PLANT SCIENCE TODAY
Vol x(x): xx–xx
https://doi.org/10.14719/pst.10878

eISSN 2348-1900

RESEARCH ARTICLE

Comprehensive quantitative genetic evaluation of phenotypic variability, heritability coefficients and expected genetic gain for yield and its associated traits in bitter gourd (*Momordica charantia* L.) under diverse agro-ecological conditions of the North Indian Plains

Harshit Tomar[1*], Bijendra Singh[1], Vipin Kumar[1], Rupesh Kumar[1], Vaishali[2], Satya Prakash[1], L K Gangwar[3] & Krashankant Sharma[4]

[1]Department of Vegetable Science, College of Horticulture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut 250 110, Uttar Pradesh, India
[2]Department of Agriculture Biotechnology, College of Agriculture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut 250 110, Uttar Pradesh, India
[3]Department of Genetics and Plant Breeding, College of Agriculture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut 250 110, Uttar Pradesh, India
[4]Department of Agronomy, College of Agriculture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut 250 110, Uttar Pradesh, India

Correspondence email - tomarharshit180@gmail.com

Received: 25 July 2025; Accepted: 02 November 2025; Available online: Version 1.0: 17 December 2025

Cite this article: Harshit T, Bijendra S, Vipin K, Rupesh K, Vaishali, Satya P, Gangwar LK, Krashankant S. Comprehensive quantitative genetic evaluation of phenotypic variability, heritability coefficients and expected genetic gain for yield and its associated traits in bitter gourd (*Momordica charantia* L.) under diverse agro-ecological conditions of the North Indian Plains. Plant Science Today (Early Access). https://doi.org/10.14719/pst.10878

Abstract

The study was conducted over two years to investigate genetic variability, heritability and genetic advance as a percentage of the mean among 40 genotypes of bitter gourd (*Momordia charantia* L.). The genotypes were cultivated at the Horticulture Research Centre, SVPUAT, Modipuram (Meerut), during the *Zaid* seasons of 2023 and 2024. The experiment followed a randomized block design (RBD) with three replications and a spacing of 1 m × 0.75 m. A total of sixteen quantative traits were recorded and analyzed to identify genetic factors contributing to enhanced yield potential. Analysis of variance (ANOVA) revealed that mean squares due to genotypes were significant for all the traits studied. The pooled phenotypic coefficient of variation (PCV) exhibited an average increase of about 5 % over the genotypic coefficient of variation (GCV), with mean values of 11.06 % and 10.07 %, respectively. In 2023, the highest genotypic and phenotypic coefficients of variation were observed for primary branches per vine (23.24 and 23.57, respectively), whereas in 2024, the maximum values were recorded for total fruit yield per vine (41.93 and 42.22 respectively). Similarly, heritability (broad sense, h^2bs) and genetic advance (GA) were highest for primary branches per vine in 2023 (97.28 % and 47.22 %, respectively, while in 2024, total fruit yield per vine recorded the maximum heritability and genetic advance (98.67 % and 85.82 %, respectively). Overall, traits exhibiting high PCV and GCV values corresponded with high heritability and genetic advance estimates for the same characters, indicating the predominance of additive gene action and the potential for improvement through simple selection.

Keywords: bitter gourd; genetic advance; heritability; variability

Introduction

Bitter gourd (*Momordica charantia* L.) is an important cucurbitaceous crop with significant production, nutritional and economic benefits. Bitter gourd is also known as balsam pear, karela, bitter melon or bitter cucumber, among others. It is widely distributed in tropical and subtropical regions of the world and is highly adaptable to a variety of growing conditions. India is the primary center of origin, whereas China and Southeast Asia are considered secondary centers of diversity. Bitter gourd is monoecious species, bearing distinct yellow male and female flowers and is predominantly cross-pollinated, leading to considerable variability in fruit and plant characteristics.

The characteristic bitter taste is attributed by momordicine, an alkaloid that also contains momordicosides (glycosides composed of tetracyclic triterpinoids with a cucurbitane structure) and has a distinct chemical structure compared to the cucurbitacins found in other members of the cucurbitaceae family. This wild cucurbit species *M. balsamina,* widely distributed across tropical Africa, can make a valuable contribution to the gene pool of cultivated bitter gourd genotypes by providing new traits such as improved quality and resistance to biological and environmental stresses. These fruits also possesses notable nutritional properties, serving as a good source of proteins, carbohydrates, lipids, different minerals and vitamins A, B_2 and C (1, 2). In India, the average vegetable consumption is only 175 g per person per day, which is considerably lower than the recommended intake of 350-400 g of vegetables and fruits for a balanced diet (3). To achieve the national nutritional goals, it is necessary to develop and promote improved varieties and hybrids and enhance other agronomic practices.

Despite the economic and nutritional significance of bitter gourd (*M. charantia* L.), comprehensive genetic studies focusing on yield and its associated traits under diverse agro-ecological conditions remain limited. Most existing research has been conducted at single locations, neglecting the influence of genotype x environment (G x E) interactions, which are crucial for stable yield performance and cultivar adaptability (4). The lack of multi-environment quantitative genetic evaluations restricts breeders' ability to identify genotypes with high heritability and genetic gain across varying conditions, especially in the ecologically diverse North Indian Plains.

