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## Assessment of genetic variability in F<sub>4</sub> segregating population of bitter melon (*Momordica charantia* L.)

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**Abstract**

A field experiment was carried out to evaluate the variability, heritability and genetic advance in F<sub>4</sub> segregating generation of bitter melon (*Momordica charantia* L.) during late *kharif* season, 2018 at Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India. Ten F<sub>4</sub> segregants along with seven parents were evaluated by adopting RBD with three replications. The analysis of variance revealed significant differences among the segregants and parents for all the characters under study. The estimation of coefficient of error variations (C<sub>v</sub>) ranged from 1.62% in days to 1<sup>st</sup> harvest to 12.04% in sex ratio (male:female). The PCV values were higher than the GCV values as expected. Relatively lower difference between GCV and PCV was recorded in characters like days to 1<sup>st</sup> female flower (7.73-7.30), fruit girth (14.24-13.60) and days to 1<sup>st</sup> male flower (8.51-7.86), thus less influenced by environmental factors. High heritability along with high GA as % of mean was noticed for characters like fruits vine<sup>-1</sup> (91.36% and 49.11%), fruit girth (91.12% and 26.74%), seeds fruit<sup>-1</sup> (89.85% and 38.21%), total green fruit yield (89.35% and 44.67%), sex ratio (88.10% and 63.38%), internodal length (87.82% and 46.83%), fruit length (87.42% and 46.43%), average fruit weight (81.16% and 34.35%) and vine length (78.16% and 26.44%) indicating that these traits are controlled by additive gene action. So, there is an ample scope for direct selection of these traits in bitter melon.

**Keywords:** bitter melon, genetic variability, GCV, PCV, heritability, genetic advance

**Introduction**

Bitter melon (*Momordica charantia* L.) is an important monoecious cross pollinated vegetable crop belongs to family Cucurbitaceae. It is locally known as Bitter Melon, Karela, Maiden apple and Balsam pear etc. It is believed to be originated in Tropical Asia, particularly eastern India (*i.e.* state of Odisha, West Bengal, Assam, Jharkhand and Bihar) and south China *i.e.* Indo Burma centre of origin (Zevan and Zhukovsky, 1975) [20].

It is an important contributor of iron, phosphorus and ascorbic acid (Singh *et al.*, 2012) [16]. The fruit contains two alkaloids *viz.*, momordicin and cucurbitacin (bitter glucoside) which prevents the spoilage of cooked vegetable and keeps fit for consumption even for two to three days (Jatav *et al.*, 2016) [7]. A hypoglycemic principle called “*charantin*” has been isolated which is used for the treatment of diabetes (Raman and Lau, 1996) [15]. A basic protein MAP-30 that inhibits human immune deficiency virus (HIV) is present both in seed and fruit (Lee *et al.*, 1995) [9]. The fruits are usually consumed fresh but can also be dried and pickled (Vinning, 1995) [18].

Different varieties of bitter melon adopted in various regions differ in their fruit characters with respect to colour, shape and size, as they are selected by the farmers. Besides these, appreciable amount of variation is also found in crop duration, vegetative parts, capability of growing in frost free winter to hot summer of subtropical regions etc. are present in genotypes distributed all over India (Gowda, 2017) [5]. Although a wide range of variability found in this crop, still our productivity is too low due to lack of high yielding varieties and hybrids. Therefore, a thorough knowledge regarding the amount of genetic variability existing for various characters is essential for initiating the crop improvement programme for exploitation, study of segregating generation would be of considerable importance. Yield is a complex character and it is mostly influenced by environment. To get a superior genotype the breeder must have the knowledge of genetic variability, heritability and genetic advance of different traits which contributes to the yield. Hence, keeping all these views in mind an attempt was made to study the genetic variability, heritability and genetic gain among ten F<sub>4</sub> segregants along with seven parents of bitter melon for various horticultural traits.

## Materials and Methods

The present study material was comprised of 17 genotypes (ten F<sub>4</sub> segregants and seven parents). This investigation was conducted at Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India during late *kharif* season, 2018. The experiment was laid out in Randomized Block Design with three replications. All the recommended package of practices was adapted uniformly to all the 17 genotypes in order to raise a good crop stand. All the observations were recorded from randomly selected four plants per replication for 13 traits *viz.*, vine length (cm), primary branches vine<sup>-1</sup>, internodal length (cm), days to 1<sup>st</sup> male flower, days to 1<sup>st</sup> female flower, sex ratio (male: female), days to final harvest, fruit length (cm), fruit girth (cm), average fruit weight (g), fruits vine<sup>-1</sup>, total green fruit yield (kg) and seeds fruit<sup>-1</sup>. The genotypic and phenotypic coefficients of variations (GCV and PCV) were calculated by the formula given by Burton (1952). Heritability in broad sense and genetic advance (GA) were estimated as per the formula described by Allard (1960) and Johnson *et al.* (1955), respectively.

