

## Morphological Analyses Define the Genetic Diversity of Indian Bitter Gourd (*Momordica charantia* L.)

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### ABSTRACT

Twenty seven diverse bitter gourd genotypes were collected from NBPGR, Thrissur, Kerala, India and grown in a Randomized Block Design (RBD) with three replications at Sri KondaLaxmanTelangana State Horticultural University, Hyderabad (Telangana) during the *rabi* season of 2017-2018. There were significant differences among the genotypes for the traits examined. A wide range of variation was observed for all characters which represents the variation was high and genotypes were rich in diversity. The wide variation in these yield related traits will be useful for selecting best genotypes with high yield. The long sized fruits with wide diameter generally consisted more number of seeds as compare to normal and small fruited genotypes because it consisted more space for seed development within the flesh. Cluster analysis of 27 genotypes based on 18 quantitative traits was indicated that all the genotypes

were resolved into eight major clusters. The genotypes from these distant clusters may be used in crop improvement program to produce populations with wide variability and with transgressive segregants possessing high yielding and nutrition rich fruits.

**Keywords** Bitter gourd, Genotypes, Diversity, Cluster analysis, Yield.

### INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is one of the most important cucurbitaceous vegetable crops grown widely all over the world. It is a very versatile vegetable for culinary purposes. Bitter gourd belongs to the family cucurbitaceae and is native of India, with a secondary center of diversity in China and South East Asia (Gruthe 1977). Bitter gourd is a typical day neutral plant and is mainly cross-pollinated. It is a warm season crop reasonably tolerant to saline conditions and grows under wide range of soil and climatic conditions. In India bitter gourd is grown in wild and cultivated form covering an area of 96,000 ha with an annual production of 1085 lakh MT with productivity of 11 MT/ha (NHB 2017-2018). Bitter gourd (syn. bitter melon or bitter squash ; *Momordica charantia* L.) is an economically important and nutritious vegetable of Cucurbitaceae family that is widely cultivated in India, China, Malaysia, Africa, and South America (Raj *et al.* 1993). Bitter gourd possesses comparatively high concentrations of ascorbic acid and iron as compared to other cucurbits (Behera 2004). Fruits of bitter gourd also have anti-oxidant, anti-microbial, antiviral activities and also

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used as a very popular traditional medicine in India, China and Central America for diabetes (Yeh *et al.* 2003) and other health promoting substances such as charantin (Yeh *et al.* 2003) and vicine (Dutta *et al.* 1981). Bitter melon also reported to have anti-cancer property, seeds are rich in  $\alpha$ -eleostearic acid and fruits contain 15, 16-dihydroxy- $\alpha$ -eleostearic acid which have been found to induce apoptosis of leukemia cells *in vitro* (Kobori *et al.* 2008), extract from bitter melon or *Karela* causes a chain of events which helps to kill breast cancer cells and prevents them from multiplying (Ray 2010, Ray *et al.* 2010). White-fruited Indian varieties are very rich in polypeptide-p,

phenolics, polyphenolic compounds and natural oxidants and antioxidants (Krawinkel and Keding 2006). In India *M. charantia* have relatively broad phenotypic species variation (i.e., sex expression, growth habit, maturity and fruit shape, size, color and surface texture (Behera *et al.* 2006) of provide for genetic diversity analysis on morphological basis has is the pre-breeding step to know the diversity and similarity among genotypes. Therefore, a study was designed to assess the genetic diversity among 27 diverse bitter melon accessions using morphological parameters to identify potentially useful germplasm for crop improvement.

**Table 1 (a).** Mean performance of 27 genotypes of bitter melon in terms of yield and its related characters.

Sl. No.	Genotypes	Vine length (cm)	Number of primary branches per vine	Number of nodes per vine	Inter-nodal 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
	Grand mean	269.80	435.66	46.50	6.03	40.54	49.06	10.48	13.89
	SEm $\pm$	13.39	1.2831	1.27	0.36	1.57	1.14	0.42	0.48
	CV (%)	8.60	0.51	4.73	10.43	6.74	4.02	6.94	6.02
	CD (p=0.05)	38.01	3.64	3.60	1.03	4.48	3.23	1.19	1.37
	Range	177.73-363.30	8.60-21.63	30.30-66.10	4.30-9.08	32.40-48.73	42.40-60.06	7.10-14.88	10.63-19.40