Analyzing variability in traits and understanding the relationship of traits to yield, as well as yield-contributing traits, forms an essential component of crop improvement programs (5). Such analyses allow breeders to estimate the expected genetic advance (GA) from selection within populations and to evaluate alternative breeding strategies (6). High heritability combined with substantial GA indicates additive gene action, providing favourable conditions for effective selection of high-yielding cultivars (7). Breeders can thus utilize existing genetic variation to develop high-yielding open-pollinated varieties or hybrids, contributing to the genetic improvement of bitter gourd.

Accordingly, the objective of this study was to determine the degree of genetic variability, heritability and GA in bitter gourd populations by analyzing and quantifying variation in desirable traits. This evaluation will help identify characteristics that are strongly inherited and can be effectively improved through selective breeding. Understanding these parameters is essential for developing superior bitter gourd varieties with enhanced yield, disease resistance and other agronomic traits.

Materials and Methods

Experimental site and layout

The field experiment was carried out during the *Zaid* seasons in the 2023 and 2024 at the Horticulture Research Centre, College of Horticulture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh (latitude 29.094876° N and longitude 77.695616° E), using 40 genotypes of bitter gourd. In total, 38 genotypes were procured from ICAR-NBPGR, New Delhi, while 2 additional varieties were sourced (Table 1). These genotypes were sown in a randomized block design (RBD) with three replications in the field. The number of plants per replication was three and the net plot size was 2.25 m^2. Irrigation was provided weekly to maintain soil moisture in the root zone, which promotes rapid taproot development. Well-decomposed farmyard manure (15-20 t ha^{-1}) was incorporated into the soil during ploughing to improve soil fertility. The recommended dose of fertilizers (RDF) per hectare was applied as 70 kg nitrogen (N), 50 kg phosphorus (P) and 40 kg potassium (K), placed in a ring 6-7 cm away from the stem base. Red pumpkin beetle, a major pest of bitter gourd, was controlled by spraying malathion at 0.05 % (10 kg ha^{-1}).

Observations were recorded by randomly selecting three plants for various characters, including days to germination, vine length (m), primary branches per vine, days to first male flower appearance, days to first female flower appearance, total number of male flowers, total number of female flowers, days to first picking, fruit weight (g), fruit length (cm), fruit girth (cm), number of fruits per vine, number of seeds per fruit, total fruit yield per vine (kg), total yield (q ha^{-1}) and total soluble solids (TSS, %).

The experiment was conducted in the subtropical region of the Upper Gangetic Plain in India, where summer temperatures reach 40 °C to 45 °C in June-July. During the crop growth period, the mean daily temperature was 27.1 °C and 28.4 °C, the average relative humidity was 50.8 % and 42.37 % and the average rainfall recorded was 26.6 mm and 7.33 mm in year 1 and year 2, respectively. These climatic variations likely contributed to differences in trait expression, as reflected in the higher estimates of phenotypic coefficient of variation (PCV) compared to genotypic coefficient of variation (GCV), indicating that environmental factors played a greater role in phenotypic variability than the genetic component alone. Weather parameters for 2023-2024 crop periods are shown in Fig. 1, 2.

The edaphic characteristics of the experimental field were as follows: the soil exhibited a slightly alkaline pH of approximately 7.8 and an electrical conductivity (EC) value of 0.291 dS m^{-1}, indicating low salinity. The organic carbon content was low (0.312 %), reflecting limited organic matter. The soil texture was identified as sandy loam, contributing to moderate fertility levels suitable for plant growth. These factors collectively influence soil nutrient availability and overall productivity.

Table 1. List of genotypes included in the trial

S. No.	Genotypes	Source	S. No.	Genotypes	Source
1.	IC 68230	ICAR-NBPGR, New Delhi	21.	IC 50526	ICAR-NBPGR, New Delhi
2.	IC 85643	ICAR-NBPGR, New Delhi	22.	IC 44423	ICAR-NBPGR, New Delhi
3.	IC 264770	ICAR-NBPGR, New Delhi	23.	IC 50516	ICAR-NBPGR, New Delhi
4.	IC 505632	ICAR-NBPGR, New Delhi	24.	IC 44426	ICAR-NBPGR, New Delhi
5.	IC 470550	ICAR-NBPGR, New Delhi	25.	IC 470555	ICAR-NBPGR, New Delhi
6.	IC 85650	ICAR-NBPGR, New Delhi	26.	IC 505626	ICAR-NBPGR, New Delhi
7.	IC 505623	ICAR-NBPGR, New Delhi	27.	IC 470535	ICAR-NBPGR, New Delhi
8.	IC 505635	ICAR-NBPGR, New Delhi	28.	IC 505630	ICAR-NBPGR, New Delhi
9.	IC 44424	ICAR-NBPGR, New Delhi	29.	IC 470554	ICAR-NBPGR, New Delhi
10.	IC 45346	ICAR-NBPGR, New Delhi	30.	IC 505621	ICAR-NBPGR, New Delhi
11.	IC 213308	ICAR-NBPGR, New Delhi	31.	IC 470556	ICAR-NBPGR, New Delhi
12.	IC 50520	ICAR-NBPGR, New Delhi	32.	IC 505638	ICAR-NBPGR, New Delhi
13.	IC 66023	ICAR-NBPGR, New Delhi	33.	IC 469656	ICAR-NBPGR, New Delhi
14.	IC 85647	ICAR-NBPGR, New Delhi	34.	IC 68309	ICAR-NBPGR, New Delhi
15.	IC 68314	ICAR-NBPGR, New Delhi	35.	IC 213307	ICAR-NBPGR, New Delhi
16.	IC 68232	ICAR-NBPGR, New Delhi	36.	IC 68275	ICAR-NBPGR, New Delhi
17.	IC 44419	ICAR-NBPGR, New Delhi	37.	IC 470553	ICAR-NBPGR, New Delhi
18.	IC 44413	ICAR-NBPGR, New Delhi	38.	IC 68272	ICAR-NBPGR, New Delhi
19.	IC 33275	ICAR-NBPGR, New Delhi	39.	Pusa Vishesh	Local Market
20.	IC 469512	ICAR-NBPGR, New Delhi	40.	Green long -32	Local Market

