



Evaluation of Genetic Variability for Yield Improvement 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

The degree of genetic variability found in any particular germplasm is a major factor in determining the best breeding program or technique to be used. Exploitation of the natural genetic variability present within a crop species can aid in meeting the rising demand through the identification and

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modification of the adaptive and productive genes present. Breeders thus identify natural genetic variability as the key to crop improvement. The present investigation was undertaken at the Experimental field of Urban Technological Park Habbak, Srinagar, Jammu and Kashmir during *kharif*-2022. To investigate several aspects of genetic variability, including mean, range, PV, GV, PCV, GCV, heritability, genetic gain, and genetic advance among the genotypes, the experiment was set up in a Randomized Block Design with three replications and a plant spacing of 2×1 m for thirty genotypes. For every character under study, it was discovered that the estimates of the phenotypic coefficient of variation were marginally greater than the respective genotypic coefficient of variation, indicating a possible involvement of environment in the expression of these traits. Fruit yield hectare⁻¹ (q) exhibited the largest genotypic and phenotypic coefficient of variation (39.788 and 38.970). For yield hectare⁻¹ (q), high heritability and high genetic gain (0.95 and 78.62) were observed. This suggests that additive gene effects are most likely the cause of the heritability and increases the likelihood that this characteristic would be fixed by selection. For every characteristic, the estimates of broad sense heritability were high. All these factors help in selection of better parents for the development of commercial varieties/hybrids. Considering the potential nutritional and economic benefits of bitter gourd (*Momordica charantia* L.), there is an imperative necessity to isolate such breeding lines having desirable traits, high yield potential along with better quality.

Keywords: Bitter gourd; Cucurbitaceae; vegetable crop; genetic variability.

1. INTRODUCTION

Bitter gourd, botanically known as "*Momordica charantia* L.", is a fairly well-known member of the herbaceous vine family "Cucurbitaceae". Bitter gourd is a quite popular "tropical and subtropical" commercially significant vegetable crop [1]. The name "*Momordica*" is derived from a Latin word, which means "to bite", which is in reference to the ridges present on the edges of the seed, appearing as if chewed. Some other common names used to refer to bitter gourd include bitter melon, balsam pear, maiden apple, casislla, karela, bitter cucumber and African cucumber [2,3]. The origin of bitter gourd remains obscure, but most scientists presume this crop to be a native of Tropical Asia particularly Eastern India and South China. It is now being thoroughly cultivated across countries including India, Japan, China, Malaysia, Indonesia as well as tropical parts of Africa and Southern America.

Bitter gourd is well known for its high nutritive value, being especially rich in ascorbic acid and iron content [4,5]. The plant shows a high level of cross pollination and is in turn, highly heterozygous due to monoecism [6]. A useful medicinal and vegetable plant for maintaining human health, it is one of the most promising plants for diabetes management. Considerable variation in different nutrients, including carbohydrates, ascorbic acid, zinc, iron, calcium, magnesium, phosphorus and protein content has been observed in bitter gourd [7]. The fruits are

frequently eaten boiled, fried, or stuffed and are utilized in a variety of ways as vegetable. In addition, the fruits are dehydrated, canned, and pickled. The plant is utilized medicinally in all parts. The fruits are useful in treating flatulence, blood disorders, rheumatism, and asthma. They also have cooling, digestive, laxative, antipyretic, and antidiabetic effects. The leaf is applied topically on wounds and taken internally as a laxative. The fruit powder is said to be beneficial to treat cancerous ulcers, leprosy, and wounds. It is said to be helpful for snakebite injuries. There is abortifacient activity in the roots. According to reports, the immunological deficiency virus (HIV-1) was inhibited in humans by the bitter gourd protein. Fresh leaf juice is recommended for diabetes in Ayurveda [8].

In India, the bitter gourd crop covers 101,000 hectares and produces 1174 thousand metric tonnes of fresh yield annually [9]. The leading bitter gourd producing states are Maharashtra, Uttar Pradesh, Gujarat, Rajasthan, Punjab, Tamil Nadu, Karnataka, Kerala, Andhra Pradesh, West Bengal, Odisha, Assam and Bihar. In Kashmir, this crop is cultivated on a marginal scale and as a result, precise data on area and production is unavailable [10].

