



ISAH Indian Journal of Arid Horticulture

Year 2025, Volume-7, Issue-2 (July-December)

Genetic variability, heritability and genetic advance in bitter gourd (*Momordica charantia* L.)

Anil Kumar^{*1}, Vivek Pandey², Raj Narayan³, Ashish Kumar Singh⁴, Virendra Kumar⁵, Vipin⁵ and Parvesh Kumar⁵

^{1&4}Department of Vegetable Science, ANDUA&T, Ayodhya (U.P.)

²PAU, RRS, Gurdaspur, Punjab

³Division of Horticulture and Forestry, ICAR-CIARI, Bathubasti, Garacharma (A&N Islands)

⁵Research Scholar, Department of Vegetable Science, ANDUA&T, Ayodhya (U.P.)

ARTICLE INFO

Received: 09 June 2025

Accepted: 05 September 2025

Keywords: Bitter gourd, Genetic advance, Heritability, Variability.

doi:10.48165/ijah.2025.7.2.11

ABSTRACT

Greater diversity in the initial breeding stock increases the likelihood of developing desirable crop varieties. The key aim of germplasm conservation is to gather and safeguard genetic variation in native crop species for both current and future breeding efforts. The analysis of variance revealed significant differences among the hybrids across all traits studied, with average performance data presented for 10 genotypes that exhibited low, moderate, and high levels of phenotypic (PCV) and genotypic coefficient of variation (GCV). The greatest GCV was observed for sex ratio (20.93%) and the number of primary branches per plant (21.30%). Traits such as number of seeds per fruit (17.93%) and fruit yield per plant (17.53%) showed moderate GCV, whereas lower GCV values were recorded for days to first staminate flower anthesis (8.78%) and fruit circumference (7.74%). In general, PCV values exceeded GCV values. Heritability was high for days to first staminate flower anthesis (85%), moderate for vine length (53%), and low for number of seeds per fruit (25%). Traits like number of primary branches per plant exhibited high heritability along with high genetic advance, suggesting the predominance of additive gene action. Genetic advance expressed as a percentage of the mean was high for fruit yield per plant (41.79%) and number of primary branches per plant (40.55%). Moderate genetic advance was seen in traits like internodal length (18.67%), highlighting their considerable potential for improvement through direct selection.

Introduction

The bitter gourd (*Momordica charantia* L.) name itself indicate that bitter nature and it is due to momordicine, is an important cucurbit which was highly cross pollinated due to Monoecy condition and somatic chromosome number of $2n=2x=22$. According to Singh *et al.* (2023), bitter gourds can be cooked, curried, stuffed, sliced, and fried. They can also be pickled, preserved, and dehydrated. They are also rich in therapeutic characteristics, such as carminative, purgative,

and anti-diabetic effects. It is actually a tonic fruit that is used to treat diabetes, gout, and rheumatism (Khulakpam *et al.*, 2015).

Yield in bitter gourd is a complex trait influenced by multiple factors such as the number of primary branches per vine, number of nodes per vine, sex ratio, number of fruits per vine, and primarily, the average fruit weight. Heritability reflects the proportion of phenotypic variation that is attributed to genetic causes and provides essential guidance for genetic selection. In order to design an effective breeding program

aimed at enhancing crop yield, it is crucial to gather sufficient information regarding the extent and nature of genetic variability, along with their associated heritability estimates. According to Dey *et al.* (2009), yield is a complicated trait that is impacted by a number of genetic factors interacting with the environment. In order to improve selection, it is necessary to provide a better understanding of the ancillary features. A crop's breeding strategy is largely determined by the type and extent of gene activities that contribute to the development of both quantitative and qualitative features. Selection efficiency improves when traits are chosen based on high heritability combined with high genetic advance over the mean. The magnitude of these estimates also indicates the potential for improvement through selection. The present study was conducted to estimate the components of variance, heritability, and genetic advance over the mean in bitter melon.