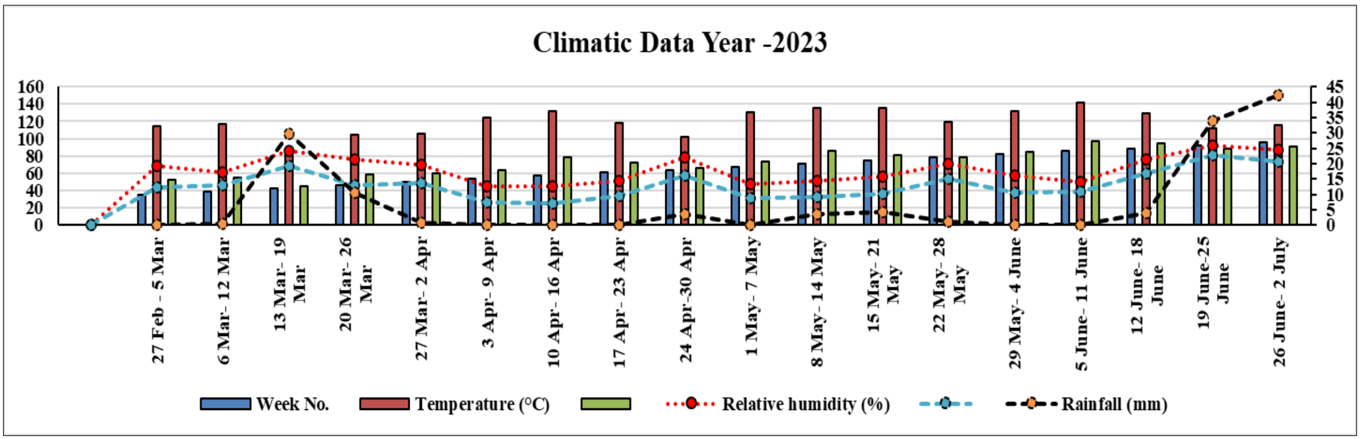

Fig. 1. Weekly climate data of Year 2023.

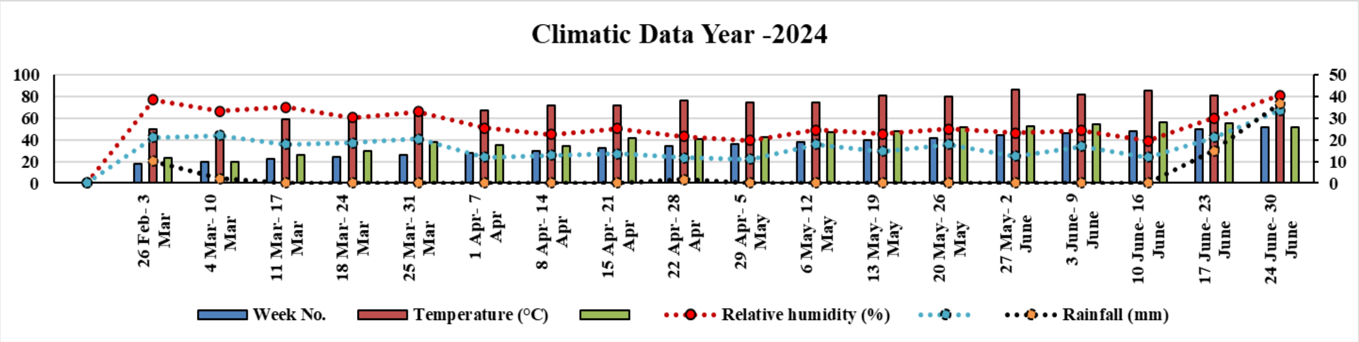

Fig. 2. Weekly climate data of Year 2024.

