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Evaluation of Performance of Bitter Gourd (*Momordica charantia* L.) Genotypes under Coastal Conditions of Odisha

Pratibha Sharma[1]*, Gouri Shankar Sahu[2], Anita Mohanty[3], Pradyumna Tripathy[4], Neeraj Kumar[1] and S. Karubakee[5]
[1]Research Scholar, Department of Vegetable Science,
Odisha University of Agriculture and Technology Bhubaneshwar (Odisha), India.
[2]Professor and Head, Department of Vegetable Science,
Odisha University of Agriculture and Technology Bhubaneshwar (Odisha), India.
[3]Senior Vegetable Breeder and OIC, AICRP on Vegetable Crops,
Odisha University of Agriculture and Technology, Bhubaneshwar (Odisha), India.
[4]Professor, Department of Vegetable Science,
Odisha University of Agriculture and Technology Bhubaneshwar (Odisha), India.
[5]Research Scholar, Department of Agronomy,
Odisha University of Agriculture and Technology Bhubaneshwar (Odisha), India.

(Corresponding author: Pratibha Sharma)*

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ABSTRACT: A field experiment was carried out using 16 genotypes during *spring-summer* season (2022). The experiment was conducted using a RBD with three replications to study the nature and extent of genetic variability in bitter gourd genotypes for improvement in fruit yield and yield attributing traits. Significant variations in the genotypes for each character were found using the analysis of variance. The PCV was greater than GCV for every character under study. The characters such as average fruit weight, days to 50% flowering, days to first female flower opening and sex-ratio observed relatively low difference of GCV and PCV. High heritability and high GA as per cent of mean was recorded for characters like average fruit weight, fruit yield per vine, sex-ratio, vine length, number of primary branches, number of fruits per vine and fruit diameter indicating that these characters are highly influenced by additive gene action and hence, direct selection through these characters would be more effective in improvement programme.

Keywords: Bitter gourd, GCV, PCV, heritability, genetic advance.

INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is a popular cucurbitaceous vegetable crop belonging to family Cucurbitaceae, with 2n=2x=22 where immature fruits are eaten as vegetables. It is thought to be indigenous to tropical regions of Asia. In India, it is commonly referred to as 'karela'. The states of Eastern India i.e. Odisha, West Bengal, Assam, Jharkhand and Bihar may be considered as a probable primary centre of diversity of bitter gourd. It is an excellent source of vitamin B_1, B_2, B_3, vitamin C, magnesium, potassium, calcium, phosphorous, manganese, folic acid, zinc, and has high dietary-fibre (Krawinkel and Keding 2006; Singla *et al.*, 2023). It is rich in therapeutic qualities such as purgative, carminative, anti-diabetic, anthelmintic, antiemetic and anti-cancerous (Dhangar, 2024; Saha *et al.*, 2024). Bitter gourd is cultivated round the year in Odisha and the vegetable also fetches a premium price in the market.

The Bitter gourd plants are monoecious annuals with medium size vines which are highly cross-pollinated crop in nature and such pollination mechanism can be used to generate hybrids because nature has a plethora of genetic variability. Given the varied agroclimatic conditions of Odisha, little is known about the genetic diversity and trait associations of bitter gourd genotypes. The presence of genetic variation in crops is necessary for their improvement as they respond to selection pressure. The extent to which the desirable characters are heritable and the magnitude of genetic variability already present in the genotype determines the effectiveness of any breeding program for the genetic improvement of quantitative characters. Therefore, the present investigation was carried out to study the presence of genetic variability, heritability and genetic advance among different bitter gourd genotypes.

MATERIALS AND METHODS

The present investigation entitled "Evaluation of performance of Bitter gourd (*Momordica charantia* L.) genotypes under coastal conditions of Odisha" was carried out during the spring-summer season of the year, 2022 at the Horticultural Research Farm, OUAT, Bhubaneswar. The experiment was conducted in Randomized Block Design (RBD) in three replications with plot size of 3.0 × 2.7 m^2. Each plot had three basins, and each basin had three plants. The 16 genotypes were used in the experiment, which were procured from AICRP on Vegetable Crops, OUAT. The cultural and management practices were implemented in accordance with the package of practices. Observations on fifteen quantitative characters namely days to first male flower opening, days to first female flower opening, days to 50% flowering, vine length, number of primary branches per vine, internodal length, leaf area, fruit length, fruit diameter, average fruit weight, number of fruits per vine, sex-ratio, fruit yield per vine, fruit yield per plot, and fruit yield per hectare and four morphological characters *viz.* fruit-color, ridges, presence of tubercles and shape of the fruit were recorded from five plants in each replication. The mean value was subjected to statistical analysis of variance (Panse and Sukhatme 1956). The phenotypic and genotypic coefficients of variation were computed as per Burton and De Vance (1953). The heritability in broad sense and genetic advance as percent mean (GAM) were determined by using the formula given by Lush (1949); Johnson *et al.* (1955) respectively.

