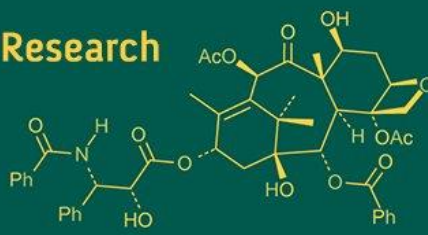


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(6): 1701-1706
www.biochemjournal.com
Received: 20-03-2026
Accepted: 22-04-2026

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Estimation of Genetic Variability, Heritability and Genetic Advance for Yield and Quality Traits in Bitter Gourd (*Momordica charantia* L.)

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i6St.8909>

Abstract

The quantity of exploitable variation for economically significant features determines how much bitter gourd can be genetically improved. During the 2025 *Zaid* season in Kumarganj, Ayodhya, India, the current study assessed thirty bitter gourd genotypes, including Arka Harit as a check. Twenty growth, earliness, yield, and fruit-quality characteristics were observed in the experiment, which was set out in a randomized block design with three replications. Significant genetic variety was confirmed by analysis of variance, which revealed extremely significant variations between genotypes for each variable. Although the discrepancies were small for a few traits, phenotypic coefficients of variation were generally higher than their genotypic equivalents. The number of seeds per fruit had the highest GCV and PCV (24.35 and 25.18%), followed by fruit diameter, length, and total soluble solids. Days to first pistillate flower anthesis had a broad-sense heridity of 19.84%, while total soluble solids had a heritability of 99.38%. In terms of node number to first staminate and pistillate flower appearance, number of primary branches per plant, vine length, fruit length, fruit diameter, average fruit weight, seed flesh ratio, number of seeds per fruit, and total soluble solids, high heritability and high genetic advancement were noted as percentage of mean. Because a significant amount of their variance is probably heritable, these features should react well to phenotypic selection. The yield per hectare showed low genetic advancement (16.36%) but significant heritability (78.31%), indicating that direct selection and concurrent emphasis on its component qualities should be used to improve output. A useful foundation for choosing parental material and developing superior bitter gourd genotypes for increased yield and quality is provided by the identified variability.

Keywords: Bitter melon, GCV, PCV, broad-sense heritability, selection response, total soluble solids

Introduction

Bitter gourd (*Momordica charantia* L.; $2n = 2x = 22$) is an important cucurbitaceous vegetable grown throughout tropical and subtropical regions. Its young fruits are prized for their nutritional content and as a source of chemicals that promote health. The crop contains cucurbitane-type triterpenoids and other phytochemicals linked to its distinctive bitterness and nutraceutical value, in addition to vitamin C, minerals, and dietary fibre. A breeding purpose that goes beyond fruit output to include earliness, fruit size, marketable appearance, and biochemical quality is created by these various end uses. The amount and kind of diversity in the breeding material determine how effective a crop-improvement programme is. Because environmental factors might change how quantitative features are expressed, phenotypic variation alone cannot determine how much of the observed difference is transmissible. Heritability describes the proportion of genetic variance to total phenotypic variance, whereas genotypic and phenotypic coefficients of variation offer a scale-independent measure of variability. When combined with genetic advancement, which forecasts the anticipated improvement under a specified selection intensity, heritability becomes more valuable for selection (Johnson *et al.*, 1955; Allard, 1960) [6, 1]. High heritability and high genetic advancement together typically suggest a better potential for improvement through direct selection as well as a stronger contribution from additive genetic effects. Significant variation in blooming behaviour, fruit dimensions, average fruit weight,

number of fruits, and yield has been documented in earlier bitter gourd research. However, the production environment and genotype set affect the size of genetic parameters. While Kumanan *et al.* (2024) ^[8] obtained close GCV and PCV estimations for significant yield attributes under sodic soil, Bhati *et al.* (2023) ^[2] found substantial heritability for a number of yield-related parameters. More recently, Hasan *et al.* (2025) ^[5] highlighted the importance of yield-component features in selection and reported wide variety among bitter gourd accessions. These results emphasise that rather than projecting genetic factors across places, it is necessary to assess locally adapted germplasm under the intended environment.