For the release of a new variety, the first basic requirement is the presence of sufficient diversity amongst the genotypes to be crossed. Exploitation of the natural genetic variability present within a crop species can aid in meeting the rising demand through the identification and modification of the adaptive and productive

genes present. Breeders thus identify natural genetic variability as the key to crop improvement. The degree of variability found in the available germplasm can be measured with the aid of the genotypic and phenotypic coefficients of variation. The more positively the yield and its component characters are correlated, the more effective the selection process is.

2. MATERIALS AND METHODS

2.1 Experimental style and layout

The current study was conducted during Kharif-2022 at the Urban Technological Park Experimental Field of SKUAST, Habbak Srinagar, Jammu & Kashmir. Situated between 34.16° North latitude and 74.83° East longitude, at a height of 1608 meters above mean sea level, is the Urban Technological Park, Habbak. The mild summers are a hallmark of the temperate climate. In October and August-September, the mean minimum and maximum recorded temperatures are 2.42 °C and 30°C, respectively. June is the month when there is the most rainfall received.

During Kharif-2022, thirty genotypes of bitter gourd with distinct phenotypes that were gathered from different sources were assessed for a variety of yield-related characteristics. Three replications of the single factor experiment were set up using a Randomized Complete Block Design (RCBD). For every replication, five plants per genotype were planted at a spacing of 2 × 1 m between rows and plants, respectively. To generate a healthy crop, recommended cultural techniques were adhered to during the growth and developmental phase.

Observations were recorded on twenty four traits viz. days to appearance of 1st male flower, days to appearance of 1st female flower, number of male flowers plant⁻¹, node at which 1st female flower appears, number of female flowers plant⁻¹, vine length (m), fruit length (cm), fruit diameter (cm), number of fruits plant⁻¹, average fruit weight (g), leaf area (cm²), 100 seed weight (g), number of seeds fruit⁻¹, seed weight fruit⁻¹ (g), days to 1st fruit harvest, fruit yield plant⁻¹ (kg), fruit yield hectare⁻¹ (q), TSS (°Brix), crude protein (%), vitamin C content (mg/100g), iron content (mg/100g), total chlorophyll content (mg/100g), dry matter content (%) and total phenols (mg/100g). The observations on different

quantitative and quality parameters were recorded from three randomly selected plants from each line of all replications.

2.2 Statistical Analysis

2.2.1 Analysis of variance

According to the procedure outlined by Panse and Sukhatme [11], analysis of variance was performed for each character in accordance with the design of the experiment (RCBD). The significance levels for the treatment means were 5% and 1%.

2.2.2 Estimation of the components of variances

2.2.2.1 Genotypic variance

Genotypic variance was calculated by using the method suggested by Johnson *et al.* [12].

2.2.2.2 Phenotypic variance

Phenotypic variance was estimated as per the procedure described by Johnson *et al.* [12].

$$\sigma_g^2 = \frac{MSt - MSe}{r}$$

Where,

$\hat{\sigma}_g^2$	=	Genotypic variance,
MSG	=	mean sum of squares due to genotypes,
MSE	=	mean sum of squares due to error and
r	=	number of replications

$$\hat{\sigma}^2 p = \hat{\sigma}_g^2 + \hat{\sigma}_e^2$$

Where,

$\hat{\sigma}^2 p$	=	Phenotypic variance
$\hat{\sigma}_g^2$	=	genotypic variance and
$\hat{\sigma}_e^2$	=	error variance

2.3 Phenotypic and Genotypic Co-Efficient of Variation

Burton [13] provided the following formulas, which were used to calculate the genotypic and

phenotypic co-efficients of variation (GCV) for the multitude of parameters under study:

$$PCV = \frac{\sqrt{\hat{\sigma}^2 p}}{\bar{X}} \times 100$$

Where,

$$\begin{aligned} \hat{\sigma}^2 p &= \text{Phenotypic variance and} \\ \bar{X} &= \text{Grand mean of the character} \\ &\text{under study} \end{aligned}$$

$$GCV = \frac{\sqrt{\hat{\sigma}^2 g}}{\bar{X}} \times 100$$

Where,

$$\begin{aligned} \hat{\sigma}^2 g &= \text{Genotypic variance and} \\ \bar{X} &= \text{Grand mean of the character} \\ &\text{under study} \end{aligned}$$