RESULTS AND DISCUSSION

Results of analysis of variance as presented in Table 1 showed significant differences among genotypes for all the 15 examined quantitative characters thereby suggesting existence of wide range of variations among the genotypes.

The widest range was recorded for average fruit weight (33.63g to 102.56g) followed by leaf area (128.96cm^2 to 161.61cm^2) and number of fruits per vine (11.76 to 24.03), indicating the presence of sufficient variability among the genotypes used in the present study thus, aiding in the selection of the best genotype from existing collection as presented in Table 2. The results contradicted the findings of Murlee *et al.* (2013), who found that yield per hectare had the greatest range of variation, followed by fruit weight, days to first appearance of the male flower, and fruit length. The general mean results indicated wide variation ranging from fruit yield per vine (1.03kg) to leaf area (144cm^2). The genotypic variance ranged from 0.19 for fruit yield per vine to 378.57 for average fruit weight while, the phenotypic variance varied from 0.21 for fruit yield per vine to 397.66 for average fruit weight. In general all the values showed values parallel between these two variances showing higher values for the later than the former.

The study of data in Table 2 revealed that the estimates of phenotypic co-efficient of variation (PCV) was higher than the estimates of genotypic co-efficient of variation (GCV) for all the characters suggesting relative influence of environment on expression of different characters. Similar results were reported by Dey *et al.* (2009); Maurya *et al.* (2018); Talukder *et al.* (2018); Tyagi *et al.* (2018); Bhati *et al.* (2023); Sagar *et al.* (2024). The difference between PCV and GCV was very less in traits like average fruit weight, days to 50% flowering, fruit yield per plot, days to first female flower opening, sex-ratio, vine length, number of primary branches, days to first male flower opening, leaf area and number of fruits per vine indicating less environmental influence on these traits. Hence, these traits may be considered stable thus selection of such traits on phenotypic values may be considered rewarding. On the other hand traits like fruit length, internodal length, and fruit diameter relatively showed large differences among PCV and GCV indicating high environmental influence on expression of such characters. These results coincide similar with the results obtained by Singh *et al.* (2017); Kumanan *et al.* (2024) who reported close relation between PCV and GCV for almost all the characters whereas, Prasanth *et al.* (2020) reported close relation for number of fruits, fruit weight and fruit yield.

Heritability estimates provide the basis for selection of phenotypic performance but heritability estimated with genetic advance (GA) should always be considered simultaneously for obtaining an effective selection of characters in crop improvement programme (Johnson *et al.,* 1955). In the current investigation (Fig. 1 & 2), high heritability coupled with high GA as percent of mean was recorded for characters like fruit yield per plot, average fruit weight, fruit yield per vine, sex-ratio, vine length, number of primary branches, number of fruits per vine, and fruit diameter indicating the predominance of additive components for these characters. Hence, direct selection through these characters would be more effective in future improvement programme. High heritability and low GA as percent of mean was observed for characters like days to 50% flowering, days to first female flower opening, leaf area indicating that non-additive gene effects were involved in the expression of these characters and that selection for such characters would not be rewarding. Characters such as days to first male flower opening, and internodal length showed moderate heritability and low GA as percent of mean suggesting that these characters are highly influenced by environment and selection for such characters would be less effective. Similar findings were reported by Dey *et al.* (2009); Pathak and Pahwa (2014); Rani *et al.* (2014); Rani *et al.* (2015); Maurya *et al.* (2018); Kumar *et al.* (2018); Talukder *et al.* (2018); Tyagi *et al.* (2018); Alekar *et al.* (2019); Prakash *et al.* (2021); Triveni *et al.* (2021); Nithinkumar *et al.* (2022); Bhati *et al.* (2023); Sagar *et al.* (2024).

In the present investigation, morphological characters like fruit color, ridges (continuous/discontinuous), presence of tubercles and shape of the fruit of all accessions were recorded (Table 3). The results revealed that genotypes BG-4 and BG-12 were green in color while genotype BG-9 was pale-green in color.

