Genetic variability studies in Bitter gourd (*Momordica charantia* L.) genotypes

Abstract

The magnitude of genetic variability present in any given germplasm plays a key role in deciding the method or type of breeding programme to be adopted.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 present investigation was undertaken at the Experimental field of Urban Technological Park Habbak, Srinagar, Jammu and Kashmir during *kharif*-2022. The experiment was laid out in Randomized Block Design with three replications and plant spacing of 2×1 m for thirty genotypes in order to study the different components of genetic variability such as mean, range, PV, GV, PCV, GCV, heritability, genetic advance and genetic gain among the genotypes.The estimates of phenotypic coefficient of variation were found to be slightly higher than the corresponding genotypic coefficient of variation for all the characters studied suggesting some role of environment in the expression of these traits. The highest phenotypic and genotypic coefficient of variation were noted for fruit yield hectare^{-1} (q) (39.788 and 38.970). High heritability coupled with high genetic gain was recorded for yield hectare^{-1} (q) (0.95 and 78.62), indicating that the heritability is most likely due to additive gene effects and thus the chances of fixing this trait by selection are more. The estimates of heritability in broad sense were high for all the traits.

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 (Singh *et al.,* 2013). 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 (Morton, 1967 and Heiser, 1979). 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 (Behera, 2004 and Bharati *et al.,* 2010). The plant shows a high level of cross pollination and is in turn, highly heterozygous due to monoecism (Singh *etal.*, 2014). 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. (Zehra *et al.,* 2023). The fruits are used as a vegetable in many ways and quite commonly consumed in cooked, fried and stuffed forms. The fruits are also pickled, canned and dehydrated. Every part of the plant is used medicinally. The fruits consists of cooling, digestive, laxative, antipyretic and antidiabetic

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properties and its administration is useful in biliousness, blood diseases, rheumatism and asthma. The leaf is used internally as a laxative and as an ointment for sours. It is claimed that the fruit powder is used for healing wounds, leprous and malignant ulcers. It is reported for its usefulness in snakebites. The roots have abortifacient activity. It has been reported that protein of bitter gourd inhibited the growth of immune deficiency virus (HIV-1) in human beings. In Ayurveda, the juice of fresh leaves is prescribed for diabetes (Sagar *et al.*).

In India, the bitter gourd crop covers 101,000 hectares and produces 1174 thousand metric tonnes of fresh yield annually (NHB, 2020-21). 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. (Aftab *et al.*, 2024).

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 phenotypic and genotypic coefficients of variation help in quantifying the amount of variability present in the available germplasm. Higher the magnitude of positive association between yield and its component characters, better is the efficiency of the selection exercise.

Materials and methods

Experimental style and layout

The present was undertaken at the experimental field of Urban Technological Park of SKUAST, Habbak Srinagar, Jammu and Kashmir during *Kharif*-2022. The experimental field of Urban Technological Park, Habbak is located at an altitude of 1608 meters above mean sea level lying between 34.16° North latitude and 74.83º East longitude. The climate is temperate characterized by mild summers. The mean minimum and maximum temperatures are 2.42 ºC and 30ºC recorded in the months of October and August-September (respectively). The maximum rain fall is received during June.

Thirty phenotypically diverse genotypes of bitter gourd collected from various sources were evaluated for various yield and yield attributing traits during *Kharif*-2022. The single factor experiment was laid down in a Randomized Complete Block Design (RCBD) with three replications. Five plants of each genotype in each replication were planted at a spacing of 2×1 m between rows and plants respectively. Recommended cultural practices were followed during the growth and developmental period in order to raise a healthy crop. 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 (cm^2), 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

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

Statistical analysis

Analysis of variance

Analysis of variance for all the characters as per the design of experiment (RCBD) was carried out as per the method explained by Panse and Sukhatme (1957).The treatment means were tested at 5% and 1% level of significance.

Estimation of the components of variances

Genotypic variance

Genotypic variance was calculated by using the method suggested by Johnson *et al*. (1955).

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

Where,

$\hat{\sigma}^2_g$ = Genotypic variance,

MSG = mean sum of squares due togenotypes,

MSE = mean sum of squares due to error and

r = number of replications

Phenotypic variance

Phenotypic variance was estimated as per the procedure described by Johnson *et al*. (1955).

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

Where,

$\hat{\sigma}^2$ Phenotypic variance

$\hat{\sigma}^2$ genotypic variance and

$\hat{\sigma}^2$ error variance

Phenotypic and genotypic co-efficient of variation

The magnitude of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) existing in the parameters under study was worked out by the formula given by Burton (1952):

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$$PCV = \frac{\sqrt{\hat{\sigma}^2 p}}{\bar{x}} x100$$

Where,

$\hat{\sigma}^2 p$ Phenotypic variance and

$\bar{x}$ Grand mean of the character under study

$$GCV = \frac{\sqrt{\hat{\sigma}^2 g}}{\bar{x}} x100$$

Where,

Genotypic variance and

Grand mean of the character under study

The estimates of PCV and GCV were classified into low, moderate and high according to Sivasubramanian and Madhavmenon (1973) as follows:

0 – 10%: Low

10 – 20%: Moderate

> 20%: High

Heritability (broad sense)

Heritability (h^2) for yield and its components was estimated from the ratio of the genotypic variance to the phenotypic variance and expressed in percentage. The calculation was performed as per the procedure presented by Burton and Devane (1953), Johnson *et al*. (1955) and Hanson *et al*. (1956).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

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.* (1949):

0-30%: Low

30-60%: Moderate

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> 60%: High

Genetic advance

Genetic advance at 5 per cent selection intensity was worked out by using the procedure suggested by Lush (1949) and Johnson *et al*. (1955).