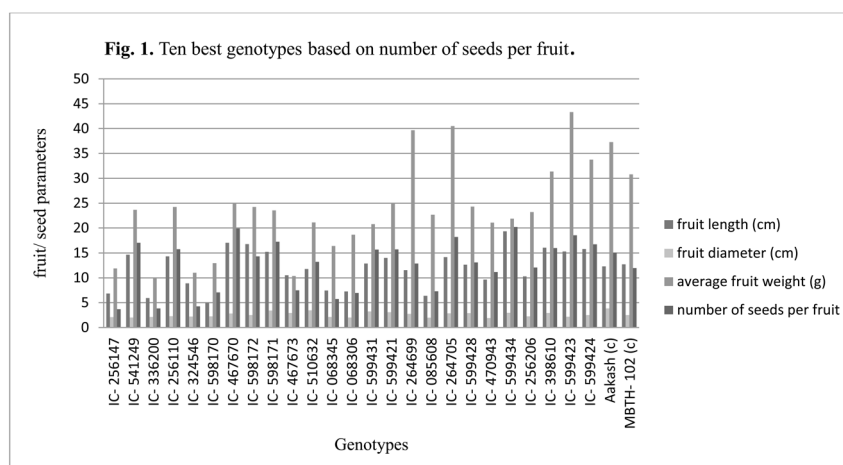
Table 1 (b). Continued..

Sl. 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
	Grand mean	62.608	135.999	16.29	24.01	12.02	2.53	27.33	12.63	15.02	2.19
	SEm ±	3.78	8.43	0.71	1.77	0.40	0.15	3.12	0.47	0.35	0.12
	CV (%)	10.47	10.74	7.58	12.75	5.87	10.16	19.82	6.49	4.07	9.76
	CD (p=0.05)	10.74	23.93	2.02	5.02	1.15	0.43	8.87	1.34	1.00	0.35
	Range	43.51-74.76	90.60-170.96	13.46-20.70	9.86-43.3	4.93-19.30	1.91-3.85	12.26-51.93	3.66-20.20	7.96-21.81	0.46-6.93

## MATERIALS AND METHODS

Twenty seven diverse bitter gourd genotypes viz., IC-256147, IC-541249, IC-336200, IC-256110, IC-324546, IC-598170, IC-467670, IC-598172, IC-598171, IC-467673, IC-510632, IC-068345, IC-068306, IC-599431, IC-599421, IC-264699, IC-085608, IC-264705, IC-599428, IC-470943, IC-599434, IC-256206, IC-398610, IC-599423, IC-599424 were collected from NBPGR, Thrissur, Kerala, India and with two check varieties Aakash (c) MBTH-102 (c) grown in a Randomized Block

Design (RBD) with three replications at college of horticulture, Mojerla, SKLTSHU, Hyderabad (Telangana) during the *rabi* season of 2017-2018. In each replication, seeds of each genotype were sown on 2 m long rows at spacing of 0.5 m between plants. The crop was managed as per recommended package of practices. Ten randomly selected plants were tagged for data recording for eighteen horticultural traits viz., vine length (cm), number of primary branches per vine, number of nodes per vine, intermodal length (cm), number of days to first male flower appearance, number of days to first female flower