The estimates of PCV and GCV were classified into low, moderate and high according to Sivasubramanian and Madhavmenon [14] as follows:

0 – 10%: Low
10 – 20%: Moderate
> 20%: High

2.4 Heritability (Broad Sense)

The ratio of genotypic variance to phenotypic variance was used to determine the heritability (h^2) for yield and its component traits, which was then reported as percentage. The computation was carried out following the guidelines provided by Hanson et al. [15] Johnson et al.[12], and Burton and Devane [16].

$$h^2 = \sigma^2 g / \sigma^2 p$$

Where,

h^2 = Estimate of heritability in broad sense,
 $\sigma^2 g$ = Genotypic variance, and
 $\sigma^2 p$ = Phenotypic variance

The estimates of broad sense heritability, expressed in percentage were then categorized as low, moderate and high as suggested by Robinson et al. [17]:

0-30%: Low
30-60%: Moderate
> 60%: High

2.5 Genetic advance

Genetic advance at 5 per cent selection intensity was worked out by using the procedure suggested by Lush [18] and Johnson et al. [12].

$$GA = \frac{\sigma^2 g}{\sigma^2 p} \times (\sigma^2 p)^{1/2} \times K$$

Where,

GA = Genetic advance of the trait,
 $\sigma^2 g$ =genotypic variance of the trait,
 $\sigma^2 p$ =phenotypic variance of the trait, and
K = selection differential; (K = 2.06 at 5% selection intensity)

2.6 Expected Genetic Gain (Genetic Advance as Per Cent Of Mean)

It was estimated as per the method suggested by Johnson et al. [12]

$$\text{Genetic gain} = \frac{GA}{\bar{X}} \times 100$$

Where,

G.A.=Genetic advance of the trait
 \bar{X} =mean of the trait

The GA as per cent of mean was categorised as low, moderate and high as suggested by Johnson et al. [12]

0-10%: Low
10-20%: Moderate
>20%: High

All the above computations were carried out using the software Windostat at the Division of Genetics and Plant Breeding, SKUAST-Kashmir, Shalimar and “Variability package” in R software at the Division of Agri-Statistics, SKUAST-K, Shalimar.

3. RESULTS AND DISCUSSION

The analysis of variance disclosed that all the twenty-four characters exhibited highly significant differences among all the genotypes studied, thus suggesting existence of sufficient variability in the germplasm studied (Table-1a and 1b).

Table 1a. Analysis of variance (ANOVA) with respect to MSS for various growth, yield attributing and quality characters in bitter gourd (*Momordica charantia* L.)

S. No.	Source of variation	d.f	Mean sum of squares											
			Days to 1 st male flower appearance	Days to 1 st female flower	No. of male flowers plant ⁻¹	Node number at which 1 st female flower appeared	No. of female flowers plant ⁻¹	Vine length (m)	Fruit length (cm)	Fruit diameter (cm)	No. of fruits plant ⁻¹	Average fruit weight (g)	Leaf area (cm ²)	100 seed weight (g)
1.	Replication	2	0.99	0.84	3.71	1.10	1.58	0.15*	0.59	0.18*	1.25	3.10	2.80	1.03
2.	Genotype	29	51.53**	52.99**	20464.60**	24.69**	155.12**	2.15**	20.72**	0.28**	135.50**	508.77**	905.61**	83.72**
3.	Error	58	0.26	0.45	1.90	0.35	0.59	0.01	0.24	0.01	0.48	0.91	0.76	0.26

*, **= Significant at 5% and 1% probability level respectively

Table 1b. Analysis of variance (ANOVA) with respect to MSS for various growth, yield attributing and quality characters in bitter gourd (*Momordica charantia* L.)