Statistical analysis

The analysis of variance (ANOVA) followed the methodology outlined in the literature (9). Both the PCV and GCV for each trait were calculated using a previously described standard formula (10). These coefficients were classified into three different categories as defined by earlier researchers: low (0 %-10 %), moderate (10 %-20 %) and high (above 20 %) (11). Broad-sense heritability (h^2) values were determined according to the method described earlier studies (12). The heritability values were grouped into low (0 %-30 %), moderate (30 %-60 %) and high (60 % and above), as recommended by previous researchers (13).

GA under 5 % selection intensity was calculated using established formulas (14, 15). Following the methodology described GA as a percentage of the mean was categorized into three groups: low (0 %-10 %), moderate (10 %-20 %) and high (above 20 %). All the genetic parameters-including genetic variability, heritability, GA, correlation and path coefficient analysis (PCA)-were computed using R software. The level of significance was set at $p < 0.05$.

Results and Discussion

Analysis of variance

ANOVA conducted on sixteen morphological and yield-related traits of bitter gourd showed that the mean squares among genotypes were statistically highly significant ($p < 0.01$) for all examined traits (Table 2). This indicates substantial genetic variability among the genotypes, suggesting considerable potential for crop improvement through selection breeding. The traits showing significant variation included days to germination, days to first male flower appearance, days to first female flower appearance, days to first picking, vine length (m), number of primary branches per vine, total number of male flowers, total number of female flowers, fruit weight (g), fruit length (cm), fruit girth (cm), number of fruits per vine, TSS (%), number of seeds per fruit, total fruit yield per vine (kg) and total yield (q ha^{-1}).

The calculated F-values ranged from 13.47 (days to germination) to 52.59 (total yield, q ha^{-1}) in 2023 and from 11.94 (days to germination) to 45.57 (total yield, q ha^{-1}) in 2024. The wide range of variation observed among different genotypes for each trait demonstrates ample scope for genetic enhancement through selective breeding programs. These findings are consistent with previous studies, where significant variations in bitter gourd traits have also reported by several researchers (8, 16-18).

Genotypic and phenotypic coefficient of variance

The GCV and PCV are useful indicators for assessing the extent of variability in specific traits and for comparing the degree of variation across quantitative characteristics. The calculated coefficients revealed that PCV values were higher than GCV values for all measured traits, indicating that environmental factors contributed to the observed variability (Table 3). A larger difference between PCV and GCV values suggests a greater environmental influence on trait expression.

For the 2023 season, the highest estimates of both GCV and PCV were recorded for primary branches per vine (23.57 %) (Fig. 3A, B). Moderate PCV vales were observed for fruit length (18.17 %), followed by vine length (15.30 %), total fruit yield per vine (15.13 %), fruit girth (13.85 %) and number of seeds per fruit (10.10 %). Traits such as fruit weight (8.47 %), days to germination (8.46 %), number of fruits per vine (8.32 %), total yield (q ha^{-1}) (7.98 %), total number of male flowers (7.50 %), total number of female flowers (7.25 %), days to first male flower appearance (6.22 %), days to first female flower appearance (5.78 %), TSS (5.14 %) and days to first picking (4.99 %) exhibited low PCV values.

During the *Zaid* season of 2024, the maximum PCV and GCV values were recorded for total fruit yield per vine (42.22 %) and primary branches per vine (23.19 %) (Fig. 3A, 3B). Moderate phenotypic variability was recorded for fruit length (18.47 %), vine length (13.37 %) and fruit girth (13.32 %), whereas low phenotypic

Table 2. Mean sum squares of genotypes

	Characters	**Sources of variation for year 1 (2023)**			**Sources of variation for year 2 (2024)**		
		Replications	**Treatments**	**Error**	**Replications**	**Treatments**	**Error**
	d.f.	2	39	78	2	39	78
1.	Days to germination	0.21	1.93**	0.19	0.09	2.03**	0.17
2.	Days taken to first male flower appearance	3.29	10.58**	2.10	1.78	12.17**	2.06
3.	Days taken to first female flower appearance	2.57	13.66**	3.08	3.13	15.50**	3.11
4.	Days taken to first picking	1.59	13.82**	5.02	6.57	13.44**	5.29
5.	Vine length (m)	0.002	0.609**	0.014	0.018	0.510**	0.019
6.	Primary branches per vine	0.02	3.39**	0.03	0.05	3.46**	0.04
7.	Total number of male flowers	38.97	946.78**	98.51	87.52	914.63**	109.76
8.	Total number of female flowers	0.50	4.63**	0.47	0.17	4.85**	0.56
9.	Fruit weight (g)	5.99	93.59**	6.41	0.73	92.39**	7.88
10.	Fruit length (cm)	0.22	16.75**	0.22	0.17	18.00**	0.26
11.	Fruit girth (cm)	0.16	7.49**	0.19	0.05	7.07**	0.22
12.	Number of fruits per vine	0.54	4.99**	0.37	0.34	5.07**	0.38
13.	TSS (%)	0.007	0.078**	0.021	0.028	0.216**	0.019
14.	Number of seeds per fruit	0.072	4.309**	0.213	0.189	3.798**	0.219
15.	Total fruit yield / vine (kg)	0.012	0.096**	0.002	0.001	0.934**	0.004
16.	Total yield (q/ha.)	4.89	188.96**	19.51	41.24	182.32**	16.20

*, ** significant at 5 % and 1 % level, respectively.

