



Studies on genetic divergence for yield and quality traits in bitter gourd (*Momordica charantia* L.)

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ARTICLE INFO

Article history:

Received:22nd June 2021

Revision Received:16th August 2021

Accepted:22nd September 2021

Key words: Bitter gourd, Genotypes, Genetic divergence, Yield, Quality traits

ABSTRACT

Twenty genotypes of bitter gourd (*Momordica charantia* L.) based on twenty-one characters were studied in a field experiment conducted at Horticulture Research Farm-I, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya-vihar, Rae Bareilly Road, Lucknow-226025, (U.P.), India, during the *summer season* of 2018-19 and 2019-20. The objectives of the study were to estimate the genetic diversity among the genotypes for different characters including marketable fruit yield per plant. There was a great deal of significant variation among the genotypes for all the characters. The inter-cluster distance between cluster II and V followed by cluster II and IV was the highest and distances between other clusters were more or less intermediate. Intermediate diverse parents have more chance to contribute diversity in the subsequent generations. The highest cluster means the value of marketable fruit yield per plant was observed in cluster IV followed by cluster III and cluster II. Genetically distant parents are usually able to produce maximum diversity. Considering the magnitude of genetic distance, the magnitude of cluster means for different characters and the maximum number of the genotypes was observed in cluster number I followed by cluster number II which contained 9 and 8 entries, respectively, which compared to all genotypes and the suitable for future hybridization programme.

1. Introduction

Bitter gourd (*Momordica charantia* L.; $2n=2x=22$) is a commercial and medicinal vegetable, belongs to the family Cucurbitaceae. It is an annual as well as a perennial climber. It is also considered as balsam pear, bitter melon and maidan apple (Morton, 1967). It is a monoecious and highly cross-pollinated crop in which a large amount of variation has been observed for most of the economically important traits. Wild *Momordica charantia* var. *abbreviata*, a native of Asia and possibly the ancestor of domesticated (Degener, 1947).

Cucurbits occupy a unique place among the various vegetable crop groupings. Liberty Hyde Bailey developed the term "cucurbits" to describe cultivated species. Since the early 1920 century, the word has been used to describe not just cultivated forms, but also wild forms. In the Cucurbitaceae family, there are approximately 100 genus and 750 species that are fairly evenly distributed across the new

and old world tropics (Yamaguchi, 1983). In India, there are 38 endemic species and a further 38 non-endemic species in 34 genus comprising 108 species. It is caused by a lack of explicit knowledge of their utility, untamed plant genetic modification of specific value to people in the area and even the worldwide people are frequently overlooked in germplasm expedition and cumulative impacts. Considering the implementation of novel crops and better species, wild species play an important role, particularly in forest and rural communities, in which many people appear to collect and eat wild obtained plants for nourishment. In the terms of bitter gourd ranks first among the cucurbits because of higher nutritional value due to its high content of all necessary vitamins and minerals, particularly vitamin-A. (210IU/100g), Vitamin-C (88 mg/100g), iron (1.8 mg/100g), phosphorus (55 mg/100g) calcium (20 mg/100g), and calories 25 regular use prevents many complications such as hypertension, eye

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complication, neuritis and defective metabolism of carbohydrates. It increases the body's resistance to infection. The bitter gourd is specifically used as a folk medicine for diabetes. It contains alkaloids *viz.*, Momordicin and cucurbitacin while the skeleton is rich in momordicosides-glycosides of tetracyclic triterpenoids with cucurbitane (Chandravandna and Chandra, 1990). The fruit of bitter gourd are reported to have appetising, cooling, stomachic, antihelminthic, vermifuge, antipyretic, aphrodisiac and carminative properties (Blatter *et al.* 1935). India is the second largest producer of vegetables in the world next only to China, which share about 15 percent of the world's output of vegetables and about 5 percent of the total cropped area in the country. The current vegetable production level is over 183.3 million tonnes from an area of 10 million hectares. During 2017-18, the bitter gourd crop had average productivity of 19.7 tonnes per hectare and the area was 0.97 million hectares and production was 1137 million tonnes (2017-18) all over India. However, in Uttar Pradesh, it is a major vegetable crop with area of 1.97 lakh hectares, 19.77 lakh tonnes production and 10.9 tonnes per hectare productivity based on the National Horticulture Board report (NHB) 2018.