S. No.	Source of variation	d.f	Mean sum of squares											
			No. of seeds fruit ⁻¹	Seed weight fruit ⁻¹	Days to 1 st fruit harvest	Fruit yield plant ⁻¹ (kg)	Fruit yield hectare ⁻¹ (q)	TSS (°Brix)	Crude protein content (%)	Vitamin C content (mg 100g ⁻¹)	Iron content (mg 100g ⁻¹)	Total chlorophyll content (mg 100g ⁻¹)	Dry matter content (%)	Total phenols (mg 100g ⁻¹)
1.	Replication	2	1.31	0.08	0.59	0.26*	15.63	0.92	0.25	0.39	0.86	1.50	1.14	0.34
2.	Genotype	29	44.44**	5.82**	76.52**	1.18**	2871**	0.57**	13.82**	159.61**	0.04**	20463.50**	11.05**	182.73**
3.	Error	58	0.33	0.06	0.36	0.01	4.09	0.19	0.15	0.10	0.40	0.53	0.70	0.10

*, **= Significant at 5% and 1% probability level respectively

Table-2. Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation, heritability and genetic advance (as % of mean) for various growth, yield attributing and quality characters in bitter gourd (*Momordica charantia* L.)

S. No.	Parameters	Mean	Range	Phenotypic variance (PV)	Genotypic variance (GV)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability h ² (broad sense)	Genetic gain (Genetic advance as % of mean)
1.	Days to appearance of 1 st male flower	55.45	46.22-62.25	17.35	17.09	7.51	7.45	0.98	15.24
2.	Days to appearance of 1 st female flower	63.53	57.22-72.18	17.96	17.51	6.67	6.58	0.97	13.39
3.	Number of male flowers plant ⁻¹	297.35	170.02-432.81	6822.77	6630.81	27.77	27.38	0.97	55.61
4.	Node number at which 1 st female flower appeared	13.03	6.72-19.38	8.46	8.11	22.33	21.86	0.95	44.08
5.	Number of female flowers plant ⁻¹	23.65	12.71-35.23	52.10	51.50	30.51	30.33	0.98	62.13
6.	Vine length (m)	2.62	1.48-4.53	0.73	0.71	32.59	32.15	0.97	65.35
7.	Fruit length (cm)	15.46	10.81-23.21	7.07	6.82	17.20	16.90	0.96	34.20
8.	Fruit diameter (cm)	2.72	2.06-3.43	0.10	0.09	11.78	11.032	0.87	21.26
9.	Number of fruits plant ⁻¹	19.41	9.01-30.40	45.48	45.00	34.73	34.54	0.98	70.79
10.	Average fruit weight (g)	83.13	60.58-120.88	170.19	164.32	15.69	15.41	0.96	31.20
11.	Leaf area (cm ²)	65.87	33.49-109.90	307.37	300.21	26.61	26.30	0.97	53.54
12.	100 seed weight (g)	27.37	16.52-36.80	28.08	27.81	19.35	19.26	0.99	39.50
13.	Number of seeds fruit ⁻¹	19.38	12.31-28.19	15.04	14.70	20.00	19.78	0.97	40.29
14.	Seed weight fruit ⁻¹ (g)	7.38	4.73-10.50	1.98	1.92	19.09	18.77	0.96	38.04
15.	Days to 1 st fruit harvest	77.28	70.04-86.06	25.74	25.38	6.56	6.52	0.98	13.33
16.	Fruit yield plant ⁻¹ (kg)	1.62	0.70-2.94	0.40	0.388	39.34	38.41	0.95	77.28
17.	Fruit yield hectare ⁻¹ (q)	77.85	32.53-143.60	959.72	920.63	39.78	38.97	0.95	78.62
18.	TSS (°Brix)	4.31	3.61-5.16	0.19	0.19	10.17	10.11	0.98	20.71
19.	Crude protein content (%)	14.78	11.00-19.63	4.61	4.54	14.52	14.41	0.98	29.48
20.	Vitamin C content (mg 100g ⁻¹)	51.16	41.26-66.90	53.20	52.10	14.25	14.10	0.97	28.75
21.	Iron content (mg 100g ⁻¹)	0.43	0.25-0.67	0.01	0.01	27.58	27.38	0.98	56.22
22.	Total chlorophyll content (mg 100g ⁻¹)	235.46	102.33-354.72	6821.16	6772.34	35.07	34.94	0.99	71.73
23.	Dry matter content (%)	10.80	8.07-14.02	3.72	3.68	17.85	17.77	0.99	36.43
24.	Total phenols (mg 100g ⁻¹)	37.28	24.26-50.07	60.91	58.96	20.93	20.59	0.96	41.73

Range values for the various characters under study (Table 2) showed that there was enough variation for each character, which is necessary before selecting for improvement. The results obtained are in conformity with the findings of Islam *et al.*[19], Yadav *et al.*[20], Chinthan *et al.* [21] Sowmya *et al.* [22] and Nithinkumar *et al.* [23].