However, genotypes like BG- 1, BG-2, BG-5, BG-13, BG-14 and BG-16 were light-green in color. Rests of the genotypes are dark-green in color. Genotypes BG-2, BG-8 and BG-10 showed continuous ridges while the rest other genotypes showed discontinuous ridges. The genotypes that showed continuous ridges also recorded absence of tubercles on their surface while, the rest of the genotypes showed tubercles presences on their fruit surface.

All the genotypes, based on fruit shape were categorized into three different shapes *i.e.* spindle, oblong and cylindrical. Among them, maximum number of genotypes had spindle-shaped fruits. However, three (BG-4, BG-6 and BG-16) genotypes had oblong-shaped fruits and four genotypes (BG-3, BG-7, BG-9 and BG-12) had cylindrical-shaped fruits.

Table 1: Analysis of variance for 15 characters of 16 genotypes of Bitter gourd.

Sr. No.	**Characters**	**Mean Sum of Square**			**Calculated F**
		Replication	**Genotypes**	**Error**	
	Degree of freedom	**2**	**15**	**30**	
1.	Days to first male flower opening	2.766	5.977	1.686	3.544*
2.	Days to first female flower opening	1.958	16.019	1.819	8.804*
3.	Days to 50% flowering	10.396	24.172	2.435	9.925*
4.	Vine length (m)	0.059	0.677	0.029	23.196*
5.	No. of primary branches	0.583	6.976	0.339	20.586*
6.	Internodal length	1.454	1.661	0.583	2.847*
7.	Leaf area (cm^2)	663.029	296.555	53.405	5.552*
8.	Fruit length (cm)	0.909	11.139	2.769	4.022*
9.	Fruit diameter (cm)	0.030	1.012	0.181	5.583*
10.	Avg. fruit weight (g)	14.620	1154.817	19.089	60.497*
11.	No. of fruits per vine	43.895	45.335	2.533	17.900*
12.	Sex-ratio	11.089	20.489	0.861	23.801*
13.	Fruit yield per vine (kg)	0.104	0.595	0.018	32.713*
14.	Fruit yield per plot (kg)	0.158	23.609	0.296	79.875*
15.	Yield/ha (t/ha)	0.195	29.147	0.365	79.875*

'*'at 5% level '**'at 1% level

Table 2: Estimates of genetic parameters of different characters.

Sr. No.	**Characters**	**Range**		**Mean**	**GV**	**PV**	**GCV (%)**	**PCV (%)**	**H (%)**	**GA**	**GAM**
		Min.	**Max.**								
1.	Days to first male flower opening	36.89	41.56	39.45	1.43	3.12	3.03	4.47	45.90	1.67	4.23
2.	Days to first female flower opening	45.56	54.22	48.20	4.73	6.55	4.51	5.31	72.23	3.81	7.90
3.	Days to 50% flowering	51.33	61.67	55.50	7.24	9.68	4.85	5.61	74.84	4.80	8.64
4.	Vine length (m)	1.81	3.22	2.54	0.22	0.25	18.28	19.48	88.09	0.90	35.34
5.	No. of primary branches	6.67	11.33	9.15	2.21	2.55	16.26	17.47	86.72	2.85	31.20
6.	Internodal length	7.31	9.85	8.26	0.36	0.94	7.26	11.75	38.11	0.76	9.23
7.	Leaf area	128.96	161.6	144.0	81.04	134.4	6.25	8.05	60.28	14.4	9.98
8.	Fruit length (cm)	9.45	16.93	13.29	2.79	5.56	12.57	17.75	50.19	2.44	18.35
9.	Fruit diameter (cm)	2.64	4.41	3.46	0.27	0.45	15.23	19.58	60.45	0.84	24.39
10.	Avg. fruit weight (g)	33.63	102.5	68.54	378.5	397.6	28.39	29.09	95.20	39.1	57.06
11.	No. of fruits per vine	11.76	24.03	17.71	14.26	16.80	21.33	23.15	84.92	7.17	40.50
12.	Sex-ratio	16.02	24.21	20.17	6.54	7.40	12.68	13.49	88.37	4.95	24.55
13.	Fruit yield per vine (kg)	0.44	1.93	1.03	0.19	0.21	42.54	44.51	91.36	0.86	83.76
14.	Fruit yield per plot (kg)	2.93	11.53	6.83	7.77	8.07	40.83	41.60	96.34	5.64	82.55
15.	Yield/ha (t/ha)	3.26	12.81	7.59	9.59	9.95	40.83	41.60	96.34	6.26	82.55

