%) and TSS (12.47%). The lowest genotypic coefficient of variation was seen in days to germination (9.95%) followed by number of leaves per plant (9.73%), vine length (9.49%), number of primary branches per plant (6.39%), days to first male flower (5.24%), days to first female flower (4.91%), days to first fruit harvest (4.64%).

3.1.1.2 Phenotypic Coefficient of Variation (PCV)

The phenotypic variation range recorded for 4.85% to 23.74% for the various characters studied (Table 2 and Fig. 1). The data were presented according to the table the highest phenotypic coefficient of variation was seen in fruit length (23.74%) followed by fruit diameter (23.34%), fruit yield per hectare (23.23%), fruit yield per plot (22.94%), number of fruits per plant (22.71%), node number to first male flower (21.11%), average fruit weight (20.53%) and the moderate phenotypic coefficient of variation was seen in node number to first female flower (17.57%), TSS (13.09%), days to germination (10.73%) and vine length (10.25%). However, lowest phenotypic coefficient of variation was observed. However, lowest phenotypic coefficient of variation was observed in number of leaves per plant (9.95%), number of primary branches per plant (7.28%), days to first male flower (5.40%), days to first female flower (5.34%) and days to first fruit harvest (4.85%).

3.1.2 Heritability (h^2)

Estimates of heritability and expected genetic advance for different characters are presented in Table 2 and Fig. 1. The broad sense heritability ranged from 99.45% to 77.08 %. The result revealed that the high heritability estimates in fruit diameter 99.45% followed by number of fruits per plant (99.04%), fruit yield per plot (98.53%), fruit length (97.12%), node number to first female flower (97.05%), average fruit weight (96.30%), number of leaves per plant (95.47%), node number to first male flower (94.64%), days to first male flower (94.35%), fruit yield per hectare (93.78%), days to first fruit harvest (91.64%), TSS (90.75%), days to germination (86.03%), vine length (85.73%), days to first female flower (84.54%) and number of primary branches per plant (77.08%).

3.1.3 Genetic advance

The genetic advance value ranges from 9.15% to 47.82% for the various characters studied (Table 2 and Fig. 1). The data were presented according to the table the highest value of genetic advance in percent of mean was shown by fruit diameter (47.82%), fruit length (47.50%), fruit yield per plot (46.57%), number of fruits per plant (46.32%), fruit yield per hectare (44.89%), node number to first male flower (41.15%), average fruit weight (40.72%), node number to first female flower (35.12%) and the moderate

Table 2. Estimates of Parameters of Variability, Heritability and Genetic Advance for Various Characters in Bitter Gourd Genotypes

Characters	Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to Germination	8.55	6.75	10.58	0.72	0.84	86.03	1.62	19.01	9.95	10.73
Node to First Male Flower	10.18	7.50	17.50	4.37	4.62	94.64	4.19	41.15	20.53	21.11
Node to First Female Flower	12.46	8.50	20.25	4.65	4.79	97.05	4.38	35.12	17.31	17.57
Days to First Male Flower	38.26	34.83	44.08	4.03	4.27	94.35	4.01	10.49	5.24	5.40
Days to First Female Flower	41.81	38.67	47.08	4.21	4.98	84.54	3.89	9.30	4.91	5.34
Number of Primary Branches /Plants	11.34	9.42	12.00	0.53	0.68	77.08	1.31	11.56	6.39	7.28
Number of Leaves Per Plant	40.62	29.92	47.75	15.60	16.34	95.47	7.95	19.57	9.73	9.95
Vine Length(M)	2.43	2.04	2.95	0.05	0.06	85.73	0.44	18.11	9.49	10.25
Days to First Fruit Harvest	53.69	50.08	60.50	6.21	6.78	91.64	4.91	9.15	4.64	4.85
Fruit Length (Cm)	10.34	4.54	16.05	5.85	6.03	97.12	4.91	47.50	23.40	23.74
Fruit Diameter (Cm)	3.86	1.08	5.85	0.81	0.81	99.45	1.84	47.82	23.27	23.34
Number of Fruits Per Plant	26.81	14.58	34.92	36.70	37.05	99.04	12.42	46.32	22.60	22.71
Average Fruit Weight	51.57	16.58	63.25	107.94	112.09	96.30	21.00	40.72	20.14	20.53
TSS (°Brix)	4.26	3.25	5.25	0.28	0.31	90.75	1.04	24.47	12.47	13.09
Fruit Yield Per Plot	1.11	0.54	1.83	0.06	0.06	98.53	0.52	46.57	22.77	22.94
Fruit Yield/Ha	12.26	6.00	19.93	7.61	8.11	93.78	5.50	44.89	22.50	23.23

Note*

PCV = Phenotypic coefficient of variation {Low (L): <10%, Moderate (M): 10-20%, High (H): >20%}