Since it encompasses elements of genotype, environment, and genotype \times environment interaction and does not identify which character is exhibiting a higher degree of variability, the range in the values represents the amount of phenotypic variability, which makes it unstable. Additionally, dominance (a non-heritable factor), epistasis (non-allelic interaction), and additive gene effect (a heritable factor) all affect a crop's phenotypic behaviour. Therefore, the observed variability must be divided into the phenotypic and genotypic coefficients of variation. This will finally illustrate how variable different traits are.

Table-2 displays the estimated genotypic and phenotypic coefficients of variation for each character under study. The environment plays a significant impact in the expression of the traits that are being observed, as seen by the generally nearly identical genotypic and phenotypic coefficients of variation, with somewhat larger phenotypic coefficients of variation. This was consistent with research conducted by Maurya *et al.*[24], Ziaul *et al.* [25], Prakash *et al.*[26], Reddy *et al.* [27] Tiwari *et al.* [28], Rani *et al.*[29], and Ziaul *et al.* [25].

Traits with moderate to high coefficients of variation have a greater chance of improving through selection. Wide range of variability and high estimates of the genotypic and phenotypic coefficients of variation further imply that these traits would be responsive to selection.

It is evident from the data presented in Table-2 that the number of male flowers plant⁻¹ (27.77, 27.38), node number at which 1st female flower appeared (22.33, 21.86), number of female flowers plant⁻¹ (30.51, 30.33), vine length (32.59, 32.15), number of fruits plant⁻¹ (34.73, 34.59), leaf area (26.61, 26.30), fruit yield plant⁻¹ (39.34, 38.41), fruit yield hectare⁻¹ (39.78, 38.97), iron content (27.58, 27.38), total chlorophyll content (35.07, 34.94) and total phenols (20.93, 20.53) exhibited high values of genotypic and phenotypic coefficients of variation, respectively, suggesting that these genotypes had a wide genetic base for these characters. Fruit length (17.20, 16.90), fruit diameter (11.78, 11.03),

average fruit weight (15.69, 15.41), 100 seed weight (19.35, 19.26), number of seeds fruit⁻¹ (20.00, 19.78), seed weight fruit⁻¹ (19.09, 18.77), TSS (10.17, 10.11), crude protein content (14.52, 14.41), vitamin C content (14.25, 14.10) and dry matter content (17.85, 17.77) demonstrated moderate phenotypic and genotypic coefficients of variation suggesting the existence of moderate variability in the genetic stock studied. Low PCV and GCV values were observed for the traits; days to appearance of 1st male flower (7.51, 7.45), days to appearance of 1st female flower (6.67, 6.58) and days to 1st fruit harvest (6.56, 6.52). The results were in tune with the findings of Yadav *et al.* [20], Pathak *et al.*[30], Maurya *et al.* [24], Talukder *et al.* [31] Ziaul *et al.* [25] and Sowmya *et al.* [22].

The genotypic and phenotypic coefficients of variation do not accurately represent the degree of a character's heredity nor do they aid in determining the percentage of variation that is genuinely heritable. The heritability of a trait is therefore a reliable approach in such a situation because it allows the breeder to determine how much selection pressure to apply in a given context, thereby separating the effect of the environment from overall variability. It makes assessing the contributions of environmental and genetic factors to the observable phenotypic variance easier. According to Panse and Sukhatme [11] and Johnson *et al.* [12] the estimation of heritability has a greater role to play in determining the efficiency of character selection if it is taken into account in conjunction with the projected genetic advance. Moreover, the amount of genetic gain is closely correlated with the progress of selection. Hence, traits with high heritability and high genetic gain experience the effects of selection more quickly. High GAM (Genetic Advance as % of Mean) in conjunction with high heritability suggests that selection could be successful since the traits are likely being governed by additive gene action. When high heritability is demonstrated as a result of a favourable environment rather than genotype, selection for such traits may not be profitable. High heritability with low GAM suggests the importance of non-additive gene action. Additive gene effects are generally predominant in the case of low heritability with high GAM. In certain situations, significant environmental effects lead to low heritability, and selection may be successful. Low GAM and low heritability suggest that selection would be futile because character is heavily impacted by environmental factors.