Material and Methods

The experimental material for the present study was sourced from the Indian Institute of Vegetable Research (IIVR), Varanasi, consisting of 10 genotypes of *Momordica charantia* L. representing diverse morphological and yield characteristics. The genotypes included DVBTG-903, DVBTG-7, IC-06309, VRBTG-423, VRBTG-12-2, IC-068296, DVBTG-448, IC-068316, DVBTG-1004, and Green Long Jaunpuri. The experiment was carried out during 2022–23 at the Main Experimental Field, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, using a Randomized Block Design (RBD) with three replications. A spacing of 1.5 meters between rows and 0.5 meters between plants was maintained. Recommended agronomic practices were followed to ensure a healthy crop. Data collection involved selecting six plants from each genotype in every replication, with the chosen plants tagged and properly labelled before the flowering stage to facilitate observation.

The traits recorded for analysis included days to first staminate flower anthesis, days to first pistillate flower anthesis, node number at first staminate flower appearance, node number at first pistillate flower appearance, internodal length (cm), sex ratio (male:female), vine length (m), number of primary branches per plant, days to first fruit harvest, fruit length (cm), fruit circumference (cm), average fruit weight (g), number of fruits per plant, fruit yield per plant (kg), and number of seeds per fruit. Additional traits such as days to flowering, days to ripening, plant height (cm), number of branches per plant, number of fruits per cluster, fruit width (cm), number of locules per fruit, number of fruits per plant, and fruit weight per plant were also recorded. After calculating the mean data for each character, Panse and Sukhatme (2000)'s standard method of analysis

of variance was applied. According to Burton and Devane's (1953) formula, the genotypic and phenotypic coefficients of variation (GCV and PCV), heritability in the broadest sense (h^2), and genetic advancement as a percentage of mean were calculated.

Results and Discussion

A higher degree of diversity in the original breeding material guarantees a higher probability of generating the desired crop plant types. Therefore, the main goal of germplasm conservation is to gather and conserve the genetic diversity found in native crop species collections so that it can be used by both the current and future generations. The analysis of variance indicated the existing of significant differences among all the hybrids for all the traits studied. Mean performance of 10 genotypes for all character is presented in Table 1. The character exhibited low moderate and high PCV and GCV values in Table 2.

Highest genotypic coefficient of variation was recorded only two character i.e sex ratio (male: female) (20.93%) followed by number of primary branches per plant (21.30%). Moderate GCV was observed for number of seeds per fruit (17.93%), fruit yield per plant (17.53%), number of fruits per plant (17.19%), node at which first staminate flower appears (16.20%), node at which first pistillate flower appears (14.53%), fruit length (13.25%), vine length (13.16%), internodal length (12.20%) and average fruit weight (10.97%). Genotypic coefficient of variation was low for days to first staminate flowers anthesis (8.78%), fruit circumference (7.74%), days to first pistillate flower anthesis (6.39%) and days to first fruit harvest (6.01%). In general, PCV was higher than the GCV in the same direction. Rana and Pandit (2011) reported that in snake melon, the genotypic coefficient of variation (GCV) was high for traits such as days to seedling emergence, fruit length, total number of male flowers, total number of seeds per fruit, total number of fruits per plant, and yield per plant. According to Bhati *et al.* (2023), the GCV values ranged from 4.64% to 23.40%.

The highest GCV was recorded for 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%), and average fruit weight (20.14%). The lowest GCV was noted for days to germination (9.95%), number of leaves per plant (9.73%), vine length (9.49%), and number of primary branches per plant (6.39%). In terms of phenotypic coefficient of variation (PCV), the highest value was observed for 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%), and average fruit weight (20.53%). Moderate PCV values were found for node number to first female flower (17.57%),

total soluble solids (TSS) (13.09%), days to germination (10.73%), and vine length (10.25%). The lowest PCV values were recorded for 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%).