Table 3. Estimates of genetic variability, heritability and genetic advance

No.	**Characters**	**Year**	**Mean**	**Heritability (%)**	**GA**	**GA% mean**	**GCV (%)**	**PCV (%)**
1.	Days to Germination	Y_1	10.37	75.53	1.37	13.17	7.36	8.46
		Y_2	10.50	78.55	1.44	13.68	7.49	8.45
2.	Days taken to first male flower appearance	Y_1	35.67	57.45	2.63	7.36	4.72	6.22
		Y_2	35.99	62.02	2.98	8.27	5.10	6.48
3.	Days taken to first female flower appearance	Y_1	44.44	53.37	2.83	6.36	4.23	5.78
		Y_2	44.76	57.01	3.16	7.06	4.54	6.01
4.	Days taken to first picking	Y_1	56.50	36.86	2.14	3.79	3.03	4.99
		Y_2	57.01	33.95	1.98	3.47	2.89	4.96
5.	Vine Length (m)	Y_1	3.01	93.19	0.89	29.37	14.77	15.30
		Y_2	3.20	89.55	0.79	24.67	12.65	13.37
6.	Primary branches per vine	Y_1	4.55	97.28	2.15	47.22	23.24	23.57
		Y_2	4.69	96.67	2.16	46.18	22.80	23.19
7.	Total number of male flowers	Y_1	260.49	74.16	29.83	11.45	6.46	7.50
		Y_2	263.83	70.97	28.42	10.77	6.21	7.37
8.	Total number of female flowers	Y_1	18.78	74.78	2.10	11.17	6.27	7.25
		Y_2	19.11	71.71	2.08	10.90	6.25	7.38
9.	Fruit weight (g)	Y_1	70.33	81.94	10.05	14.29	7.67	8.47
		Y_2	71.18	78.15	9.67	13.58	7.46	8.44
10.	Fruit length (cm)	Y_1	13.17	96.11	4.74	35.98	17.82	18.17
		Y_2	13.46	95.78	4.90	36.43	18.07	18.47
11.	Fruit girth (cm)	Y_1	11.70	92.61	3.09	26.41	13.32	13.85
		Y_2	11.88	91.27	2.97	25.04	12.72	13.32
12.	Number of fruits per vine	Y_1	16.63	80.50	2.29	13.79	7.46	8.32
		Y_2	16.89	80.51	2.31	13.68	7.40	8.25
13.	TSS (%)	Y_1	3.88	47.88	0.20	5.07	3.55	5.14
		Y_2	3.91	77.56	0.46	11.87	6.54	7.43
14.	Number of seeds per fruit	Y_1	12.45	86.48	2.24	17.99	9.39	10.10
		Y_2	12.66	84.49	2.07	16.33	8.63	9.38
15.	Total fruit yield / vine (kg)	Y_1	1.21	93.53	0.35	29.15	14.63	15.13
		Y_2	1.33	98.67	1.14	85.82	41.94	42.22
16.	Total yield (q/ha.)	Y_1	109.25	74.32	13.35	12.22	6.88	7.98
		Y_2	110.20	77.37	13.48	12.24	6.75	7.68

Y_1 = 2023; Y_2 = 2024.