All of the characters in the current study had high heritability (b.s.), which ranged from 87 to 99 percent. This suggests that genetic constitution plays a major role in character expression and that selection based on phenotypic expression can be trusted because the characters are less affected by environmental factors and are effectively passed down to the progeny. Pathak *et al.* [29] Singh *et al.* [32] Alekar *et al.* [33] , Prasanth *et al.* [34] , and Sowmya *et al.* [22] all reported similar outcomes.

The characters *viz.*, number of male flowers plant⁻¹, node number at which 1st female flower appeared, number of female flowers plant⁻¹, vine length,, fruit length, average fruit weight, number of fruits plant⁻¹, leaf area, 100 seed weight, number of seeds fruit⁻¹, seed weight fruit⁻¹, fruit yield plant⁻¹, fruit yield hectare⁻¹, iron content, total chlorophyll content, dry matter content and total phenols shown substantial genetic advance as a percentage of mean (GAM) and high estimates of heritability, suggesting that additive gene action predominates in the control of these traits. This implies that actual advancements in yield-based selection could be accomplished. These results are in conformity with several workers *viz.* Islam *et al.* [19] Alekar *et al.* [32], Ziaul *et al.* [24] Prasanth *et al.* [34] and Sowmya *et al.* [22].

A key factor that determines the hybrid or variety's commercial viability is fruit yield hectare⁻¹. Therefore, in every breeding effort, this feature should be given top importance. The prospect of choosing high yielding cultivars from the current collection was suggested by the trait's high heritability and high genetic progress as a percentage of mean. Islam *et al.* [19] Kumari *et al.* [35] Nithinkumar *et al.* [23] and Wan *et al.* [36], all backed up this claim.

4. CONCLUSION

Analysis of variance revealed significant variation existed among various characters under study; this indicates that there is tremendous potential for converging the elite allelic resources present in these bitter melon genotypes through a systematic breeding and selection approach, with the goal of recovering high yielding recombinants, with good quality characteristics.

For every character under investigation, the estimates of phenotypic variances were greater than the corresponding genotypic variances,

demonstrating the influence of environment on the expression of these traits, according to the results obtained for various variability and heritability parameters. In order to draw meaningful findings, the phenotypic and genotypic coefficients of variation were also computed, since these values by themselves do not offer a way to evaluate the nature of genetic variability. In general, the phenotypic and genotypic coefficients of variation were almost similar with somewhat higher values phenotypic coefficients of variation indicating minor role of environment in the expression of the studied traits. The phenotypic and genotypic coefficients of variability ranged from 6.65-39.78 and 6.52-38.97 respectively. The highest phenotypic and genotypic coefficients of variability in the present investigation were observed for the trait fruit yield hectare⁻¹ (39.78, 38.97) followed by fruit yield plant⁻¹ (39.34, 38.40), total chlorophyll content (35.07, 34.94) and number of fruits plant⁻¹ (34.73, 34.59). The present investigation indicates a great scope of fast improvement of majority of the traits studied as these characters in general exhibited high heritability coupled with high genetic advance (as per cent of mean), except for the traits days to appearance of 1st male flower, days to appearance of 1st female flower and days to 1st fruit harvest which although had high heritability but it was coupled with low genetic advance (as per cent of mean).