Heritability estimates in narrow sense was high for three parameters while, moderate for five parameters and low for seven out of fifteen parameters taken in experiment. The high narrow sense heritability was observed for days to first staminate flowers anthesis (85%), days to first pistillate flower anthesis (79%) and node at which first staminate flower appears (70%), whereas, moderate heritability recorded by node at which first pistillate flower appears (58 %), vine length (53 %), days to first fruit harvest (52%), number of fruits per plant (49%) and fruit yield per plant (43%). It was heritability low for number of seeds per fruit (25%), fruit length (21%), number of primary branches per plant (18%), sex ratio (16%), average fruit weight (15%), fruit circumference (9%) and internodal length (7%). Bannatti *et al.* (2024) reported that high heritability (>60%) combined with high genetic advance as a percentage of the mean (>20%) was observed for traits such as number of primary branches per plant, days to first male flowering, node number at first male flower opening, sex ratio, node number at first female flower opening, vine length, fruit yield per vine, fruit length, average fruit weight, ascorbic acid content, fruit yield per hectare, beta carotene

content, and exocarp thickness. This suggests that these traits are predominantly governed by additive gene action. Thus, there is considerable potential for direct selection to enhance these traits. According to Sagar *et al.* (2024), moderate heritability and high genetic advancement were observed for fruit yield per plant, average fruit weight, fruit length, and the number of primary branches per vine. Additionally, high heritability and high genetic advancement were found for vitamin C content, average fruit weight, number of primary branches per vine, and fruit yield per plant as a percentage of the mean.