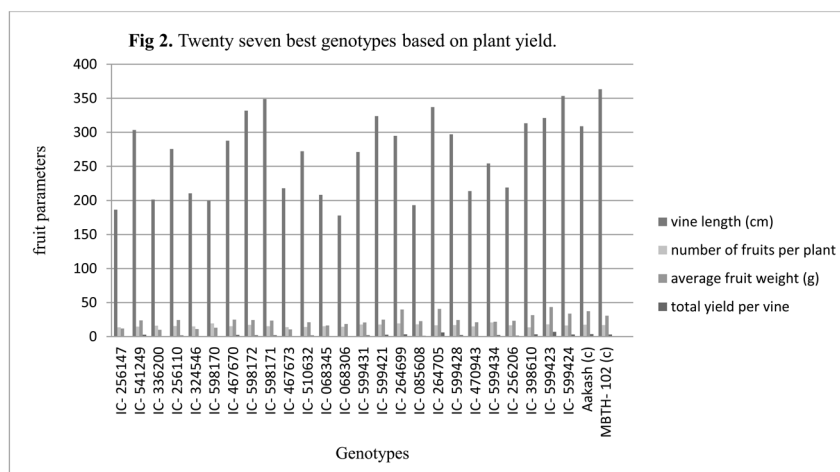


**Fig. 1.** Ten best genotypes based on number of seeds per fruit.

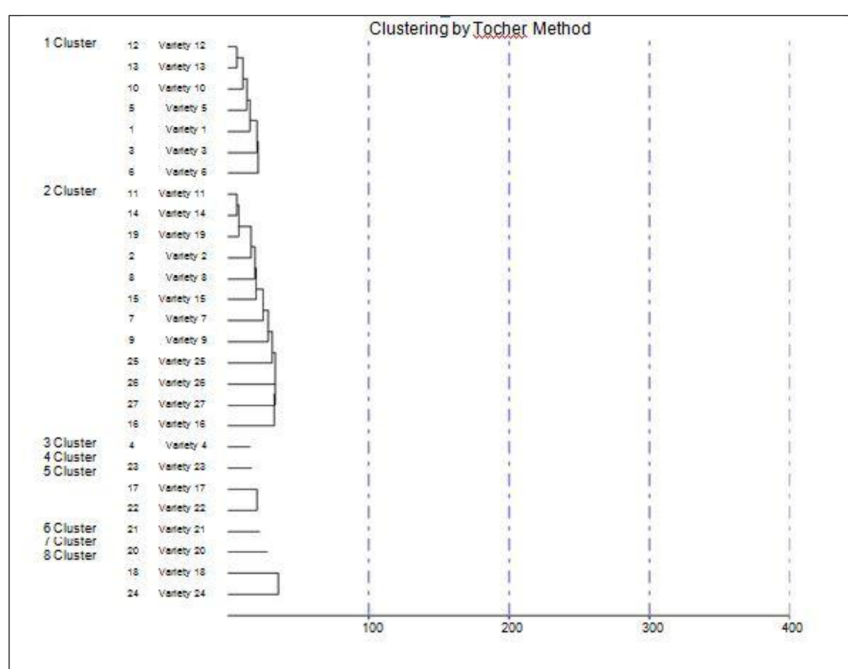
appearance, node at which first male flower appears, node at which first female flower appears, days to first fruit harvest, days to last fruit harvest, number of fruits per vine, average weight of the fruit (g), fruit length (cm), fruit diameter (cm), fruit yield per vine (kg), number of seeds per fruit, 100 seed weight, incidence of fruit fly infestation (%). The data were analyzed following standard statistical techniques and subjected to analysis of variance according to Panse and Sukhatme (1967).

## RESULTS AND DISCUSSION

The mean performance, range and standard error of difference (SE) values are presented in Table 1. A wide range of variation was observed for all characters which represents the variation was high and genotypes were rich in diversity. The widest range was recorded for vine length (177.73–363.30 cm) followed by days to last fruit harvest (90.60–170.96 days), fruit fly infestation (12.26–51.93 %), number



**Fig 2.** Twenty seven best genotypes based on plant yield.



**Fig. 3.** Genetic similarity relationships based on Jaccard's coefficient of similarity (Jaccard 1908) after cluster analysis of Indian bitter gourd (*Momordica charantia* L.) accessions on phenotypic basis.

of nodes per vine (30.30–66.10), average fruit weight (9.86–43.30 g), days to first fruit harvest (43.51–74.76 days), number of days to first female flower appearance (42.40–60.06 days), number of seeds per fruit (3.66–20.20), number of days to first male flower appearance (32.40–48.73), 100 seed weight (7.96–21.81 g), number of primary branches per vine (8.60–21.63), fruit length (4.93–19.30 cm), nodes at which first female flower appears (10.63–19.40), nodes at which first male flower appears (7.10–14.88), number of fruits per vine (13.46–20.70), fruit yield per vine (0.46–6.93 kg), internodal length (4.30–9.08 cm) and fruit diameter (1.91–3.85 cm). The wide variation in these yield related traits will be useful for selecting best genotypes with high yield.

The graphical presentation (Fig. 1) revealed that fruit length and fruit diameter was positively associated with number of seeds per fruits. The long sized fruits with wide diameter generally consisted more number of seeds as compare to normal and small fruited genotypes because it consisted more space for

seed development within the flesh. Moreover, there were non-significant relationship between number seeds per fruit and fruit yield per vine (kg).

However, (Fig. 2) represented that the collective effects of vine length(cm), number of fruits per vine and average fruit weight (g) enhanced fruit yield per vine (kg). Therefore these three parameters i.e., vine length (cm), number of fruits per vine and average fruit weight (g) were major yield contributing traits in bitter gourd. Similar results were obtained for two important traits contributes towards genetic divergence were number of fruits per vine and fruit yield per plant in bitter gourd (Quamruzzaman *et al.* 2008a), pumpkin (Masud *et al.* 1995) and days to first female flower anthesis, fruit diameter, average fruit weight and number of fruits per plant contributing major portion of the total genetic diversity in ridge gourd (Quamruzzaman *et al.* 2008b) offer a scope for genetic improvement and deserve to be included as selection criteria in bitter gourd.