The present study included a diverse set of thirty genotypes assembled from institutional collections and newly maintained NDK lines. The objective was to quantify variability, broad-sense heritability and expected genetic advance for 20 earliness, growth, yield and quality traits, and to identify characters that can be used as reliable selection criteria in a bitter gourd breeding programme.

Material and Method

The field experiment was conducted during the *Zaid* season of 2025 at the Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India. The site lies in the humid subtropical zone of the eastern Gangetic plains at approximately 113 m above mean sea level. The experimental material comprised thirty genotypes; NDK 24-2, NDK-11/24, IC-44438, VRBTG 70-2, IC-065639, NDK-12/24, NDK-13/24, NDK-14/24, NDK-15/24, NDK-16/24, NDK-17/24, NDK-18/24, NDK-19/24, NDK-20/24, NDK-21/24, NDK-22/24, NDK-23/24, NDK-24/24, NDK-25/24, NDK-26/24, NDK-27/24, NDK-28/24, NDK-29/24, NDK-30/24, NDK-31/24, NDK-32/24, NDK-33/24, NDK-34/24, NDK-35/24 and Arka Harit (check variety). The accessions represented material maintained at ANDUAT, Ayodhya and collections obtained from IIVR, Varanasi and IIHR, Bengaluru.

The trial was laid out in a completely randomized block design with three replications. Each genotype was grown in a 3.0 m × 3.0 m plot at a spacing of 3.0 m between rows and 0.5 m between plants. Recommended cultural and plant-protection practices were followed uniformly. Observations were recorded from five randomly selected plants in each plot and averaged before analysis.

Twenty characters were evaluated: days to first staminate flower anthesis, days to first pistillate flower anthesis, days to first fruit harvest, node number to first staminate flower appearance, node number to first pistillate flower appearance, number of primary branches per plant, vine length, fruit length, fruit diameter, average fruit weight, internodal length, seed flesh ratio, number of fruits per plant, number of seeds per fruit, total soluble solids, moisture content, dry matter content, ascorbic acid, fruit yield per plant and fruit yield per hectare. Total soluble solids were measured with a digital refractometer and expressed as °Brix. Ascorbic acid was estimated by the 2, 6-dichlorophenol-indophenol titration method and expressed as mg 100 g⁻¹ fresh fruit.

Statistical analysis was performed using analysis of variance (ANOVA) following the procedure described by Panse and Sukhatme (2000) ^[9] to determine the significance of differences among genotypes. The genotypic coefficient of

variation (GCV) and phenotypic coefficient of variation (PCV) were estimated according to the method of Burton and DeVane (1953). Broad-sense heritability (h²_{bs}) was computed following Hanson *et al.* (1956), while genetic advance (GA) and genetic advance as per cent of mean were calculated using the methodology proposed by Johnson *et al.* (1955) ^[6]. These genetic parameters were used to assess the magnitude of variability and the effectiveness of selection for yield and quality traits in bitter gourd.

Result and Discussion

Treatment mean squares were highly significant ($P \leq 0.01$) for all 20 traits (Table 1). The result demonstrates that the germplasm panel was sufficiently diverse for the estimation of genetic parameters and for selection. Significant variability covered flowering, vine growth, fruit morphology, biochemical quality and yield, showing that the material contains contrasting alleles across the main components of the breeding objective. Similar significant differences among bitter gourd genotypes have been reported by Reddy *et al.* (2021) ^[12], Bhati *et al.* (2023) ^[2] and Kumanan *et al.* (2024) ^[8].

Table 1: Analysis of variance for 20 yield and quality traits in bitter gourd.

S. No.	Trait	Replication	Genotypes	Error
df		2	29	58
1	Days to first staminate flower anthesis	0.56	10.94**	2.58
2	Days to first pistillate flower anthesis	9.13	15.49**	8.89
3	Days to first fruit harvest	14.30	33.85**	6.39
4	Node number to first staminate flower appearance	0.15	5.06**	0.43
5	Node number to first pistillate flower appearance	0.03	11.54**	1.02
6	Number of primary branches per plant	0.103	1.792**	0.193
7	Vine length (m)	0.016	0.637**	0.019
8	Fruit length (cm)	1.11	18.88**	1.09
9	Fruit diameter (cm)	0.055	1.076**	0.064
10	Average fruit weight (g)	69.59	372.95**	8.76
11	Internodal length (cm)	0.48	1.13**	0.25
12	Seed flesh ratio (%)	2.32	20.27**	1.20
13	Number of fruits per plant	4.58	25.08**	2.31
14	Number of seeds per fruit	0.38	54.09**	1.22
15	Total soluble solids (°Brix)	0.03	2.57**	0.01
16	Moisture content (%)	0.24	4.04**	1.01
17	Dry matter content (%)	0.11	4.19**	0.75
18	Ascorbic acid (mg 100 g ⁻¹)	21.52	256.84**	8.20
19	Fruit yield per plant (kg)	0.082	0.101**	0.023
20	Fruit yield (q ha ⁻¹)	62.40	380.64**	32.17