## Results and Discussion

The analysis of variance (ANOVA) for 23 different characters revealed significant differences among the breeding lines for all the characters (Table 1) which implies that there was existence of appropriate amount of variations among them and it gives more scope for their further improvement. The C<sub>V</sub> values were around 10% for all the characters except for sex ratio (12.04%) indicating overall moderate precision being maintained in the present investigation.

The extent of genetic variability present in the breeding lines under study was measured in terms of range, general mean, Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability (h<sup>2</sup>), Genetic advance (GA), GA as % of mean is presented in (Table 2). These parameters were calculated for all the 13 quantitative characters. The range of different traits between maximum and minimum values varied from 132.60-145.13 days (28.74%) for days to final fruit harvest to minimum of 7.96-13.36 cm (4.63%) in fruit girth (Table 2).

It was revealed that the estimates of PCV were higher than that of GCV for all the traits indicating relatively low influence of environmental factors for expression of different traits. This was supported by several scientists in bitter melon (Bhave *et al.*, 2003; Narayan *et al.*, 2006; Rajput *et al.*, 2012; Singh *et al.*, 2012 and Gupta *et al.*, 2016)<sup>[2, 11, 14, 16, 6]</sup>. The higher magnitude of PCV and GCV was observed in characters like internodal length (25.88 and 24.26), sex ratio (34.92 and 32.78), fruit length (25.78 and 24.11), fruits vine<sup>-1</sup> (26.10 and 24.94) and total green fruit yield (24.27 and 22.94) showed that genotypes evaluated under present study had sufficient extent of genetic variability to generate transgressive segregation of green fruit yield vine<sup>-1</sup> and other yield attributes. Similar findings were also reported by Rajput

(2012)<sup>[14]</sup>, Dalamu and Behera, (2013)<sup>[4]</sup>, Nandakumar (2014)<sup>[10]</sup>, Singh *et al.* (2015)<sup>[17]</sup>, Gupta *et al.* (2016)<sup>[6]</sup> and Gowda (2017)<sup>[5]</sup> in bitter melon. Relatively lower difference between GCV and PCV was recorded in characters like days to 1<sup>st</sup> female flower (7.73-7.30), fruit girth (14.24-13.60) and days to 1<sup>st</sup> male flower (8.51-7.86), indicating that genes play a major role in the expression of these characters. While, low magnitude of PCV and GCV was observed for days to 1<sup>st</sup> male flower (8.51 and 7.86), days to 1<sup>st</sup> female flower (7.73 and 7.30) and days to final harvest (3.76 and 2.68).

It has been established that estimation of GCV does not indicate the magnitude of heritable variation with a particular trait. So, in order to measure the proportion of total genetic variation, there is also need to estimate heritability in broad sense. Higher heritability means the character is more stable under different environment conditions which provide a better opportunity for selecting a good genotype. According to Panse (1957)<sup>[12]</sup>, high GA occurs only due to additive gene action. Therefore, heritability coupled with GA would be more efficient for selecting superior genotype(s) rather heritability alone.

High heritability estimates were recorded for fruits vine<sup>-1</sup> (91.36%), fruit girth (91.12%), seeds fruit<sup>-1</sup> (89.85%), total green fruit yield (89.35%), days to 1<sup>st</sup> female flower (89.17%), sex ratio (88.11%), internodal length (87.82%), fruit length (87.42%), primary branches vine<sup>-1</sup> (85.95%), days to 1<sup>st</sup> male flower (85.19%), average fruit weight (81.16%) and vine length (78.16%). On the other hand, moderate heritability was recorded for days to final fruit harvest (50.77%) in the present investigation. Genetic advance was found to be highest for Fruits vine<sup>-1</sup> and lowest for sex ratio. The characters sex ratio (63.38%), fruits vine<sup>-1</sup> (49.11%), internodal length (46.83%), fruit length (46.43%), number of seeds fruit<sup>-1</sup> (38.21%), average fruit weight (34.35%), fruit girth (26.74%) and vine length (26.44%) recorded comparatively higher value of expected GA (%).