2. Materials and methods:

The experimental material comprised of 20 bitter gourd genotypes obtained from various institutes was carried out at the field of the Horticulture Research Farm-I of the Department of Horticulture, School of Agricultural Sciences and Technology, Babasaheb Bhimrao Ambedkar University Vidya vihar Raebareli Road Lucknow- 226025 (U.P.), India during the *summer season* 2018-19 and 2019-20. Geographically Lucknow is situated at 26° 76' North and latitude, 80° 92' East longitude and the altitude of 123 meters above mean sea level (MSL). The experiment was laid out in Randomized Block Design (RBD) and replicated thrice at individual plot size (3.0 m × 2.0 m). Row-to-row and plant-to-plant distances are maintained (2.5 m × 0.5 m), respectively. The field had sandy loam soil, low in organic carbon and slightly alkaline in nature (pH 8.0). Intercultural practices were carried out on a regular basis across the cropping season to ensure optimum growth and development of plants. For optimal seedling survival and prosperity, solely healthy seedlings were maintained per pit. To grow healthy crops, all conventional agronomic methods for the region were being used. For the data observation, 15 physical characters and 6 chemical characters in the field as well as laboratory condition were considered *viz.*, Node number to first staminate flowers, Node number to first pistillate flowers, Days to anthesis of first staminate flowers, Days to anthesis of first pistillate flowers, Days to first fruit harvest, Vine length (m), Fruit length (cm), Nodes per plant, Number

of branches per plant, Number of seeds per fruit, Fruit diameter (cm), Number of fruits per plant, Seeds weight per fruit (g), Average fruit weight (g), Ascorbic acid (mg/100g), Reducing sugar (%), Non-reducing sugar (%), Total sugars (%), Total soluble solids (T.S.S.)⁰Brix, Titratable acidity (%) and Marketable fruit yield per plant (kg). The standard technique for calculating statistical analysis of the data acquired in many sets of experiments was followed by **Mahalanobis D²** statistics.

3. Results and discussion:

Mahalanobis D² statistics were used to investigate genetic divergence within twenty genotypes of bitter gourd. Twenty bitter gourd genotypes were classified into five different non-overlapping clusters in this study. The results suggested that the genotypes had a lot of variation. The genotypes of genetically diverse were frequently sold in the main groups in the aforementioned genetic divergence evaluation. However, genotypes from the same specific region were identified to be clustered together with the same cluster. It became possible to see genotypes from various origins places or from the same geographical area grouped together in the same cluster. It is suggested there is no relationship between genetic and geographical diversity. A perusal of data shows various clustering patterns of different genotypes of bitter gourd in Table-1. Grouping of genotypes into V clusters revealed that the extant germplasm included a great deal of variation among the various characteristics. Cluster number I was followed by cluster number II which contained 9 and 8 entries, respectively. The minimum number of clusters III, IV and V which had one entry from the remaining clusters, respectively, which compared to all genotypes. A similar revelation was also reported by Dey *et al.* (2007), Remsi (2012), Shalini *et al.* (2000) and Khan (2006). The D² values had signed deals at intra and inter-cluster distances given in Table-2. The intra cluster D² values varied from 0.00 (cluster III, VI and V) to 127.20 (cluster II). The maximum inter-cluster distance was observed between clusters II to V (401.57), members of these two clusters were genetically extremely different from one another, implying that they were genetically quite different. The inter-cluster values between cluster II and V (401.57) followed by cluster II and IV (295.76), cluster IV and V (276.66), cluster II and III (272.23), cluster I and V (231.71), cluster I and II (201.99), cluster I and IV (167.65), cluster III and V (164.50) and cluster I and III (161.99) were very high. The minimum inter-cluster D² values were recorded in the case of clusters III and IV (155.11). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters. While lower inter-cluster values between the clusters suggested that the genotypes of these clusters were not much genetically diverse from each other.

Further the crossing between lines of distant clusters may give rise desirable segregates. Similar findings were also recorded by Rashid (2000), Rao (1964) and Ganesh *et al.* (2007). An assessment of the significance of features in the genetic divergence of twenty genotypes of bitter gourd had been given in Table-3. The highest manifestation of the contribution of genetic divergence was made by average fruit weight (28.95%) followed by total sugars (15.79%), total soluble solids (12.11%), days to anthesis of first pistillate flowers (9.47%) and Titratable acidity (8.95%). The genetic divergence were moderate in manifestation genetically in the available genotypes of characters was a number of branches per plant and reducing sugar (4.74%) followed by nodes per plant and non-reducing sugar (4.21%), days to anthesis of first staminate flowers (2.63%), number of seeds per fruit (1.58%), days to first fruit harvest and ascorbic acid (1.05%) and number of fruits per plant (0.53%) were low in the manifestation of total genetic divergence in the available germplasm. The genetic divergence were negligible in the available genotypes of characters was node number to first staminate flowers was after that node number to first pistillate flowers, vine length, fruit length, fruit diameter, seeds weight per fruit, marketable fruit yield per plant (0.00). The contribution of these traits for total genetic divergence was also reported by Biju (2001), Devmore *et al.* (2007) and Parhi (1993).