** Significant at $P \leq 0.01$.

For each character, PCV was greater than GCV (Table 2; Figure 1), indicating that environmental influences influenced phenotypic expression. However, in terms of total soluble solids, average fruit weight, number of seeds per fruit, vine length, ascorbic acid, and seed:flesh ratio, there was little difference between the two estimates. The little variations suggest that phenotypic performance can serve as a helpful indicator of genetic value and show relatively constant expression of these features in the test setting.

The single characteristic in the high-variability category for both parameters was the number of seeds per fruit, which had the greatest GCV (24.35%) and PCV (25.18%). Fruit length (18.60%), total soluble solids (18.76%), fruit diameter (16.42%), vine length (15.38%), seed:flesh ratio (15.23%), node number to first staminate flower (15.42%), node number to first pistillate flower (14.59%), average fruit

weight (14.36%), primary branches (13.37%), dry matter (11.85%), internodal length (11.25%), and number of fruits per plant (10.52%). Compared to qualities with low GCV, these characteristics offer greater potential for genotype discrimination. Ascorbic acid, yield, moisture content, and

earliness traits all displayed low GCV, suggesting a comparatively smaller genetic variation on the mean scale. (Singh *et al.*, 2017; Thampi and Sarada, 2023; Bhati *et al.*, 2023) ^[14, 15, 2].

