

## Studies on Genetic Variability, Heritability and Genetic Advance for Yield and Yield Attributes in Bitter Gourd (*Momordica charantia* L.) Genotypes

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(Received 15 May 2021, Accepted 14 July, 2021)

(Published by Research Trend, Website: [www.researchtrend.net](http://www.researchtrend.net))

**ABSTRACT:** The present investigation was undertaken during *Kharif* 2017-18, College of Horticulture, Mojerla, Sri Konda Laxman Telangana State Horticultural University, Telangana. The trial was laid out in Randomized Block Design with twenty seven bitter gourd genotypes. Analysis of variance revealed significant differences among all the genotypes for all the characters. The genetic parameters were studied to elucidate the genetic variability, heritability and genetic advance in bitter gourd (*Momordica charantia* L.). The genotypes exhibited a large range of variability for all the characters. Phenotypic coefficient of variation (PCV) was more than genotypic coefficient of variation (GCV) for all the characters studied. PCV was higher than the appropriate GCV in all aspects that describe the environmental factors that influence their expression to some degree or another. Heritability (> 60) have been observed for vine length, number of primary branches per vine, number of nodes per vine, Internodal length, Days to first male flower appearance, Days to first female flower appearance, Nodes at which first male flower appearance, Nodes at which first female flower appearance, Number of fruits per vine, average fruit weight, fruit length, fruit diameter, number of seeds per fruit, 100 seed weight, total fruit yield per vine and fruit fly infestation per cent. Genetic advance, i.e., genetic gain, ranged from 0.91 to 108.80. High genetic gain (> 20%) was observed for vine length and days to last fruit harvest. High heritability combined with high genetic advance was observed for the characters vine length. High heritability combined with high genetic advance indicates that additive gene action plays a serious role in governing these traits and these traits will be improved by simple selection.

**Keywords:** Variability, heritability, RBD, PCV, GCV, genetic advance.

### INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is one in all the world's most extensively cultivated vegetable crops. It is a versatile vegetable when it involves cooking. The cucurbitaceae family includes sour bitter, which is native to India and incorporates a second centre of diversity in China and geographical region (Gruthe, 1977). It is a day neutral plant, and heavily cross pollinated. It's summer time crop that grows during a form of soils and climates and tolerates salty conditions. The bitter gourd is grown in India in an exceedingly wild and planted technique over a 96,000 ha region, with an annual production of 1085 lakh MT per 11 MT/ha (NHB, 2017-2018). Extra (inherited) and extra differences, like dominance and epistasis, compose the genetic variation of any

limited component (non-allelic interactions). As a result, proper indices like phenotypic and genotypic coefficients for genetic diversity are required to separate the apparent phenotypic variability in its genetic and non-genetic variants. Furthermore, genetic improvement will be utilised to predict selection efficacy.

### II. MATERIALS AND METHODS

With 27 genotypes, the study was done at the college of Horticulture in Mojerla, SKLTSHU. There have been 25 native clusters and two check variants, Aakash and MBTH-102, among them. The research is carried out in the Randomized Block Design. The sphere is split in three replications. Each genotype is planted with a 2.0 m row to row spacing and a 0.5 m plant to plant

spacing. The information is gathered supported the bitter gourd's description. The investigation was meted out with the assistance of the Windows software package. The variation in fruit-related symptoms within the bitter gourd between genotypes is assessed as follows.

#### A. Genotypic variance and phenotypic variance

Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox (1957).

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MSS due to genotypes} - \text{MSS due to error}}{r}$$

$$\text{Phenotypic variance} = \text{Genotypic variance } (\sigma_g^2) + \text{Error variance } (\sigma_e^2)$$

#### B. Co-efficient of variability

Together, phenotypic and genotypic co-efficient of variability for all characters were estimated using the formula of Burton (1952).

$$\text{Phenotypic Co-efficient of Variability (PCV\%)} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \times 100$$

$$\text{Genotypic Co-efficient of Variability (GCV\%)} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \times 100$$

PCV and GCV were classified as per Sivasubramanian and Madha menon (1973) and as shown below:

Less than 10 % : Low, 10-20 % : Moderate, More than 20 % : High

#### C. Heritability in broad sense ( $h^2$ )

The broad sense heritability ( $h_{bs}^2$ ) was estimated for all characters as the ratio of genotypic variance to the total or phenotypic variance as suggested by Lush (1949) and Hanson *et al.* (1956).

$$h^2 = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

According to Robinson *et al.* (1966) heritability estimates in cultivated plants can be placed in following categorizes.