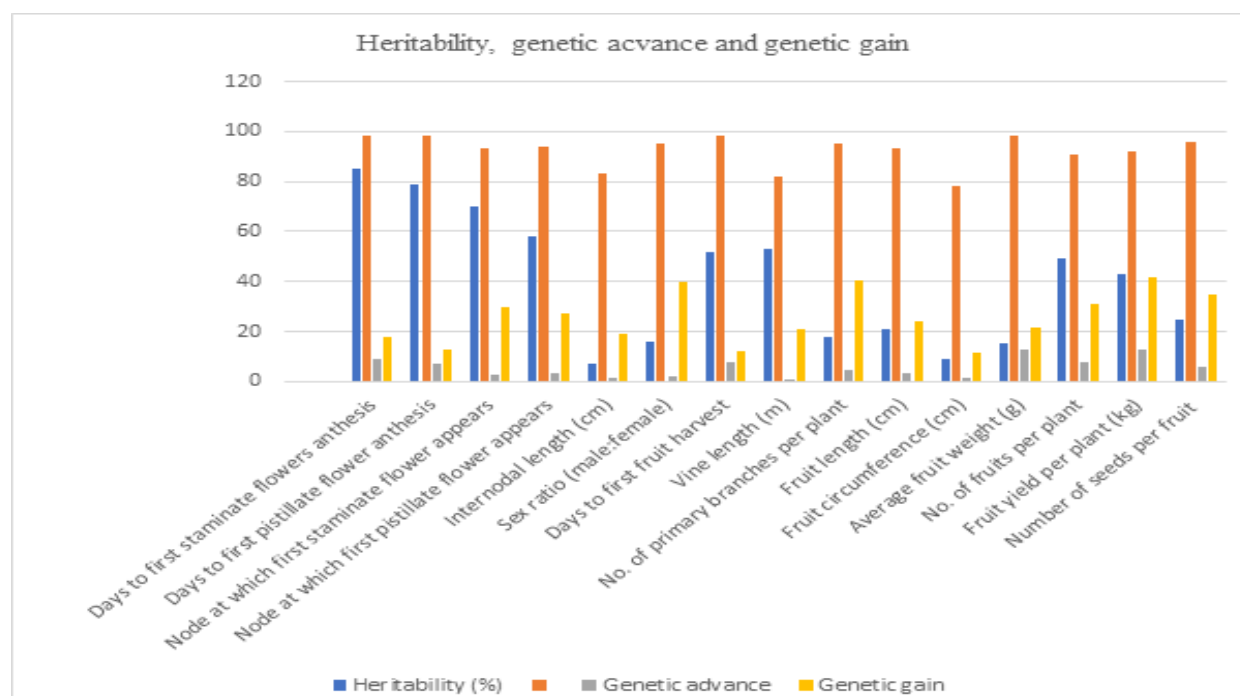
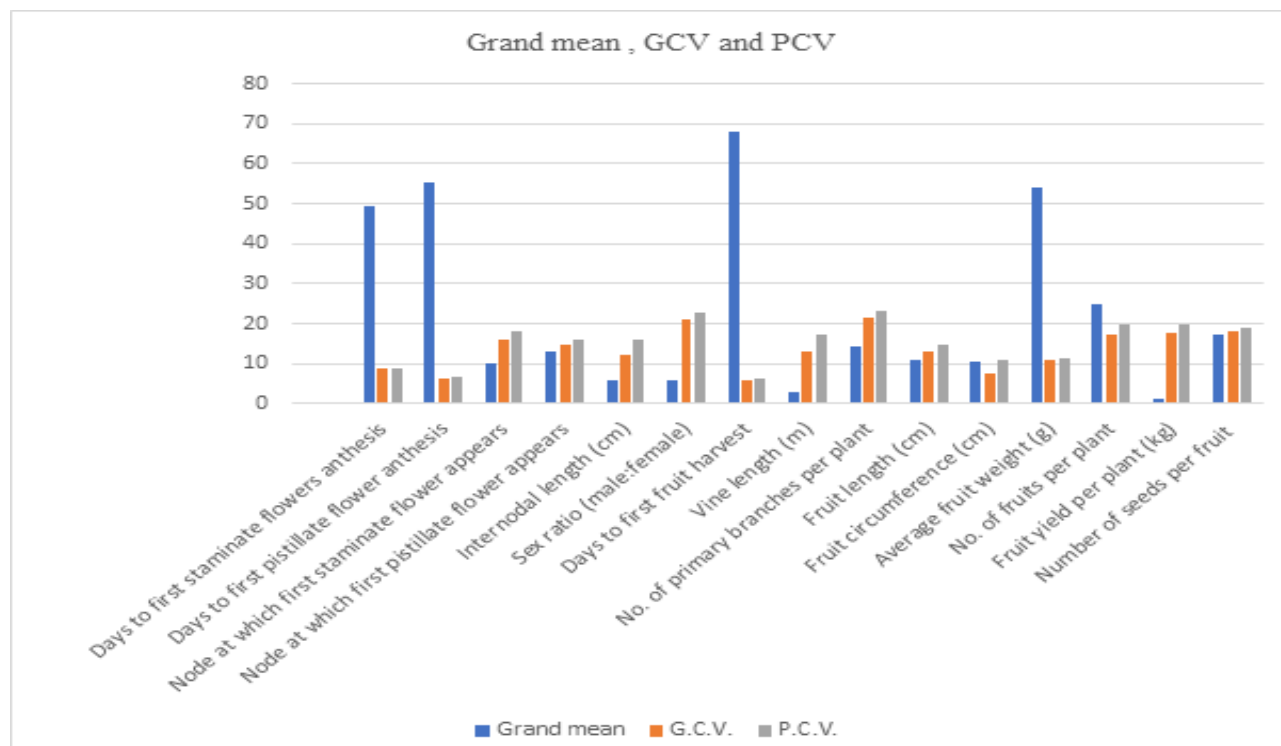
Genetic advance as per cent of mean was high for nine parameters i.e. fruit yield per plant (41.79%), number of primary branches per plant (40.55%), sex ratio (39.80%), number of seeds per fruit (34.53%), number of fruits per plant (30.77%), node at which first staminate flower appears (30.02%), node at which first pistillate flower appears (27.24%), fruit length (24.23%), average fruit weight (21.87%), vine length (20.88%), and whereas, moderate genetic advance as per cent of mean was observed for internodal length (18.67%), days to first staminate flower anthesis (17.67%), days to first pistillate flower anthesis (12.70%), days to first fruit harvest (11.98%) and fruit circumference (11.97%). Singh *et al.* (2014) high heritability coupled with high genetic advance as percent of mean was observed for fruit length, yield per plant, fruit diameter, fruit weight, branch per plant and seeds per fruit.