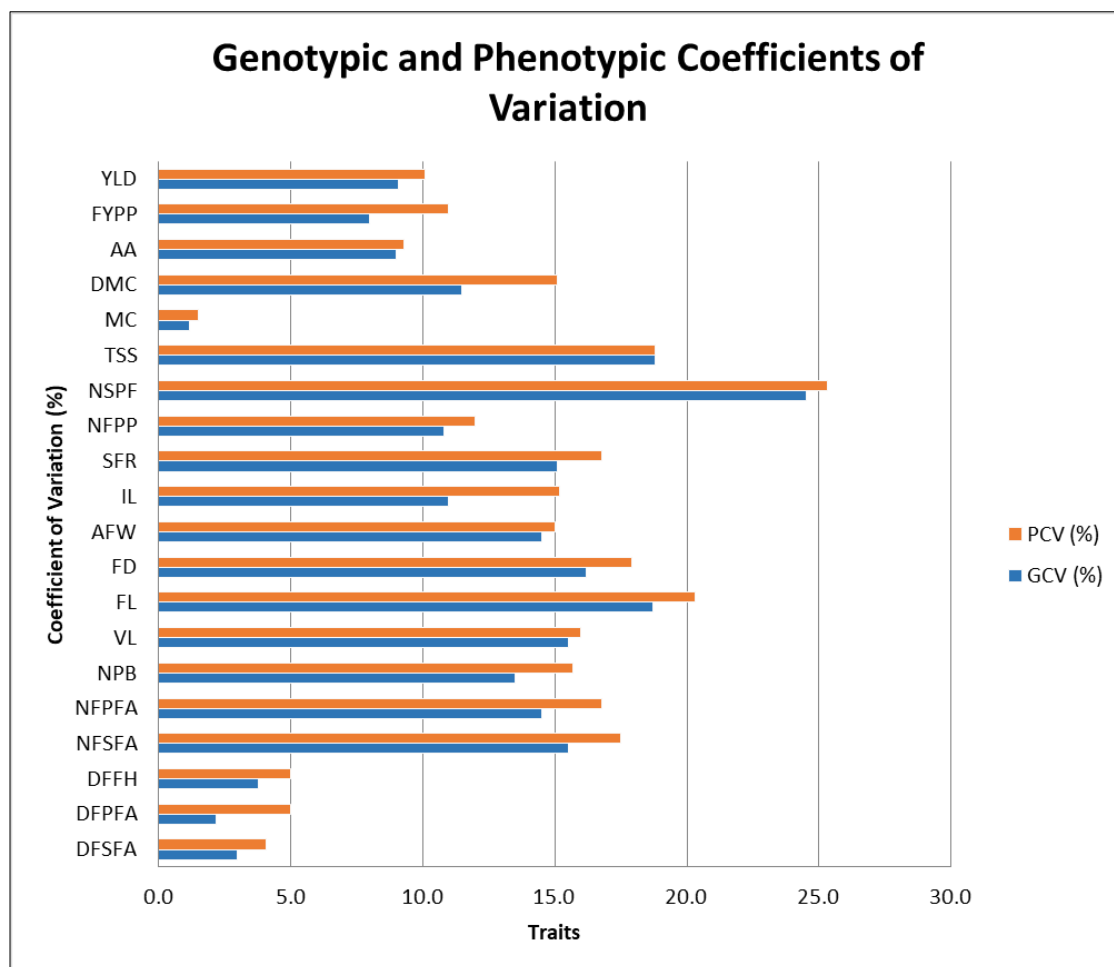


Fig 1: Genotypic (GCV) and phenotypic (PCV) coefficients of variation for 20 traits. Trait abbreviations are defined in the note to Table 2.

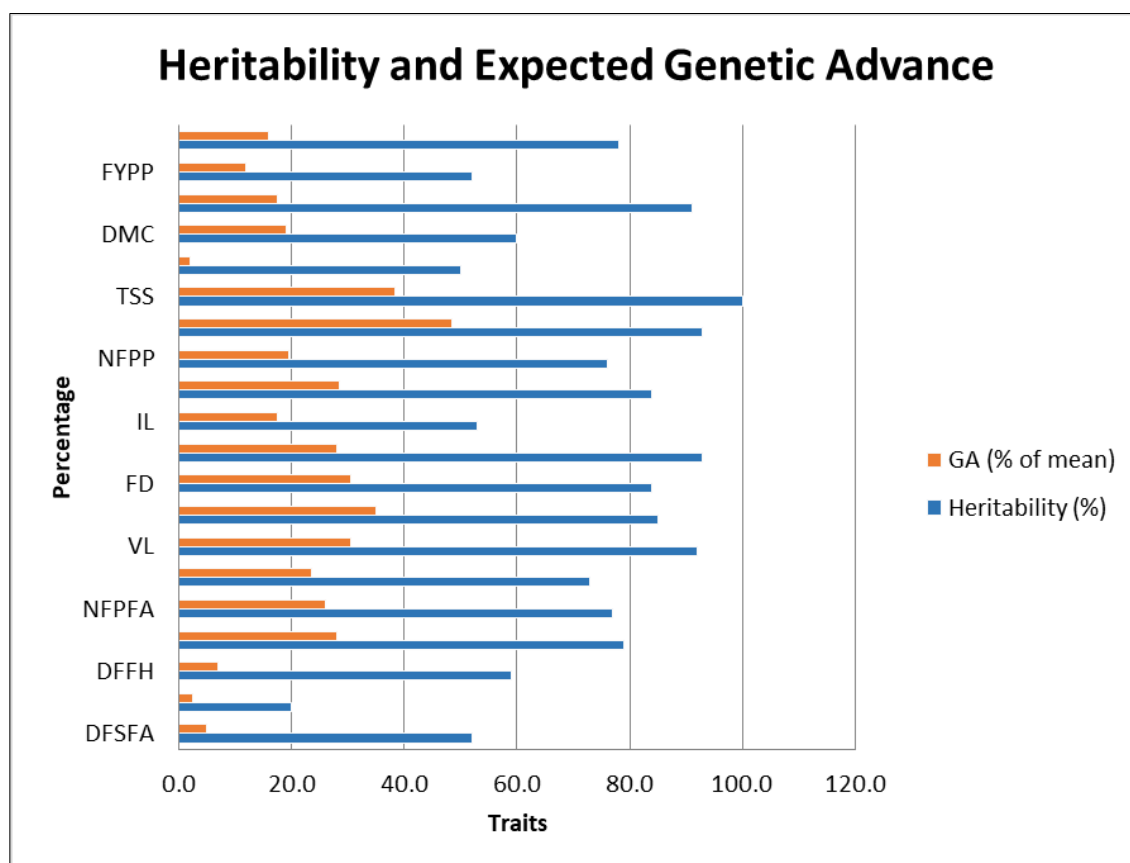
The broad-sense heritability ranged from 99.38% for total soluble solids to 19.84% for days to first pistillate flower anthesis. Node number to first staminate flower (78.31%), node number to first pistillate flower (77.41%), vine length (91.44%), fruit length (84.48%), fruit diameter (83.95%), average fruit weight (93.27%), seed flesh ratio (84.13%), number of fruits per plant (76.66%), number of seeds per fruit (93.54%), total soluble solids (99.38%), dry matter (60.38%), ascorbic acid (91.00%), and fruit yield per hectare (78.31%). While internodal length, moisture content, fruit yield per plant, days to first staminate flower, days to first fruit harvest, and days to first pistillate flower anthesis all demonstrated modest heritability. The expected size of the selection response is not indicated by heritability alone. The percentage of mean genetic advancement varied from 1.61% for moisture content to 48.51% for the quantity of seeds per fruit. Fruit length (35.22%), fruit diameter (30.98%), vine length (30.29%), seed flesh ratio (28.77%), average fruit weight (28.56%), node number to first staminate flower (28.11%), node number to first pistillate flower (26.45%), and primary branches (23.60%) all had high GAM. These characteristics exhibited high GAM and high heritability at