High range of heritability along with high range of GA as % of mean was observed for characters like fruits vine<sup>-1</sup> (91.36% and 49.11%), fruit girth (91.12% and 26.74%), seeds fruit<sup>-1</sup> (89.85% and 38.21%), total green fruit yield (89.35% and 44.67%), sex ratio (88.11% and 63.38%), internodal length (87.82% and 46.83%), fruit length (87.42% and 46.43%), average fruit weight (81.16% and 34.35%) and vine length (78.16% and 26.44%) indicating the role of additive gene action in the expression of these characters. Hence, simple selection method can be employed for improving these characters. This was in line with the findings of Narayan *et al.* (2006)<sup>[11]</sup>, Singh *et al.* (2015)<sup>[17]</sup> and Yadagiri *et al.* (2016)<sup>[19]</sup>. The characters days to 1<sup>st</sup> female flower (89.17% and 14.20%), primary branches vine<sup>-1</sup> (85.95% and 18.43%) and days to 1<sup>st</sup> male flower (85.19% and 14.94%) showed high heritability coupled with moderate GA as % of mean. This was agreed with the findings of Pathak *et al.* 2014<sup>[13]</sup> and Gowda (2017)<sup>[5]</sup> for the character days to 1<sup>st</sup> female flower and days to 1<sup>st</sup> male flower.

**Table 1:** Analysis of variance for 23 characters in 17 breeding lines (F4 segregants and parents) of bitter gourd

Sl. No.	Characters	Mean sum of squares		
		Replication (2)	Genotype (16)	Error (32)
1	Vine length	0.32	1.21**	0.10
2	Primary branches vine <sup>-1</sup>	1.57	7.08**	0.37
3	Internodal length	0.69	5.82**	0.26
4	Days to 1 <sup>st</sup> male flower	4.50	37.31**	2.04
5	Days to 1 <sup>st</sup> female flower	8.77	46.39**	1.81
6	Node of 1 <sup>st</sup> male flower	2.07	4.65**	0.17
7	Node of 1 <sup>st</sup> female flower	5.48	3.83**	0.31
8	Sex ratio (male: female)	0.00	0.01**	0.00
9	Days to 1 <sup>st</sup> harvest	2.55	24.46**	1.29
10	Days to final harvest	91.73	54.04**	13.21
11	Fruit length	1.39	18.91**	0.87
12	Fruit girth	0.69	6.93**	0.22
13	Average fruit weight	24.03	299.58**	21.51
14	Fruits vine <sup>-1</sup>	59.00	278.52**	8.51
15	Marketable green fruit yield	0.07	0.76**	0.03
16	Unmarketable green fruit yield	0.01	0.01**	0.00
17	Total green fruit yield	0.07	0.77**	0.03
18	Seeds fruit <sup>-1</sup>	10.23	40.26**	1.46
19	TSS	0.51	0.55**	0.24
20	Ascorbic acid	97.72	86.20**	18.47
21	Reducing sugar	0.001	0.01**	0.000
22	Non-reducing sugar	0.003	0.01**	0.001
23	Total sugar	0.004	0.02**	0.002

**Table 2:** Estimation of different parameters of variability and genetic advances under selection (5%) for 13 characters in 17 breeding lines (F4 segregants and parents)

Sl. No.	Characters	Range	Mean	CVe	GCV	PCV	h <sup>2</sup> (bs)	GA	GA as % of mean
1	Vine length	3.19-5.17	04.18	7.68	14.52	16.43	78.16	1.11	26.44
2	Primary branches vine <sup>-1</sup>	12.50-17.97	15.50	3.90	9.65	10.41	85.95	2.86	18.43
3	Internodal length	3.87-8.50	05.61	9.03	24.26	25.88	87.82	2.63	46.83
4	Days to 1 <sup>st</sup> male flower	40.61-51.17	43.81	3.27	7.86	8.51	85.19	6.52	14.94
5	Days to 1 <sup>st</sup> female flower	45.27-59.70	52.16	2.54	7.30	7.73	89.17	7.50	14.20
6	Sex ratio	0.09-0.27	0.13	12.04	32.78	34.92	88.11	0.08	63.38
7	Days to final harvest	132.60-145.13	134.07	6.07	2.68	3.76	50.77	5.42	3.94
8	Fruit length	5.20-13.57	10.17	9.14	24.11	25.78	87.42	4.72	46.43
9	Fruit girth	7.97-13.37	11.00	4.24	13.60	14.24	91.12	2.94	26.74
10	Average fruit weight	26.65-76.17	52.01	8.92	18.51	20.55	81.16	17.87	34.35
11	Fruits vine <sup>-1</sup>	21.87-55.95	38.03	7.67	24.94	26.10	91.36	18.86	49.11
12	Total green fruit yield	1.56-3.18	2.16	7.92	22.94	24.27	89.35	0.97	44.67
13	Seeds fruit <sup>-1</sup>	12.81-24.07	18.37	6.58	19.57	20.65	89.85	7.02	38.21

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