Heritability (b. s.) was found to be high for all the characters and ranged from 87 to 99 per cent indicating that the characters are less influenced by environmental effects and are likely to be effectively transmitted to the progeny. The present investigation indicates a great scope of fast improvement of majority of the traits studied as these characters in general exhibited high heritability coupled with high genetic advance (as per cent of mean) indicating the preponderance of additive gene action for control of these traits. This suggests that real progress in improvement through selection could be made for yield and thus the chances of fixing by selection are more to improve such traits through pure line selection, mass selection, progeny selection, hybridization and selection through pedigree breeding. However, an exception in this regard was observed for the traits; days to appearance of 1st male flower, days to appearance of 1st female flower and days to 1st fruit harvest which although had high heritability but it was coupled with low genetic advance (as per cent of mean). These characters are likely being governed by non-additive gene action and thus, recombinant

breeding would prove beneficial for improving them.

COMPETING INTERESTS

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

REFERENCES

1. Singh B, Singh AK, Kumar S. Genetic divergence studies in bitter gourd (*Momordica charantia* L.). Academic Journal of Plant Sciences. 2013;6(2):89-91.
2. Morton JF. The Balsam Pear-An edible, medicinal and toxic plant. Journal of Economic and Taxonomic Botany. 1967;21:57-68.
3. Heiser CB.. The gourd book. University of Oklahoma Press, Norman, UK; 1979.
4. Behera TK. Heterosis in bitter gourd. In: PK. Singh PK, Dasgupta SK, Tripathi SK. (eds.) Hybrid vegetable development. Haworth Press, New York. 2004;217-221.
5. Bharati LK, John KJ, Behera TK, Behera S, Simon PW, Staub JE. Bitter gourd: Botany, horticulture and breeding. Horticultural Reviews 2010;37:101-141.
6. Singh HK, Singh VB, Kumar R, Baranwal DK, Ray PK. Assessment of genetic diversity based on cluster and principal component analyses for yield and its contributing characters in bitter gourd. Indian Journal of Horticulture. 2014;71(1): 55-60.
7. Zehra SB, Nazir G, Hussain K, Masoodi U, Amin A, Afroza B, Malik A. Combining ability studies for earliness and quality traits in bitter gourd (*Momordica charantia* L.). SKUAST Journal of Research 2023;25 (3):437-451.
8. Sagar KR, Babu BR, Babu MR, Rao MP. Mean performance of different bitter gourd genotypes for various growth and yield characters. The Pharma Innovation Journal. 2022;11(8):41-1246.
9. NHB. Indian Horticulture Database. Ministry of Agriculture. Government of India;2020-21. Available:www. nhb. gov. in
10. Aftab O, Nazir G, Hussain K, Masoodi UH., Bashir K, Nazir N. Correlation and Path Coefficient Analysis in Bitter Gourd (*Momordica charantia* L.) Genotypes. Journal of Scientific Research and Reports. 2024;30(3):14-20.
11. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi. 1957;157-165.
12. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47:314-318.
13. Burton GW. Quantitative inheritance in grasses. Proceedings of 6th International Grassland Congress. 1952;11:277-283.
14. Sivasubramanian J, Madhavamenon P.. Genotypic and phenotypic variability in rice. Madras Agricultural Journal. 1973;12: 15-16.
15. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean Lespedeza. Agronomy Journal. 1956;48(6):268-272.
16. Robinson HF, Comstock RE, Harvey PH. Estimation of heritability and degree of dominance in corn. Journal of Agronomy. 1949;4:353-359.
17. Burton GW, Devane CH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
18. Lush JL. Heritability of quantitative characters in farm animals. *Proceedings of the 8th International Congress on Genetics*. Genetics Supplement volume. *Heredity*, 1949;356-395.
19. Islam MR, Hossain MS, Bhuiyan MSR, Husna A, Syed MA. Genetic Variability and Path-Coefficient Analysis of Bitter gourd (*Momordica charantia* L.). International Journal of Sustainable Agriculture. 2009;1 (3):53-57.
20. Yadav M, Pandey TK, Singh DB, Singh GK.. Genetic variability, correlation coefficient and path analysis in bitter gourd. Indian Journal of Horticulture. 2013; 70(1):144-149.
21. Chinthan KN, Rathod V, Hanchinamani CN, Nishani S, Dileepkumar AM, Bhat AS. Studies on genetic variability among local landraces of bitter gourd (*Momordica charantia* L.) for yield attributing traits under northern dry zone of Karnataka. The Pharma Innovation Journal. 2021;10(3):17 4-178.