the same time, which is frequently linked to a significant additive component and favourable chances of responding to direct phenotypic selection. Reddy *et al.* (2021) ^[12], Bhati *et al.* (2023) ^[2], and Thampi and Sarada (2023) ^[15] have also demonstrated high heritability and genetic gain for fruit size, yield components, and associated variables.

Fruit yield per hectare, dry matter, ascorbic acid, and the number of fruits per plant all had high heritability and moderate GAM. Therefore, before progressing lines, they should be ranked across replications and, ideally, other settings. While yield per hectare had high heritability (78.31%) but moderate GAM (16.36%), fruit yield per plant had intermediate heritability (53.27%) and moderate GAM (12.20%). This trend suggests that direct selection for yield may be helpful, but when yield is enhanced in conjunction with highly heritable component traits like average fruit weight, fruit dimensions, vine length, and flowering-node characteristics, a stronger response is probably in store. The very high heritability and high GAM for total soluble solids are particularly useful for quality breeding because this trait can be screened rapidly and nondestructively in breeding populations.

Table 2: Estimates of genetic variability, broad-sense heritability and genetic advance in bitter gourd.

No.	Trait	Min.	Max.	Mean	GCV (%)	PCV (%)	h ² bs (%)	GA	GAM (%)
1	Days to first staminate flower anthesis	51.33	58.78	55.48	3.01	4.18	51.94	2.48	4.47
2	Days to first pistillate flower anthesis	59.67	68.00	64.81	2.29	5.14	19.84	1.36	2.10
3	Days to first fruit harvest	70.70	84.33	78.28	3.87	5.04	58.91	4.78	6.11
4	Node number to first staminate flower appearance	6.07	10.33	8.06	15.42	17.43	78.31	2.27	28.11
5	Node number to first pistillate flower appearance	8.00	16.53	12.83	14.59	16.59	77.41	3.39	26.45
6	Number of primary branches per plant	4.16	7.73	5.46	13.37	15.60	73.40	1.29	23.60
7	Vine length (m)	2.40	4.07	2.95	15.38	16.08	91.44	0.89	30.29
8	Fruit length (cm)	9.63	18.39	13.09	18.60	20.24	84.48	4.61	35.22
9	Fruit diameter (cm)	2.58	4.59	3.54	16.42	17.92	83.95	1.10	30.98
10	Average fruit weight (g)	57.89	97.25	76.75	14.36	14.86	93.27	21.92	28.56
11	Internodal length (cm)	3.50	5.97	4.82	11.25	15.27	54.29	0.82	17.07
12	Seed flesh ratio (%)	11.94	21.00	16.56	15.23	16.60	84.13	4.76	28.77
13	Number of fruits per plant	21.10	31.70	26.20	10.52	12.01	76.66	4.97	18.97
14	Number of seeds per fruit	10.44	23.11	17.24	24.35	25.18	93.54	8.36	48.51
15	Total soluble solids (°Brix)	3.90	6.72	4.93	18.76	18.82	99.38	1.90	38.52
16	Moisture content (%)	89.42	92.98	90.93	1.11	1.56	50.05	1.47	1.61
17	Dry matter content (%)	7.02	10.58	9.03	11.85	15.26	60.38	1.71	18.98
18	Ascorbic acid (mg 100 g ⁻¹)	92.88	122.14	102.34	8.90	9.33	91.00	17.89	17.48
19	Fruit yield per plant (kg)	1.74	2.43	1.99	8.11	11.12	53.27	0.24	12.20
20	Fruit yield (q ha ⁻¹)	104.30	146.10	120.10	8.97	10.14	78.31	19.65	16.36