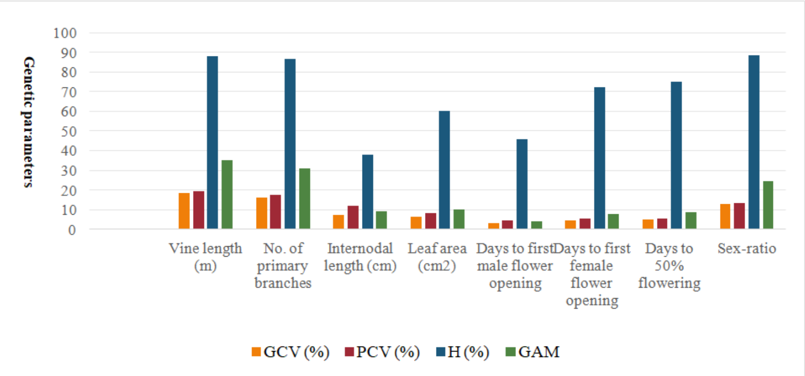

Fig. 1. Growth and flowering characters.

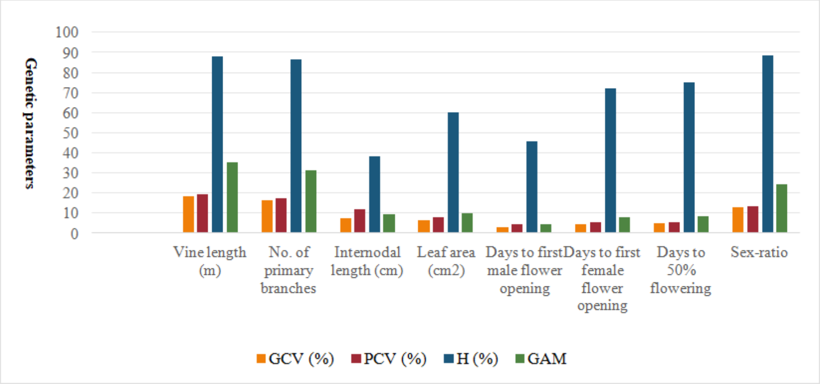

Fig. 2. Yield and yield attributing characters.

Table 3: Variation in morphological features in bitter gourd.

Sr. No.	Genotypes	Fruit color	Ridges (Continuous/discontinuous)	Presence of tubercles	Shape of fruit
1.	BG-1	Light-green	Discontinuous	Present	Spindle
2.	BG-2	Light-green	Continuous	Absent	Spindle
3.	BG-3	Dark-green	Discontinuous	Present	Cylindrical
4.	BG-4	Green	Discontinuous	Present	Oblong
5.	BG-5	Light-green	Discontinuous	Present	Spindle
6.	BG-6	Dark-green	Discontinuous	Present	Oblong
7.	BG-7	Dark-green	Discontinuous	Present	Cylindrical
8.	BG-8	Dark-green	Continuous	Absent	Spindle
9.	BG-9	Pale-green	Discontinuous	Present	Cylindrical
10.	BG-10	Dark-green	Continuous	Absent	Spindle
11.	BG-11	Dark-green	Discontinuous	Present	Spindle
12.	BG-12	Green	Discontinuous	Present	Cylindrical
13.	BG-13	Light-green	Discontinuous	Present	Spindle
14.	BG-14	Light-green	Discontinuous	Present	Spindle
15.	BG-15	Dark green	Discontinuous	Present	Spindle
16.	BG-16	Light-green	Discontinuous	Present	Oblong

CONCLUSIONS

In the present investigation, analysis of variance revealed that significant variation existed among various characters. The PCV was found higher than GCV for all the characters. Characters like fruit yield per plot, average fruit weight, fruit yield per vine, sex-ratio, vine length, number of primary branches, number of fruits per vine, and fruit diameter showed high heritability with genetic advance as percent of mean indicating the preponderance of additive gene effect for these characters. Therefore, direct selection will be effective through such traits for improvement of bitter gourd.

FUTURE SCOPE

The present study provides the basis of selecting superior bitter gourd genotypes based on genetic variability. Future research can focus on multi-location trials, molecular characterization and hybrid development. This will help in breeding high yielding, disease-resistant and region-specific varieties.

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Conflict of Interest. None.

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