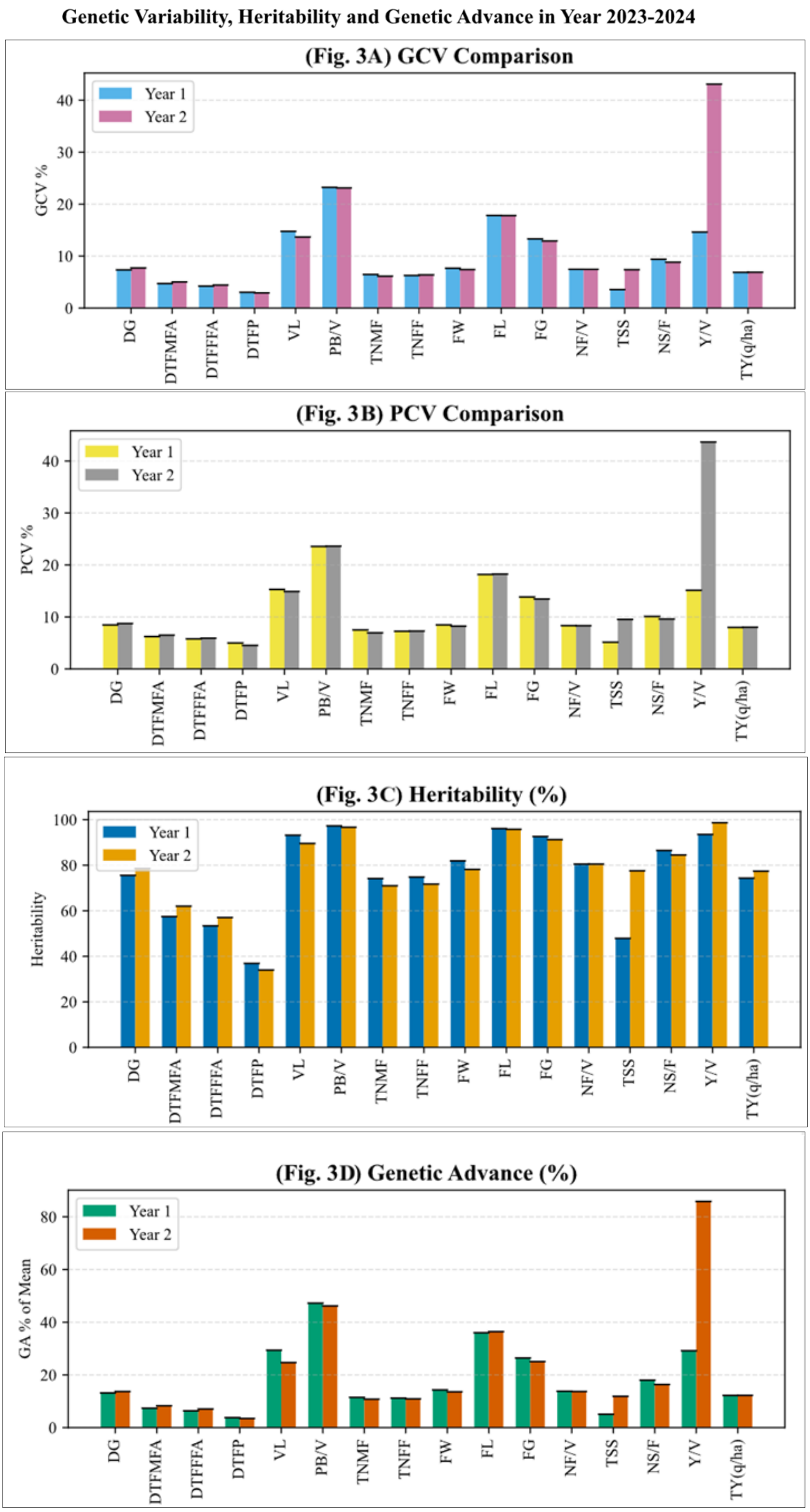

Fig. 3. Comparison between genetic variability, heritability and genetic advance in year 2023 and 2024.

DG= days to Germination, DTFMFA= days taken to first male flower appearance, DTFFFA= days taken to first female flower appearance, DTFP= days taken to first picking, VL= vine length, PB/V= primary branches per vine, TNMF= total number of male flowers, TNFF= total number of female flowers, FW= fruit weight, FL= fruit length, FG= fruit girth, NF/V= number of fruits per vine, TSS= total number of soluble solid, NS/F= number of seeds per fruit, Y/V= total fruit yield per vine and TY(q/ha)= total yield quintal per hectare.

variability was observed for number of seeds per fruit (9.38 %), days to germination (8.45 %), fruit weight (8.44 %), number of fruits per vine (8.25 %), total yield (q ha^{-1}) (7.68 %), TSS (7.43 %), total number of female flowers (7.38 %), total number of male flowers (7.37 %), days to first male flower appearance (6.48 %), days to first female flower appearance (6.01 %) and days to first picking (4.96 %).

The high PCV and GCV estimates observed for certain traits indicate substantial genetic variability among the genotypes, suggesting that selection based on phenotypic performance could be effective for crop improvement. The results of the present study are in agreement with previous research on bitter gourd and other crops, which reported similar pattern of genotypic and phenotypic variation across quantitative traits (1, 17-21).

Heritability and genetic advance as percent of mean

When high heritability is combined with substantial GA, it provides greater value for selection purposes compared to considering heritability alone. This combination enables more accurate prediction of genetic gain and more effective identification of superior individuals, leading to significant improvements in desired traits (15). The broad-sense heritability estimates (h^2bs) and GA expressed as a percentage of the mean for sixteen different characteristics evaluated in bitter gourd genotypes (Table 3).

The highest estimates of h^2bs for the *Zaid* season (2023) were observed for primary branches per vine (97.28 %), followed by fruit length (96.11 %), total fruit yield per vine (93.53 %), vine length (93.19 %), fruit girth (92.61 %), number of seeds per fruit (86.48 %), fruit weight (81.94 %), number of fruits per vine (80.50 %), days to germination (75.53 %), total number of female flowers (74.78 %), total yield (q ha^{-1}) (74.32 %) and total number of male flowers (74.16 %) (Fig. 3C). Moderate heritability was recorded for days to first male flower appearance (57.45 %), followed by days to first female flower appearance (53.37 %), TSS (47.88 %) and days to first picking (36.86 %).

Similarly, the highest h^2bs for the *Zaid* season (2024) were observed for total fruit yield per vine (98.67 %), followed by primary branches per vine (96.67 %), fruit length (95.78 %), fruit girth (91.27 %), vine length (89.55 %), number of seeds per fruit (84.49 %), number of fruits per vine (80.51 %), days to germination (78.55 %), fruit weight (78.15 %), TSS (77.56 %), total yield (q ha^{-1}) (77.37 %), total number of female flowers (71.71 %), total number of male flowers (70.97 %) and days to first male flower appearance (62.02 %), while moderate heritability was recorded for days to first female flower appearance (57.01 %) and days to first picking (33.95 %).