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

#### D. Genetic advance (GA)

Genetic advance for each character was estimated by using the following formula of Johnson *et al.*, (1955).

$$GA = h_{bs}^2 \times \sigma_p \times K$$

Where,

$h_{bs}^2$  = Heritability estimate in broad sense

$\sigma_p$  = Phenotypic standard deviation of the trait

K = Standard selection differential which is 2.06 at 5 per cent selection intensity.

Genetic advance was classified as high (>20 %), moderate (10-20 %) and low (<10 %).

Further the Genetic advance as per cent of mean was computed by using the following formula

$$GA \text{ as per cent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

Genetic advance as per cent mean was categorized as given below as suggested by Johnson *et al.*, (1955).

Less than 10 % : Low; 10-20 % : Moderate; More than 20 % : High.

## RESULTS AND DISCUSSION

The mean performance of all twenty-seven genotypes of bitter reeds was recorded (Table 1). Differential analysis (Table 2) showed significant differences between the genotypes of all eighteen characters studied. Limitations of different statistical and genetic parameters such as mean, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability, genetic advance as percent means are presented (Table 3). PCV and GCV were high (> 20) in vine height, number of nodes per vine, and Medium fruit weight, fruit length, seed fruit per fruit, 100 seed weight, fruit per fruit per grape, and fruit fly high phenotypic and genotypic differences between accessibility and sensitivity to symptoms to make them more selective in choice. PCV and GCV were estimated for internodal lengths, nodes where the first male flower appears, nodes where the first female flower appears, dates to harvest fruit, and number of fruits per vine. PCV was higher than GCV for all trained characters showing natural traits that influence their speech. PCV was higher than the appropriate GCV in all aspects that describe the environmental factors that influence their expression to some degree or another.

In the present study, the high genetic variation observed in the characters number of nodes per vine, medium fruit weight, fruit length, seed number per fruit, weight of 100 seeds, and total fruit yield per vine indicates the importance of these seeds to be used to select high genotypes. A similar trend for high GCV has already been reported by Devmore *et al.*, (2010), Yadav *et al.* (2013) on the number of areas of each vine, Ullah *et al.*, (2012) on fruit weight and fruit length, Pornornsuriya *et al.* (2011) number of seeds per fruit, and Veena *et al.*, (2012) per 100 seed weight.

Tightness with the highest strength values (> 60) is based on vine length, number of basic branches per vine, number of seeds per fruit, 100 seed weight, and total fruit yield per vine indicate the significance of these characters for being used for selecting superior genotypes. A similar trend of high GCV has already been reported by Devmore *et al.*, (2010), Yadav *et al.*, (2013) for number of nodes per vine, Ullah *et al.*, (2012) for fruit weight and fruit length, Pornsuriya *et al.*, (2011) for number of seeds per fruit, and Veena *et al.*, (2012) for 100 seed weight.