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

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)

Expected genetic gain (genetic advance as per cent of mean)

It was estimated as per the method suggested by Johnson *et al*. (1955).

$$\text{Genetic gain} = \frac{GA}{\overline{x}} \times 100$$

Where,

G.A. = Genetic advance of the trait

$\overline{x}$ = mean of the trait

The GA as per cent of mean was categorised as low, moderate and high as suggested by Johnson *et al*. (1955).

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.

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).

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Range values for various characters studied (Table-2) indicated existence of sufficient variability for all the characters, which is prerequisite for making improvement through selection. The results obtained are in agreement with Islam *et al.* (2009), Yadav *et al.* (2013), Chinthan *et al.* (2021), Sowmya *et al.* (2021) and Nithinkumar *et al.* (2022).

The range in the values reflect the amount of phenotypic variability, which is not very reliable since it includes genotypic, environmental and genotype × environmental interaction components and does not reveal as to which character is showing higher degree of variability. Additionally, the phenotype of a crop is influenced by the additive gene influence (heritable), dominance (non-heritable) and epistasis (non-allelic interaction). Hence, it becomes necessary to split the observed variability into phenotypic coefficient of variation and genotypic coefficient of variation, which ultimately indicates the extent of variability existing for various traits.

The estimates of phenotypic and genotypic coefficients of variation for all the characters studied are presented in Table-2. In general, the phenotypic and genotypic coefficients of variation were almost similar with slightly higher phenotypic coefficients of variation, which indicates the role of environment in the expression of traits under observation. This was in agreement with the study of Rani *et al.* (2015), Maurya *et al.* (2018), Ziaul *et al.* (2019), Prakash *et al.* (2021), Reddy *et al.* (2021) and Tiwari *et al.* (2021).

The possibility for improvement through selection is higher for traits with moderate to high coefficients of variation. High estimates of the phenotypic and genotypic coefficients of variation, together with a wide range of variability, further suggest 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 phenotypic and genotypic coefficients of variation respectively, indicating that genotypes had broad 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.* (2013), Pathak *et al.* (2014), Maurya *et al.* (2018), Talukder *et al.* (2018), Ziaul *et al.* (2019) and Sowmya *et al.* (2021).

Characters which possessed moderate to high coefficients of variation suggested that there is better potential for improvement through selection. Wide ranges of variability along with high estimates of phenotypic and genotypic coefficients of variation further indicate that these attributes would likely respond to selection.

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The phenotypic and genotypic coefficients of variation do not give a true picture about the extent of inheritance of the character nor they help to estimate the proportion of variation that is truly heritable. In such a situation, the heritability of a character can be relied upon, as it enables the breeder to decide the extent of selection pressure to be applied under a particular environment, which separates out the environmental influence from the total variability. It facilitates the evaluation of hereditary and environmental effects in the observable phenotypic variation. The estimation of heritability has a greater role to play in determining the effectiveness of selection of a character provided it is considered in conjunction with the predicated genetic advance as suggested by Panse and Sukhatme (1957) and Johnson *et al.* (1955). Furthermore, the progress in selection is also directly proportional to the amount of genetic gain. Therefore, the effect of selection is realized more quickly in those characters which have high heritability as well as high genetic gain. When high heritability is accompanied with high GAM (Genetic advance as per cent of mean), it indicates additive gene effects and selection may be effective. High heritability with low GAM indicates importance of non-additive gene action where high heritability is exhibited due to favourable influence of environment rather than genotype and the selection for such traits may not be rewarding. Low heritability with high GAM is governed by additive gene effects in which low heritability is exhibited due to high environmental effects and the selection may be effective in such cases. Low heritability coupled with low GAM indicates that character is highly influenced by environmental effects and selection would be ineffective.

In the present study, heritability (b.s.) was high for all the characters and ranged from 87 to 99 per cent indicating that the characters are less influenced by environmental effects and the characters are effectively transmitted to the progeny, suggesting major role of genetic constitution in the expression of a character and thus selection based on phenotypic expression could be relied upon. Similar results were observed by Pathak *et al.* (2014), Singh *et al.* (2015), Alekar *et al.* (2019), Prasanth *et al.* (2020) and Sowmya *et al.* (2021).

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 showed the high estimates of heritability coupled with high genetic advance as per cent of mean (GAM), 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. These results are in conformity with several workers *viz.* Islam *et al.* (2009), Alekar *et al.* (2019), Ziaul *et al.* (2019), Prasanth *et al.* (2020) and Sowmya *et al*. (2021).

Fruit yield hectare^{-1} is an important character, which decides the commercial viability of the hybrid/variety. Thus, this trait deserves the highest priority in any breeding programme. High heritability along with high genetic advance as per cent of mean for this trait suggested the possibility of selecting high yielding cultivars from the present collection. This argument was supported by Islam *et al.* (2009),Kumari *et al.* (2018), Nithinkumar *et al.* (2022) and Wan *et al.* (2022).

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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 1st male flower appearance	Days to 1st female flower	No. of male flowers plant^{-1}	Node number at which1st 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 1st 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

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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 1st 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 1st 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 1st 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 1st 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

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Conclusion

It is clear from the above discussion that tremendous potential exists for converging the elite allelic resources present in these bottle gourd genotypes through a systematic breeding and selection approach so as to recover high yielding recombinants, with good quality characteristics. Analysis of variance revealed that significant variation existed among various characters under study.

The results obtained for various variability and heritability parameters pointed out that the estimates of phenotypic variances were higher than the corresponding genotypic variances for all the characters under study indicating the influence of environment in the expression of these traits. Since these estimates alone do not provide means to assess the nature of genetic variability, the phenotypic and genotypic coefficients of variation were also estimated in order to draw valid conclusions. 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.

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