**Fig 2:** Broad-sense heritability and genetic advance as percentage of mean for 20 traits.

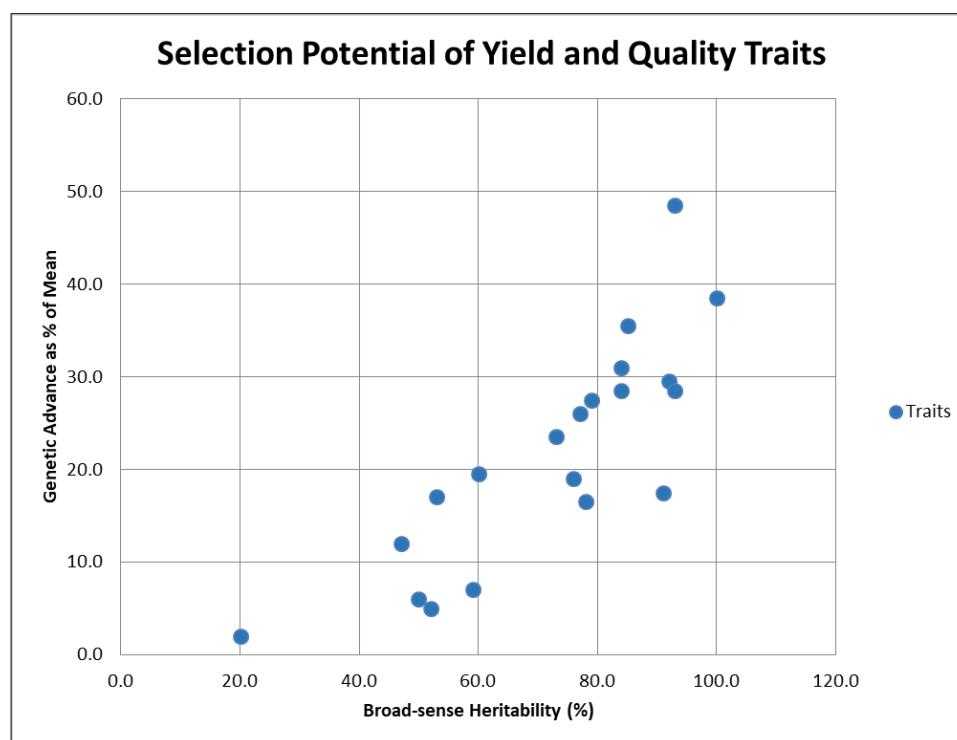


Fig 3: Trait prioritization based on heritability and genetic advance. Dashed lines indicate high heritability (>60%) and high genetic advance (>20% of mean).

Conclusion

For every one of the twenty traits examined, there was considerable genetic variation among the thirty genotypes of bitter melon. Although PCV values were higher than GCV values, there were only slight variations for a number of important fruit and quality characteristics. The highest overall diversity was found in the number of seeds per fruit. High heritability and high genetic advancement were combined in total soluble solids, number of seeds per fruit, fruit length, fruit diameter, vine length, average fruit weight, seed flesh ratio, flowering-node characteristics, and primary branches, making them dependable targets for direct selection. Fruit yield per hectare showed moderate genetic advancement and strong heritability, suggesting that simultaneous selection for its constituent traits might enhance yield improvement. While validation across seasons and places is advised prior to the final development of superior genotypes, the results offer a clear foundation for selecting characteristics and parental lines in bitter melon improvement.

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