**Table 1 (a): Mean Performance of 27 genotypes of bitter gourd in terms of yield and its related characters.**

Sr. No.	Genotypes	Vine length (cm)	Number of primary branches per vine	Number of nodes per vine	Internodal length (cm)	Days to first male flower appearance	Days to first female flower appearance	Nodes at which first male flower appears	Nodes at which first female flower appears
1.	IC-256147	186.26	16.30	38.63	4.96	36.83	45.88	8.96	13.16
2.	IC-541249	303.30	12.20	43.63	6.87	41.20	46.63	9.63	14.40
3.	IC-336200	201.16	8.60	33.73	5.56	45.50	50.55	8.87	15.30
4.	IC-256110	275.50	12.96	30.30	9.08	36.76	45.40	9.63	14.26
5.	IC-324546	210.43	15.16	32.30	5.13	42.76	49.43	10.63	14.20
6.	IC-598170	199.60	14.96	35.20	5.83	36.40	43.16	9.20	13.33
7.	IC-467670	287.76	14.40	48.20	5.89	36.20	43.30	11.63	13.20
8.	IC-598172	331.96	18.40	48.83	6.78	37.63	44.76	11.76	16.50
9.	IC-598171	348.86	16.53	60.63	5.75	32.40	42.40	10.96	14.06
10.	IC-467673	217.86	19.43	44.96	4.43	44.96	52.83	10.50	14.53
11.	IC-510632	272.20	17.63	44.50	6.08	46.66	52.40	9.10	13.50
12.	IC-068345	208.16	17.30	48.96	6.03	36.50	48.06	12.73	14.83
13.	IC-068306	177.73	12.33	42.96	5.93	47.63	56.96	11.86	15.06
14.	IC-599431	271.06	19.30	41.10	6.58	48.16	57.43	8.73	12.86
15.	IC-599421	323.86	20.40	43.76	7.35	38.53	47.40	12.98	16.06
16.	IC-264699	294.96	17.63	43.20	6.77	36.43	44.73	10.21	13.20
17.	IC-085608	192.90	15.40	49.06	4.30	37.63	48.60	7.33	11.73
18.	IC-264705	337.20	20.26	60.53	5.61	48.73	60.06	11.22	12.60
19.	IC-599428	297.16	17.43	38.30	7.79	44.20	51.60	10.99	13.30
20.	IC-470943	213.76	10.83	63.33	4.30	38.30	48.86	14.88	19.40
21.	IC-599434	254.40	21.63	37.73	6.73	41.43	52.30	7.10	11.20
22.	IC-256206	218.83	15.73	37.40	5.93	40.63	50.83	9.22	10.63
23.	IC-398610	313.30	16.86	66.10	5.21	38.53	47.53	11.44	13.30
24.	IC-599423	321.10	21.60	52.40	6.08	37.96	47.76	12.22	14.30
25.	IC-599424	353.30	15.06	61.20	5.76	39.06	47.53	12.77	14.76
26.	Aakash	308.83	12.60	54.63	5.57	40.30	47.40	11.10	14.40
27.	MBTH-102	363.30	14.66	53.96	6.57	43.26	50.83	7.44	10.96
<b>Grand mean</b>		269.809	435.667	46.5037	6.0363	40.542	49.0632	10.4883	13.8926
<b>SEm ±</b>		13.3974	1.28312	1.27077	0.36383	1.57888	1.1412	0.42072	0.48294
<b>CV (%)</b>		8.60053	0.51012	4.73304	10.4396	6.74537	4.02873	6.94781	6.021
<b>CD(P=0.05)</b>		38.0195	3.64126	3.60623	1.03248	4.4806	3.23854	1.19393	1.37049

Table 1 (b) continued...

Sr. No.	Genotypes	Days to first fruit harvest	Days to last fruit harvest	Number of fruits per vine	Average fruit weight (cm)	Fruit length (cm)	Fruit diameter (cm)	Fruit fly infestation (%)	Number of seeds per fruit	100 Seed weight (g)	Total fruit yield per vine (kg)
1.	IC-256147	62.26	127.40	13.64	11.86	6.83	2.1	33.70	3.66	7.96	0.59
2.	IC-541249	60.96	124.50	14.78	23.66	14.67	2.02	22.40	17.06	17.50	2.72
3.	IC-336200	59.86	131.50	15.98	9.86	5.93	2.11	12.26	3.83	8.50	0.54
4.	IC-256110	61.43	119.86	15.54	24.23	14.30	2.29	33.16	15.76	16.80	1.68
5.	IC-324546	63.96	138.40	14.84	11.00	8.90	2.19	34.03	4.26	8.93	0.48
6.	IC-598170	56.16	143.86	19.40	12.96	4.93	2.26	23.03	7.06	9.53	0.74
7.	IC-467670	57.16	132.63	15.09	25.00	17.06	2.82	28.63	19.90	16.13	2.54
8.	IC-598172	60.53	90.60	17.04	24.23	16.76	2.49	27.33	14.30	17.16	1.96
9.	IC-598171	55.43	151.76	15.28	23.53	15.21	3.42	37.33	17.23	19.30	1.85
10.	IC-467673	66.20	132.30	13.92	10.37	10.53	2.93	31.03	7.50	8.43	0.46
11.	IC-510632	66.73	154.63	14.16	21.10	11.76	3.45	23.56	13.20	18.90	1.64
12.	IC-068345	62.76	159.86	15.24	16.40	7.43	2.14	21.83	5.73	10.56	0.79
13.	IC-068306	72.06	169.00	14.50	18.63	7.26	2.03	27.70	6.96	10.70	0.96
14.	IC-599431	72.20	170.96	17.61	20.76	12.87	3.24	21.03	15.66	17.56	1.95
15.	IC-599421	63.63	155.63	17.81	25.00	14.00	3.08	26.36	15.73	16.03	2.66
16.	IC-264699	60.06	133.30	19.25	39.66	11.53	2.74	24.00	12.86	20.70	3.25
17.	IC-085608	63.06	116.76	17.90	22.66	6.36	1.99	22.56	7.30	11.86	1.01
18.	IC-264705	74.76	135.30	16.70	40.50	14.16	2.84	18.36	18.20	21.81	6.23
19.	IC-599428	65.20	134.40	16.80	24.30	12.65	2.90	37.60	13.10	18.66	2.29
20.	IC-470943	61.63	127.40	14.80	21.06	9.63	1.91	29.00	11.16	11.06	0.98
21.	IC-599434	63.20	126.16	20.70	21.86	19.30	2.95	21.16	20.20	15.93	2.31
22.	IC-256206	65.96	133.20	16.66	23.20	10.27	2.24	28.03	12.06	13.20	1.50
23.	IC-398610	43.51	119.96	13.46	31.36	16.05	2.91	51.93	15.96	16.26	3.21
24.	IC-599423	61.10	124.73	17.93	43.30	15.28	2.15	39.20	18.53	17.16	6.93
25.	IC-599424	62.20	120.53	16.33	33.73	15.80	2.51	24.23	16.73	19.13	3.15
26.	Aakash	61.40	151.53	17.53	37.26	12.29	3.85	18.96	15.03	17.40	3.73
27.	MBTH-102	66.76	145.73	17.00	30.80	12.72	2.49	19.50	11.96	18.40	3.12
<b>Grand mean</b>		62.6028	135.999	16.2946	24.014	12.0215	2.59753	27.3333	12.6309	15.0241	2.19811
<b>SEm ±</b>		3.78507	8.43588	0.71361	1.7707	0.40777	0.15237	3.12857	0.474	0.35362	0.12391
<b>CV (%)</b>		10.4723	10.7438	7.58545	12.7715	5.87508	10.1602	19.825	6.49988	4.07675	9.76362
<b>CD(P=0.05)</b>		10.7414	23.9396	2.02511	5.02494	1.15717	0.4324	8.87833	1.34513	1.00352	0.35163