Table 2. Estimation of range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic gain in bitter gourd

Characters	Range		Grand mean	G.C.V.	P.C.V.	Heritability (%)		Genetic advance	Genetic gain
	Min.	Max.				Narrow Sense	Broad Sense		
Days to first staminate flowers anthesis	43.60	61.26	49.43	8.78	8.98	85	98	8.77	17.67
Days to first pistillate flower anthesis	52.46	65.34	55.44	6.39	6.62	79	98	6.92	12.70
Node at which first staminate flower appears	7.60	14.53	10.21	16.20	18.01	70	93	2.96	30.02
Node at which first pistillate flower appears	9.44	18.48	13.07	14.53	15.97	58	94	3.34	27.24
Internodal length (cm)	5.12	6.97	6.05	12.20	16.03	7	83	1.13	19.12
Sex ratio (male:female)	4.01	7.98	5.95	20.93	22.68	16	95	2.07	39.80
Days to first fruit harvest	61.80	73.81	68.09	6.01	6.21	52	98	7.76	11.98
Vine length (m)	2.20	3.80	2.96	13.16	17.09	53	82	0.58	20.88
No. of primary branches per plant	11.60	18.40	14.11	21.30	23.04	18	95	4.65	40.55
Fruit length (cm)	8.62	13.28	10.93	13.25	14.93	21	93	3.11	24.23
Fruit circumference (cm)	8.61	12.06	10.69	7.74	10.86	9	78	1.28	11.37
Average fruit weight (g)	48.57	70.60	54.12	10.97	11.33	15	98	12.80	21.87
No. of fruits per plant	16.15	35.43	24.91	17.19	19.77	49	91	7.56	30.77
Fruit yield per plant (kg)	0.83	1.76	1.33	17.53	19.93	43	92	12.75	41.79
Number of seeds per fruit	11.45	25.26	17.45	17.93	19.17	25	96	5.60	34.53

Table 1. Mean performance of the 10 parents for 15 characters of bitter gourd

Genotypes	Days to first sta- minate flower anthesis	Days to first pistillate flower anthesis	Node at first staminate flower appears	Node at which first pis- tillate flower appears	Inter- nodal length (cm)	Sex ratio (M:F)	Days to first fruit har- vest	Vine length (m)	No. of primary branch- es/ plant	Fruit length (cm)	Fruit circum- ference (cm)	Average fruit weight (g)	No. of fruits/ plant	Fruit yield/ plant (kg)	Num- ber of seeds/ fruit
DVBGTG-903 (P ₁)	43.60	52.54	9.00	12.66	6.07	6.83	66.06	3.33	13.37	9.43	9.03	49.06	31.30	1.53	18.60
DVBGTG-7 (P ₂)	44.65	53.93	12.66	13.70	6.97	7.73	73.07	3.80	16.63	11.03	8.61	49.96	35.43	1.76	13.92
IC-06309 (P ₃)	47.16	54.06	8.27	12.10	5.23	4.19	63.18	2.71	12.06	8.62	12.06	48.57	24.80	1.19	15.60
VRBTG-423 (P ₄)	51.00	53.26	10.91	12.58	5.12	4.01	73.46	2.66	12.36	9.61	10.63	57.36	22.26	1.27	11.45
VRBTG-12-12 (P ₅)	50.90	53.60	7.60	12.53	6.93	7.15	64.89	3.30	18.40	11.70	11.33	54.41	31.03	1.68	16.69
IC-068296 (P ₆)	45.33	57.06	13.51	15.93	5.86	4.71	66.20	3.07	15.13	12.70	11.66	70.60	22.66	1.59	25.26
DVBGTG-448 (P ₇)	50.24	52.46	7.90	9.44	5.60	6.40	61.80	2.20	12.80	11.83	11.76	50.93	16.15	0.83	17.80
IC-068316 (P ₈)	53.24	57.33	8.36	11.17	6.43	7.98	65.24	3.32	15.86	9.68	10.93	49.16	22.53	1.10	15.99
DVBGTG-1004 (P ₉)	61.26	65.34	14.53	18.48	6.47	6.32	73.81	2.66	11.60	13.28	10.84	59.14	22.13	1.31	17.57
Green Long Jaunpuri (P ₁₀)	46.93	54.86	9.37	12.10	5.82	4.24	73.20	2.55	12.90	11.46	10.06	52.06	20.80	1.08	21.67
C.D.	2.251	2.382	0.388	0.464	0.171	0.154	2.616	0.11	0.427	0.313	0.268	2.229	0.669	0.032	0.588
SE(m)	0.752	0.796	0.13	0.155	0.057	0.051	0.874	0.04	0.143	0.105	0.09	0.745	0.223	0.011	0.196
SE(d)	1.063	1.125	0.183	0.219	0.081	0.073	1.235	0.05	0.202	0.148	0.127	1.053	0.316	0.015	0.278
C.V.	2.639	2.489	2.189	2.057	1.641	1.486	2.218	2.18	1.745	1.661	1.449	2.376	1.556	1.397	1.949