Cluster analysis of 27 genotypes based on 18

quantitative traits was performed by statistical software and a dendrogram was constructed as depicted in Fig. 3. It was observed that all the genotypes were resolved into eight major clusters. Some of genotypes were so divergent in all the character; hence each single genotype formed a separate cluster. Thus four clusters viz., III (IC-256110), IV (IC-398610), VI (IC-599434), VII (IC-470943) were solitary with one genotype in each cluster. The two genotypes were also divergent in some character, hence they have formed two separate clusters viz., V (IC-085608, IC-256206), VIII (IC-264705, IC-599423). The remaining two clusters were having maximum number of genotypes. Cluster II was largest with 12 genotypes viz., (IC-510632, IC-599431, IC-599428, IC-541249, IC-598172, IC-599421, IC-467670, IC-598171, IC-599424, IC-264699, Aakash (C), MBTH-102 (C) followed by cluster I with 7 genotypes viz., (IC-068345, IC-068306, IC-467673, IC-324546, IC-256147, IC-336200 and IC-598170). The diversity in morphological traits, i.e., growth habit, maturity and fruit length and fruit diameter of *M. charantia* L. in India provide for relatively broad phenotypic species variation (Robinson and Decker-Walters 1999, Behera *et al.* 2006).

The genotypes from these distant clusters may be used in crop improvement program to produce populations with wide variability with transgressive-segregants possessing high yielding and nutrition rich fruits.

#### REFERENCES

- Behera TK (2004) Heterosis in bitter gourd. In: Singh PK, Dasgupta SK, Tripathi SK (eds). Hybrid Vegetable Development. The Haworth Press, New York, USA, pp 217–221.
- Behera TK, Dey SS, Sirohi PS (2006) ‘DBGy-201’ and ‘DBGy-202’: Two gynoeocious lines in bitter gourd (*Momordica charantia* L.) isolated from indigenous source. *Ind J Genet Pl Breed* 66 : 61–62.
- Dutta PK, Chakravarty AK, Chowdhary US (1981) Vicine, a favisminducing toxin from *Momordica charantia* L., seeds. *Ind J Chem* 20 : 669–671.
- Jaccard P (1908) Nouvelles recherchesurla distribution florale. *Bull Soc Vanddoise Sci Nat* 44 : 223–270.
- Kobori M, Ohnishi-Kameyama M, Akimoto Y, Yukizaki C, Yoshida M (2008) A-Elleostearic Acid and Its Dihydroxy Derivative Are Major Apoptosis Inducing Components of Bitter Gourd. *J Agric Food Chem* 56 (22) : 10515–10520.
- Krawinkel MB, Keding GB (2006) Bitter gourd (*Momordica charantia*): A dietary approach to hyperglycemia. *Nature Rev* 64 : 331–337.
- Masud MAT, Chowdhury MAZ, Hossain MA, Hossain SMM (1995) Multivariate analysis in pumpkin (*Cucurbita moschata* Duh ex Poir). *Bangladesh J Pl Breed Genet* 8 (1-2) : 45–50.
- Panse VG, Sukhatame PV (1967) Statistical Methods of Agriculture Workers, Indian Council of Agricultural Research, New Delhi.
- Quamruzzaman AKM, Rahman MH, Islam MN, Rahman SML, Sarker BC (2008a) Genetic diversity in land races of ridge gourd. *Bangladesh Res Publ J* 1 (1) : 5–8.
- Quamruzzaman AKM, Rashid MA, Ali MM, Alam AKMM, Rahman MM (2008b) Genetic diversity in bitter gourd (*Momordica charantia* L.). *Bangladesh J Agric Res* 33 (1) : 129–134.
- Raj M, Prasanna NKP, Peter KV (1993) Bittergourd *Momordica* ssp. In: Kalloo G, Berg BO (eds). Genetic Improvement of Vegetable Crops, Pergmon Press, Oxford, UK, pp 239–246.
- Ray Ratna (2010) Possible Cancer Cure in ‘Karela’, also known as Bitter Melon. The Chakra, 26 February.
- Ray RB, Raychoudhuri A, Steele R, Nerurkar P (2010) Bitter Melon (*Momordica charantia*) extract Inhibits Breast Cancer Cell Proliferation by Modulating Cell Cycle Regulatory Genes and Promotes Apoptosis. Mar 1, *Cancer Res* 70 (5) : 1925–1931.
- Robinson RW, Decker-Walters DS (1999) Cucurbits. CAB International. Wallingford, Oxford, UK, pp 226.