Table 2 (a): Analysis of variance for eighteen characters in bitter gourd.

Sources of Variation	Degrees of freedom	Vine length (cm)	Number of primary branches per vine	Number of nodes per vine	Internodal length (cm)	Number of days to first male flower appearance	Number of days to first female flower appearance	Nodes at which first male flower appears	Nodes at which first female flower appears	Days to first fruit harvest	Days to last fruit harvest
<b>Replications</b>	2	261.394	6.715	4.031	0.375	5.953	6.837	1.103	0.671	12.500	33.790
<b>Genotypes</b>	26	10293.730***	31.882***	297.247***	3.357***	56.161***	57.303***	10.552***	9.773***	105.303**	925.514***
<b>Error</b>	52	538.471	4.939	4.845	0.397	7.479	3.907	0.531	0.700	42.980	213.492
<b>SEm ±</b>	80	13.3974	1.28312	1.27077	0.36383	1.57888	1.1412	0.42072	0.48294	3.78507	8.43588
<b>CV (%)</b>		8.601	13.773	4.733	10.440	6.745	4.029	6.948	6.021	10.472	10.744
<b>CD (P=0.05)</b>		38.019	3.641	3.606	1.032	4.481	3.239	1.194	1.370	10.741	23.939

\* and \*\* significant at P = 0.05 and P = 0.01 level of significance respectively

**Table 2 (b). continued...**

Sources of Variation	Degrees of freedom	Number of fruits per vine	Average fruit (g)	Fruit length (cm)	Fruit diameter (cm)	Fruit fly infestation (%)	Number of seeds per fruit	100 Seed weight (g)	Total fruit yield per vine (kg)
Replications	2	0.814	4.029	0.630	0.013	28.634	0.739	0.550	0.022
Genotypes	26	10.328***	254.799***	44.507***	0.820***	200.509***	78.302***	52.960***	7.686***
Error	52	1.528	9.406	0.499	0.070	29.364	0.674	0.375	0.046
SEm ±	80	0.71361	1.7707	0.40777	0.15237	3.12857	0.454	0.35362	0.12391
CV (%)		7.585	12.772	5.875	10.160	19.825	6.500	4.077	9.764
CD (P=0.05)		2.025	5.025	1.157	0.432	8.878	1.345	1.004	0.352

\* and \*\* significant at P = 0.05 and P = 0.01 level of significance respectively

**Table 3 (a): Estimation of variability, heritability and genetic advance as per cent of mean for eighteen characters in 27 genotypes of bitter gourd.**