Primary branches per vine, fruit length and total fruit yield per vine all exhibited very high heritability (over 95 %) and strong genetic variability, suggesting that these traits are primarily governed by additive genetic effects and can therefore effectively improved through selection. A higher number of branches support increased flowering, longer fruits and greater yield potential, with total fruit yield per vine showing particularly strong genetic gain in the second year. Focusing on these traits in breeding programs will help maximize genetic improvement and productivity. The substantial heritability values observed in this study indicate that conventional selection strategies can lead to sustainable genetic improvement in bitter gourd populations. Similar findings have been reported by other researchers (1, 22, 23).

The high estimates of GA as a percentage of the mean for the *Zaid* season (2023) were recorded for primary branches per vine (47.22 %), followed by fruit length (35.98 %), vine length (29.37 %), total fruit yield per vine (29.15 %) and fruit girth (26.41 %) (Fig. 3D). Moderate GA values were observed for number of seeds per fruit (17.99 %), fruit weight (14.29 %), number of fruits per vine (13.79 %), days to germination (13.17 %), total yield (q ha^{-1}) (12.22 %), total number of male flowers (11.45 %) and total number of female flowers (11.17 %), whereas low GA was recorded for days to first male flower appearance (7.36 %), days to first female flower appearance (6.36 %), TSS (5.07 %) and days to first picking (3.79 %).

Similarly, for the *Zaid* season (2024), high GA was recorded for total fruit yield per vine (85.82 %), followed by primary branches per vine (46.18 %), fruit length (36.43 %), fruit girth (25.04 %) and vine length (24.67 %). Moderate GA was observed for number of seeds per fruit (16.33 %), number of fruits per vine (13.68 %), days to germination (13.68 %), fruit weight (13.58 %), total yield (q ha^{-1}) (12.24 %), TSS (11.87 %), total number of female flowers (10.90 %) and total number of male flowers (10.77 %), while low GA was recorded for days to first male flower appearance (8.27 %), days to first female flower appearance (7.06 %) and days taken to first picking (3.47 %).

Traits exhibiting both high heritability and GA-such as primary branches per vine (~ 47 % GA), fruit length (~ 36 % GA) and total fruit yield per vine (up to 85 % GA)-should be prioritized in breeding programs as they exhibit additive genetic control and are highly responsive to selection, thereby enhancing productivity. The concurrent occurrence of high heritability and high GA indicates that direct selection based on phenotypic performance could be effective in improving these traits. Breeders are encouraged to adopt breeding strategies that exploit both additive and non-additive genetic effects, as this integrated approach can accelerate the development of superior varieties and hybrids, thereby strengthening bitter gourd improvement programs. Similar findings have been reported in bitter gourd and other crops by several researchers (1, 16, 20, 22, 23).

Conclusion

The study revealed substantial genetic variation among bitter gourd genotypes for multiple traits, notably primary branches per vine, fruit length and total fruit yield per vine, which exhibited both high heritability and GA. These promising traits are predominantly governed by genetic factors and are therefore ideal targets for effective phenotypic selection in breeding programs. Considering the presence of both additive and non-additive gene effects, a combined breeding strategy that integrates conventional selection and heterosis breeding is recommended. Focusing on these traits can markedly improve yield potential and overall productivity in bitter gourd improvement programs. Overall, the selection of genotypes exhibiting higher branch numbers, longer fruits and superior yield potential offers substantial scope for developing improved varieties and hybrids with better performance and quality. This approach is well aligned with contemporary breeding objectives for bitter gourd crop improvement.

Acknowledgements

Authors are highly thankful to Director of Research and In-charge of PG Lab, Department of Genetics and Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, for providing laboratory facility for the analysis of experiment samples.

Authors' contributions

HT carried out the experiment, data collection, analyses and manuscript writing. BS and VK, providing valuable help to input in the experimental design, data analysis and interpretation of results. V, SP and LKG design of the study, supervised and guidance to identify the research problem. RK and KS support in the data analysis in lab, operating instruments and assisted in refining the overall data interpretation. All authors reviewed and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