22. Sowmya HM, Kolakar SK, Nadukeri S. Variability and heritability studies for yield and yield component traits in Bitter gourd (*Momordica charantia* L.). The Pharma Innovation Journal. 2021;10(11):652-654.
23. Nithinkumar KR, Kumar JSA, Ramachandra RK, Varalakshmi B, Mushrif SK, Prashanth SJ. Genetic variability and character association studies in Bitter gourd (*Momordica charantia* L.). Journal of Genetics, Genomics and Plant Breeding 2022;6(1):1-9.
24. Maurya D, Singh VB, Yadav GC, Kumar V. Studies on genetic variability, heritability and genetic advance in bitter gourd (*Momordica charantia* L.). Journal of Pharmacognosy and Phytochemistry 2018; 7(5):1925-1928.
25. Ziaul H, Hasan KM, Anjan KD., Eftekhar M, Najmul HG. Appraisal of Genetic Variability and Character Association of Bitter Gourd (*Momordica charantia* L.) Land Races for Yield and Yield Contributing Characters in Bangladesh. Journal of Biotechnology and BioResearch. 2019;1(4):JBB.000517.
26. Prakash S, Verma RS, Ram RB, Shivran BC, Pal H.. Variability Parameters of Yield and Quality Attributes in Bitter Gourd (*Momordica charantia* L.). International Journal of Plant & Soil Science. 2021;33(20):172-177.
27. Reddy MS, Prashanth P, Laxminarayana D, Saideah studies on genetic variability, heritability and genetic advance for yield and yield attributes in bitter gourd (*Momordica charantia* L.) Genotypes. Biological Forum – An International Journal. 2021;13(3):45-51.
28. Tiwari C, Bagri AS, Pandey A, Ganjeer B, Agnihotri A, Singh SS, Bhasker P.. Genetic variability and genetic advance in some cultivars of Bitter gourd (*Momordica charantia* L.). Journal of Pharmacognosy and Phytochemistry. 2021;10(2):979-981.
29. Rani KR, Raju Ch R, Reddy KR. Variability, correlation and path analysis studies in Bitter gourd (*Momordica charantia* L.). Agricultural Science Digest. 2015;35(2): 106-110.
30. Pathak M, Pahwa K, Manpreet. Genetic variability, correlation and path coefficient analysis in Bitter gourd (*Momordica charantia* L.). International Journal of Advanced Research. 2014;2(8):179-184.
31. Talukder ZH, Khan MH, Das AK, Uddin N.. Assessment of Genetic Variability, Heritability and Genetic Advance in Bitter gourd (*Momordica charantia* L.) for yield and yield contributing traits in Bangladesh. Scholar Journal of applied Sciences. 2018;1(6):9-18.
32. Singh HK, Singh VB, Kumar R, Baranwal DK, Ray PK. Character association, heritability and path analysis for yield and its contributing traits in Bitter gourd (*Momordica charantia* L.). Progressive Agriculture. 2015;15(1):41-47.
33. Alekar AN, Shinde KG, Khamkar MB. Studies on genetic variability, heritability, genetic advance and correlation in Bitter gourd (*Momordica charantia* L.). International Journal of Chemical Studies. 2019;7(3):1155-1159.
34. Prasanth K, Sadashiva AT, Pitchaimuthu M, Varalakshmi B. Genetic Diversity, Variability and Correlation studies in Bitter gourd (*Momordica charantia* L.). Indian Journal of Plant Genetic Resources 2020;33(2):179-186.
35. Kumari M, Kumar J, Kumari A, Singh VK, Rani N, Kumar A. Genetic Variability, Correlation and Path Coefficient Analysis for Yield and Yield Attributing Traits in Bitter Gourd (*Momordica charantia* L.). Current Journal of Applied Science and Technology. 2018;31(4):1-8.
36. Wan RWE, Noraziyah AAS, Suhana O, Farahzety AM, Norfadzilah AF, Rosniza K. Estimation of heritability and genetic variability in selected F1 bitter gourd population for yield and its contributing traits. Food Research. 2022;6(4):1-8.

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