GCV = Genotypic coefficient of variation {Low (L): <10%, Moderate (M): 10-20%, High (H): >20%}

h^2_{bs} = Heritability (broad sense) {Low (L): <30%, Moderate (M): 30-60%, High (H): >60%}

GA = Genetic advance {Low (L): <10%, Moderate (M): 10-30%, High (H): >30%}

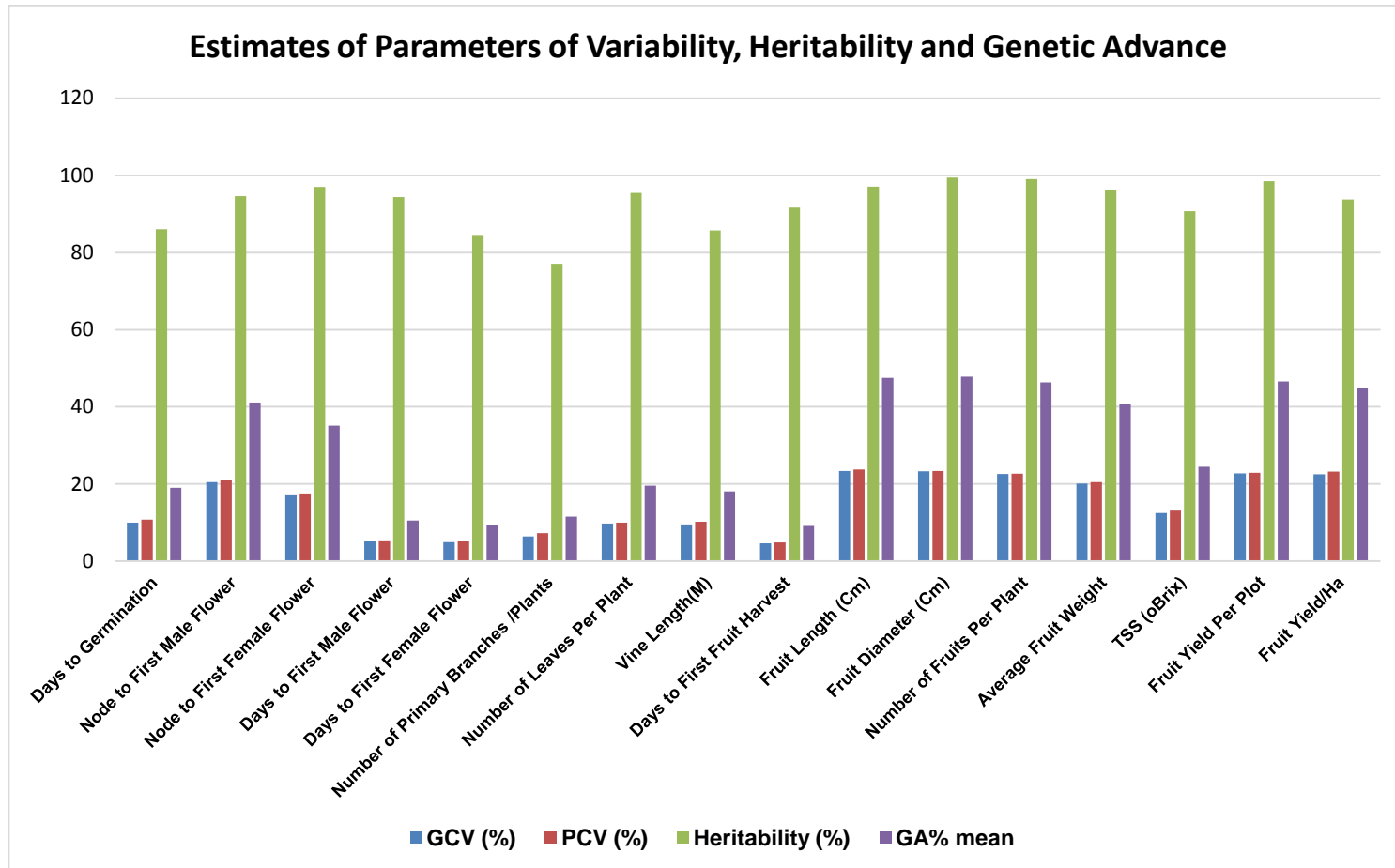


Fig. 1. Estimates of parameters of variability, heritability and genetic advance for various characters in bitter melon genotypes

value of genetic advance was observed in TSS (24.47%), number of leaves per plant (19.57%), days to germination (19.01%), vine length (18.11%), number of primary branches per plant (11.56%), days to first male flower (10.49%). The lowest value of genetic advance was observed in days to first female flower (9.30%) and days to first fruit harvest (9.15%).