References

1. Zehra SB, Parveen K, Nazir G, Hussain K, Masoodi U, Malik A. Gene action and heterosis studies for yield and its attributes in bitter gourd (*Momordica charantia* L.) under temperate ecologies. J Adv Biol Biotechnol. 2024;27(5):192–209. https://doi.org/10.9734/jabb/2024/v27i5779
2. Deng Y, Liu G, Zhang H, Zhou P, Tang X, Li P, et al. Effects of wall materials on the physicochemical properties of spray-dried bitter gourd (*Momordica charantia* L.) powders. NPJ Sci Food. 2024;8(1):37. https://doi.org/10.1038/s41538-024-00278-7
3. Srivastav A, Shukla AK, Kumar M, Kumar S, Mishra RK. Nutraceutical bioactive compounds in fruits and vegetables. In: Keservani RK, Tung BT, Kesharwani RK, Ahire ED, editors. Plant metabolites and vegetables as nutraceuticals. Oakville: Apple Academic Press. 2024. p. 111–42. https://doi.org/10.1201/9781032680125-7
4. Kusi F, Adu Amoah R, Attamah P, Alhassan S, Yahaya D, Awuku JF, et al. Genotype × environment interaction effect on grain yield of cowpea (*Vigna unguiculata* L. Walp) in deciduous forest and Sudan savanna ecologies of Ghana. PLoS One. 2025;20(1):e0314464. https://doi.org/10.1371/journal.pone.0314464
5. Hasan T, Rabbani MG, Hossain MM, Howlader NC, Hasan MM, Shourov FA, et al. Genetic variability, character association and diversity analysis in bitter gourd (*Momordica charantia* L.) for growth and yield attributing traits in Bangladesh. J Bangladesh Agric Univ. 2025;23(2):99–112. https://doi.org/10.3329/jbau.v23i2.82563
6. Roka P, Shrestha S, Adhikari SP, Neupane A, Shreepaili B, Bista MK. A review on genetic parameters estimation, trait association and multivariate analysis for crop improvement. Arch Agric Environ Sci. 2024;9(3):618–25. https://doi.org/10.26832/24566632.2024.0903029
7. Hamdi A, El-Ghareib AA, Shafey SA, Ibrahim MAM. Genetic variability, heritability and expected genetic advance for earliness and seed yield from selection in lentil. Egypt J Agric Res. 2003;81:125–37. https://doi.org/10.21608/ejar.2003.276089
8. Singh A, Singh A, Barb J, Mahama AA, Suza W. Genetic variation and germplasm usage. In: Crop improvement. 2023.
9. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. New Delhi: Indian Council of Agricultural Research. 1957. p. 157–65.
10. Burton GW. Quantitative inheritance in grasses. In: Proceedings of the 6th International Grassland Congress. 1952. p. 277–83.
11. Sivasubramanian J, Madhavamenon P. Genotypic and phenotypic variability in rice. Madras Agric J. 1973;12:15–16.
12. Burton GW, Devane CH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron J. 1953;45:478–81. https://doi.org/10.2134/agronj1953.00021962004500100005x
13. Robinson HF, Comstock RE, Harvey PH. Estimation of heritability and degree of dominance in corn. Agron J. 1949;41:353–59. https://doi.org/10.2134/agronj1949.00021962004100080005x
14. Lush JL. Heritability of quantitative characters in farm animals. In: Proceedings of the 8th International Congress on Genetics. Hereditas Suppl (Genetics). 1949. p. 356–395.
15. Johnson HW, Robinson JF, Comstock RE. Estimation of genetic and environmental variability in soybean. Agron J. 1955;47:314–18. https://doi.org/10.2134/agronj1955.00021962004700070009x
16. Gupta N, Bhardwaj M, Singh S. Genetic variability and correlation studies in bitter gourd under mid hill conditions of Himachal Pradesh. In: National Symposium on Abiotic and Biotic Stress Management in Vegetable Crops. 2013. p. 39-41.
17. Yadav M, Pandey TK, Singh DB, Singh GK. Genetic variability, correlation coefficient and path analysis in bitter gourd. Indian J Hortic. 2013;70(1):144–49.
18. Singh V, Rana DK, Shah KN. Genetic variability, heritability and genetic advance in some strains of bitter gourd (*Momordica charantia* L.) under subtropical conditions of Garhwal Himalaya. Plant Arch. 2017;17(1):564–68.
19. Narayan R, Ahmed N, Mufti S. Evaluation of some bitter gourd genotypes for yield traits and genetic parameters under Kashmir conditions. Environ Ecol. 2006;24(3A):750–52.
20. Yadagiri J, Gupta NK, Tembhire D, Verma S. Genetic variability, heritability and morphological characterization in bitter gourd (*Momordica charantia* L.). Int J Pure Appl Biosci. 2017;5(4):1322–27. https://doi.org/10.18782/2320-7051.5710
21. Tomar H, Kumar V, Singh S, Kumar R, Kumar A. Genetic variability, heritability, correlation and path coefficient analysis in amaranth (*Amaranthus* spp.) in western Uttar Pradesh (India). Int J Environ Clim Change. 2022;12(11):1780–91. https://doi.org/10.9734/ijecc/2022/v12i1131163
22. Chakraborty L, Acharya P, Ray Chaudhuri S. Diversity analysis of *Momordica charantia* L. accessions from eastern and northeastern India based on morphological, yield-related traits and molecular markers. In: Proceedings of FVHH; Thailand. 2013. p. 179–93.
23. Kumar V, Dumi T, Kumar A, Gupta A, Kumar U. Variability, heritability and genetic advance for yield and yield-related traits in tomato (*Solanum lycopersicum*). Ann Hortic. 2020;13(1):61-65. https://doi.org/10.5958/0976-4623.2020.00010.9

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc
See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

Publisher information: Plant Science Today is published by HORIZON e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.