Conclusion

The maximum genotypic coefficient of variation was recorded for two traits: sex ratio (male: female) at 20.93% and number of primary branches per plant at 21.30%, with the phenotypic coefficient of variation (PCV) exceeding the genotypic coefficient of variation (GCV) in both cases. Furthermore, high heritability and genetic advance were observed for traits such as days to first staminate flower anthesis, days to first pistillate flower anthesis, and the node position of the first staminate flower. These findings indicate

that selecting for these traits could be an effective approach to enhance bitter melon yield. Thus, selection based on these attributes would be advantageous.

Acknowledgements

I extend my sincere gratitude to the Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya for recommending this engaging research topic and providing valuable guidance,

support, and constructive feedback throughout the study.

Conflict of Interest

The authors have no conflict of interest.

Data Sharing

All relevant data are within the manuscript.

Reference

- Bannatti, R., Rathod, V., Gasti, V. D., Evoor, S., Chittapur, R. B. and Ryavalad, S. Y. 2023. Assessment of genotypic variability, heritability and genetic advance for growth, yield and quality related traits in bitter gourd (*Momordica charantia* L.) Genotypes. *Biological Forum – An International Journal*, 15:493-498.
- Bhati, S., Prakash, S., Kumar, V., Singh, B., Singh, M. K., Gangwar, L. K., Kumar, D., Gangwar, V. and Kumar, A. 2023. Genetic variability, heritability and genetic advance for yield and yield contributing characters in bitter gourd (*Momordica charantia* L.) genotypes. *International Journal of Environment and Climate Change*, 13(9):1867-1875. <https://doi.org/10.9734/ijecc/2023/v13i92418>
- Burton, G.W and Devane, E.H. 1953. Estimation of heritability in Tall Fescue (*Festuca arundinacea*) from replicated clonal materials. *Agronomy Journal*, 45:478-481.
- Dey, S.S., Behera, T.K., Munshi, A.D. and Bhatia, R. 2009. Genetic variability, genetic advance and heritability in bitter gourd (*Momordica charantia* L). *Indian Agriculturist*, 53:7-12.
- Gardner, C.O. 1963. Estimates of genetic parameters in cross fertilizing plants and their implication in plant breeding. *Statistical Genetics and Breeding*, 982: 225-252.
- Khulakpam, N. S., V. Singh and D. K. Rana 2015. Medicinal importance of cucurbitaceous Crops. *International Journal Research of Biological Sciences*, 4:1-3.
- Panse, V.G. and Sukhatme, P.V. 2000. Statistical Methods for Agricultural Workers. *ICAR Publication*. 87-89.
- Rana, N.P. and Pandit, M.K. 2011. Studies on genetic variability, character association and path analysis in snake gourd (*Trichosanthe sanguina* L) genotypes. *Journal of Crop and Weed*, 7:91-96.
- Sagar, K. R., Babu, B. R., Babu, M. R., Rao, M. P., and Sekhar, V. 2024. Studies on genetic variability, heritability and genetic advance in bitter gourd (*Momordica charantia* l.) germplasm lines. *Plant Archives*, 24:232-236.
- Singh, M. K., Bhardwaj, D. R., and Upadhyay, D. K. 2014. Genetic architecture and association analysis in bitter gourd (*Momordica charantia* L.) landraces. *The Bioscan*, 9:707-711.
- Singla, D., Sangha, M. K., Singh, M., Pathak, M., and Bala, M. 2023. Variation of mineral composition in different fruit parts of bitter gourd (*Momordica charantia* L.). *Biological Trace Element Research*, 201:4961-4971. <https://doi.org/10.1007/s12011-022-03546-3>