4. DISCUSSION

4.1 Variability

The GCV was found lower than PCV for all traits studies indicated that these characters were interacting with environment to some extent (Ram and Singh, 1993). The genotypic and phenotypic variances are of little meaning as they do not any clear limit. And at the same time, the categorization of the genotypic variance as low or high is difficult, rendering them unsuitable for comparison of two populations with desired precision when expressed in absolute values. To overcome this difficult the genotypic and phenotypic coefficients of variation that are free from the unit of measurement, can be conveniently employed for making comparison between population and different metric traits of population. Result from these present studies in this context indicated co-efficient of variation (PCV).

The moderate percent of genotypic co-efficient of variation (10-25%) was observed in fruit length followed by fruit diameter, fruit yield per plot, number of fruits per plant, fruit yield per hectare node number to first male flower, average fruit weight, node number to first female flower and TSS. Where, low genotypic co-efficient of variation (<10%) was showed in case of days to germination followed by number of leaves per plant, vine length, number of primary branches per plant, days to first male flower, days to first female flower and days to first fruit harvest.

Estimated that phenotypic coefficient of variation (PCV) for different character. The highest percent of phenotypic coefficient of variation (>20%) was observed in fruit length followed by fruit diameter, fruit yield per hectare, fruit yield per plot, number of fruits per plant, node number to first male flower and average fruit weight. While moderate phenotypic coefficient of variation (10-20%) was seen in node number to first female flower followed by TSS, days to germination and vine length. Where low

phenotypic coefficient of variation (<10%) was showed for traits like, number of leaves per plant followed by number of primary branches per plant days to first male flower, days to first female flower and days to first fruit harvest. The finding is similar in agreement with earlier reported by Chakraborty et al. [6], Singh et al. [7], Tiwari et al. (2021). If different, it indicates that the characters' varied performances are greatly influenced by their environment. But if there is a large difference, this indicates that the environment has a significant impact on how features are expressed.

4.2 Heritability

The idea of heritability is crucial for determining whether phenotypic differences between different individuals may result from genetic changes or from the influence of environmental factors. Studying the inheritance of quantitative features and arranging breeding programmes with the necessary level of anticipated genetic advancement both benefit from the information on heritability estimates. With the use of heritability estimations and genetic gain, the heritable variation can be identified; however, for the current inquiry, heredity could only be assessed in a general sense. The broad sense heritability were obtained (>80%) in various traits like, fruit diameter followed by number of fruits per plant, fruit yield per plot, fruit length, node number to first female flower, average fruit weight, number of leaves per plant, node number to first male flower, days to first male flower, fruit yield per hectare, days to first fruit harvest, TSS, days to germination, vine length and days to first female flower. The moderate heritability (<80%) was observed for number of primary branches per plant. Similar result was also finding earlier by Nithinkumar et al. [8], Selvam et al. [9]. The high heritability indicates that a significant amount of genetic influences contributed to the development of these traits and can be used to increase fruit yield. The trait with a high heritability may be caused by additive genetic components contributing more significantly to the inheritance of these traits.

4.3 Genetic Advance

For an effective see the knowledge alone on the estimates of heritability is not sufficient and genetic advance if studies along with heritability more useful. Present study, high genetic advance (>30%) for fruit diameter followed by

fruit length, fruit yield per plot, number of fruits per plant, fruit yield per hectare, node number to first male flower, average fruit weight and node number to first female flower. Whereas, moderate genetic advance (10-30%) for TSS followed by number of leaves per plant, days to germination, vine length, number of primary branches per plant, days to first male flower. while days to first female flower and days to first fruit harvest showed low genetic advance (<10%). Thereby, suggesting average response for selection based on performance. Some of these characters have been also reported by Selvam et al. [9], Tiwari et al. [10], Tiwari et al. [11].

5. CONCLUSION

Based on results, the node number to the first female flower and TSS showed considerable genotypic co-efficient of variation (10–20%). Days to germination, number of leaves per plant, vine length, number of primary branches per plant, days to first male flower, days to first female flower, and days to first fruit harvest were the areas with the lowest genotypic co-efficient of variation (10%). Fruit diameter, fruit yield per plot, number of fruits per plant, fruit yield per hectare, node number to first male flower, and average fruit weight all showed high genotypic coefficients of variance. High genetic advance as a percentage of mean (GA%) and high heritability show that both additive and non-additive genes act to enhance the effects of the environment on gene expression. High genetic advance (GA) and with high heritability (h^2) make it easier to evaluate the gain under selection. The heritability of the current experiment could only be evaluated in a broad sense. The number of fruits per plant, fruit yield per plot, fruit length, node number to first female flower, average fruit weight, number of leaves per plant, node number to first male flower, days to first male flower, fruit yield per hectare, days to first fruit harvest, TSS, days to germination, vine length, days to first female flower, and number of primary branches per plant were the other traits that showed the highest broad sense heritability (>60%). This suggested that the characteristics mentioned above may have scope for growth.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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