Sr. No.	Character	Range		Mean	Variance		PCV (%)	GCV (%)	h <sup>2</sup> (%)	Genetic Advance	GA as per cent of mean
		Minimum	Maximum		Phenotypic	Genotypic					
1.	Vine length (cm)	177.733	363.300	269.80	3790.225	3251.754	22.818	21.135	85.50	108.806	40.327
2.	Number of primary branches per vine	8.600	21.633	16.135	13.920	8.981	23.122	18.572	64.50	4.959	30.731
3.	Number of nodes per vine	30.300	66.100	46.503	102.312	97.647	21.751	21.230	95.30	19.850	42.685
4.	Internodal length (cm)	4.300	9.086	6.036	1.384	0.987	19.488	16.455	71.30	1.728	28.624
5.	Number of days to first male flower appearance	32.400	48.733	40.542	23.706	16.227	12.009	9.936	68.50	6.866	16.935
6.	Number of days to first female flower appearance	42.400	60.066	49.063	21.706	17.799	9.496	8.599	82.00	7.870	16.040
7.	Nodes at which first male flower appears	7.106	14.886	10.488	3.871	3.340	18.759	17.425	86.30	3.497	33.344
8.	Nodes at which first female flower appears	10.633	19.400	13.892	3.724	3.024	13.891	12.518	81.20	3.228	23.238
9.	Days to first fruit harvest	43.510	74.766	62.602	63.755	20.774	12.754	7.281	32.60	5.360	8.561
10.	Days to last fruit harvest	90.600	170.96	135.99	450.833	237.340	15.613	11.328	52.60	23.027	16.932
11.	Number of fruit per vine	13.466	20.700	16.294	4.461	2.934	12.962	10.511	65.80	2.861	17.558
12.	Average fruit weight (g)	9.866	43.300	24.014	91.204	81.797	39.769	37.662	89.70	17.644	73.475
13.	Fruit length (cm)	4.933	19.306	12.021	15.168	14.669	32.397	31.860	96.70	7.759	64.544
14.	Fruit diameter (cm)	1.913	3.853	2.597	0.320	0.250	21.774	19.259	78.20	0.911	35.089
15.	Number of seeds per fruit	3.666	20.200	12.630	26.550	25.876	40.794	40.273	97.50	10.345	81.903
16.	100 seed weight (g)	7.966	21.816	15.024	17.903	17.528	28.163	27.866	97.90	8.534	56.800
17.	Total fruit yield per vine (kg)	0.466	6.933	2.198	2.593	2.547	73.251	72.598	98.20	3.258	148.217
18.	Fruit fly infestation (%)	12.266	51.933	27.333	86.412	57.048	34.009	27.633	66.00	12.642	46.252

In the broad sense, higher values of heritability ( $> 60$ ) have been observed for vine length, number of primary branches per vine, number of nodes per vine, Internodal length, Days to first male flower appearance, Days to first female flower appearance, Nodes at which first male flower appearance, Nodes at which first female flower appearance, number of fruits per vine, average fruit weight, fruit length, fruit diameter, number of seeds per fruit, 100 seed weight, total fruit yield per vine and fruit fly infestation per cent. Moderate values of heritability (30-60) have been observed for days to the first fruit harvest and days to the last fruit harvest. High values of heritability suggest the greater effectiveness of selection due to less influence of the environment and improvement to be expected for these characters in future breeding programmes as the genetic variance is mostly due to additive gene action and selection based on phenotypic performance would be reliable. Genetic advance, *i.e.*, genetic gain, ranged from 0.91 to 108.80. High genetic gain ( $> 20\%$ ) was observed for vine length and days to last fruit harvest. Moderate genetic gain (10-20%) was observed for the number of nodes per vine, average fruit weight, number of seeds per fruit, and fruit fly infestation per cent. Low genetic gain (10%) was observed for the following: Number of primary branches per vine, Internodal length, Number of days to first male flower appearance, Number of days to first female flower appearance, Nodes at which first male flower appearance, Nodes at which first female flower appearance, Days to first fruit harvest, Number of fruits per vine, fruit length, fruit diameter, 100 seed weight and total fruit yield per vine. High heritability along with high genetic gain were noticed for Vine length, which might be assigned to additive gene effects governing their inheritance and phenotypic selection for their improvement, could be achieved by simple methods like pure line or mass selection or bulk or SSD method following hybridization and selection in early generations. Nevertheless, they could be improved by the development of hybrid varieties or the utilization of transgressive segregants in heterosis breeding programmes. The results are in accordance with Raja *et al.*, (2007) for the number of branches per vine, vine length, and fruit weight. Pathak *et al.* (2014) for fruit length, Singh *et al.*, (2014) for number of seeds per fruit. Islam *et al.*, (2009) for yield per plant, days to first female flower appearance, and vine length. Gupta *et al.*, (2013) for Number of branches per plant, Dalamu and behera (2013) for fruit weight.

Extensive intensity with maximum values ( $> 60$ ) is determined by vine length, number of basic branches per vine, and number of nodes per vine. Internodal Length, Dates to first male flower appearance, Dates to first female flower appearance, Nodes from which the first male flower appears, the nodes where the female flower first appears, The number of fruits per vine, The average fruit weight, fruit length, fruit width, seed fruit per fruit,

100 seed weight, total fruit yield per vine and fruit fly entry percent. Average heritability values (30-60%) were identified during the first fruit harvest and the last days of the fruit harvest. Higher robust values indicate better selective performance due to less environmental impact and the expected improvement in these characters in the upcoming breeding program as genetic variation is mainly due to increased genetic action and selections based on phenotypic performance.

Genetic improvement, *i.e.*, genetic gain from 0.91 to 108.80. The highest genetic benefit ( $> 20\%$ ) was seen in the length of vine, the last days of fruit harvesting. The average genetic gain (10-20%) is based on the number of nodes per grape, the average fruit weight, and the number of seeds per fruit. Fruits fly by fruit. The low genetic gain (10%) was seen in the number of primary branches per vine, internal length, number of days to the first appearance of the male flower, number of days to the appearance of the first female flower, nodes where the first female flower appeared, and nodes where the first female flower appeared. Days to initial fruit harvest, fruit value per vine, fruit length, fruit width, 100 seed weight and total fruit per vine. High heights and high genetic gains were noted for vine length, which could be attributed to the additional genetic impact that controls their genetic and phenotypic selection in their development can be achieved in a simple way, such as pure line or mass selection or large or SSD method following mixing and selection in early generations.

Emphasis should be laid on characters contributing maximum variability, heritability and genetic advance for the purpose of further selection and choice of parents for hybridization. However, they can be improved by the development of hybrid varieties or the use of excessive segregants in the heterosis reproductive system. The results are consistent with Raja *et al.*, (2007) number of branches per vine, vine length, and fruit weight. Pathak *et al.*, (2014) fruit length, Singh *et al.*, (2014) of the number of seeds per fruit. Muslims *et al.*, (2009) For each plant, dates to the appearance of the first female flower, length of vine. Gupta *et al.*, (2013) of the number of branches per plant, Dalam and Behera (2013) of fruit weight.

## CONCLUSION

The analysis of variance revealed significant difference for eighteen characters studied and reported that there was sufficient amount of variability exist among the genotypes. Wide range of variability was observed for vine length, number of fruits per plant, average fruit weight, fruit length, total fruit yield indicating the scope for selection of suitable initial breeding material for further improvement. High PCV and GCV estimates were recorded The difference between PCV and GCV values were minimum, indicating that the traits under study were less influenced by environment and these

characters could be improved by following phenotypic selection. Heritability estimates were high for all the characters studied except days to last fruit harvest. This suggested the greater effectiveness of selection due to less influence of environment and improvement to be expected for these characters in future breeding programme as the genetic variance is mostly due to the additive gene action. Genetic advance estimates were high (>20%) for vine length and days to last fruit harvest. Genetic advance as per cent of mean was high (>20%) for vine length, number of primary branches per vine, number of nodes per vine, internodal length, nodes at which first male and female flower appears, average fruit weight, fruit length, fruit diameter, number of seeds per fruit, 100 seed weight, total fruit yield per vine and percentage of fruit fly infestation. Thus, aforesaid traits recorded high  $h^2_{(b)}$  (>60%) estimates also. This indicated that all the above said traits were under the influence of additive gene action and simple selection process based on phenotypic performance of these traits would be effective.

**Acknowledgements.** The author express sincere thanks to P. prashanth, D. laxminarayana and P. Saidaiah, for their kind help in research programme. I am highly thankful to SKLTSHU, Mulugu, Siddipet and NBPGR, Thrissur, Kerala for providing germplasm to complete this endeavor.

**Conflict of Interest.** Nil.

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**How to cite this article:** Reddy, M.S., Prashanth, P., Laxminarayana, D. and Saidaiah, P. (2021). 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*, 13(3): 45-51.