4. Conclusion:

In the present study, maximum number of genotypes find place in cluster I while, as cluster III, IV and V is monogenetic. The cluster with high degree of divergence would produce more desirable breeding material for achieving maximum genetic advance. The genotypes of different geographic origin were randomly distributed in the clusters which means that geographical diversity does not necessarily represented genetic diversity. Hence, it is suggested to cross between the genotypes selected from most distant clusters with high mean performance to get desirable transgressive segregants.

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Table-1: Clustering pattern of 20 genotypes of bitter gourd on the basis Mahalanobis (D^2) statistics (Pooled data basis)

Cluster No.	Cluster pattern	Genotypes
I.	9	Arka Harit (G_1), Narendra Barahmasi-1 (G_3), Pusa Hybrid-1 (G_5), Narendra Barahmasi-2 (G_{14}), Ultima-1405 (G_{18}), MC-23 (G_{20}), Kashi Urvasi (G_8), US-484 (G_{19}) and Arka Sujat (G_9)
II.	8	US-475 (G_{12}), UDIT-008 (G_{17}), Kalyanpur Sona (G_4), Kalyanpur Barahmasi (G_7), Meghana-2 (G_{11}), Pusa Hybrid-2 (G_{13}), Pusa Vishesh (G_2) and VRBT-23 (G_{16})
III.	1	Sagar (G_6)
IV.	1	Selection-5 (G_{15})
V.	1	Amanshri (G_{10})

Table-2: Average intra and inter clusters distance (D^2) values for five clusters in bitter gourd (Pooled data basis)

Cluster No.	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
Cluster-I	112.39	201.99	161.99	167.65	231.71
Cluster-II		127.20	272.23	295.76	401.57
Cluster-III			0.00	155.11	164.50
Cluster-IV				0.00	276.66
Cluster-V					0.00

Bold value shows intra cluster and normal value shows inter cluster

Table-3: Percent contribution of twenty one characters towards total genetic divergence in bitter gourd (Pooled data basis)

S. No.	Source	Times ranked 1 st	Contribution Percent
		1	2
1.	Node no. to I st staminate flowers	0	0
2.	Node no. to I st pistillate flowers	0	0
3.	Days to anthesis of I st staminate flowers	5	2.63
4.	Days to anthesis of I st pistillate flowers	18	9.47
5.	Days to first fruit harvest	2	1.05
6.	Vine length (m)	0	0
7.	Fruit length (cm)	0	0
8.	Nodes per plant	8	4.21
9.	No. of branches per plant	9	4.74
10.	No. of seeds per fruit	3	1.58
11.	Fruit diameter (cm)	0	0
12.	No. of fruits per plant	1	0.53

13.	Seeds weight per fruit (g)	0	0
14.	Average fruit weight (g)	55	28.95
15.	Ascorbic acid (mg/100g)	2	1.05
16.	Reducing sugar (%)	9	4.74
17.	Non-reducing sugar (%)	8	4.21
18.	Total sugars (%)	30	15.79
19.	T.S.S. (⁰Brix)	23	12.11
20.	Titrateable acidity (%)	17	8.95
21.	Marketable fruit yield per plant (kg)	0	0

Table 3. Cluster means for twenty one characters in bitter gourd (Pooled data basis)

Characters	C ₁	C ₂	C ₃	C ₄	C ₅	C ₆	C ₇	C ₈	C ₉	C ₁₀	C ₁₁	C ₁₂	C ₁₃	C ₁₄	C ₁₅	C ₁₆	C ₁₇	C ₁₈	C ₁₉	C ₂₀	C ₂₁
Cluster No.																					
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Cluster-I	11.57	11.59	39.23	39.14	53.22	5.06	18.54	55.04	16.31	20.72	5.82	12.57	3.27	67.59	86.41	0.78	0.47	1.34	3.60	0.28	2.75
Cluster-II	12.60	12.50	38.95	44.47	52.17	4.29	19.57	61.23	19.42	23.54	6.87	15.31	3.60	107.00	86.75	0.85	0.52	1.41	2.98	0.18	2.87
Cluster-III	12.33	15.33	51.44	49.27	46.33	5.56	22.90	61.33	15.50	20.50	5.90	12.50	3.22	55.00	86.33	0.94	0.62	1.61	4.54	0.27	3.10
Cluster-IV	11.67	7.83	36.33	55.06	61.83	5.65	24.40	40.83	19.83	22.00	7.49	12.17	2.54	63.83	79.50	0.70	0.45	1.40	5.23	0.31	3.55
Cluster-V	13.83	14.33	37.81	35.97	52.50	3.25	20.24	42.00	24.83	21.17	7.75	18.50	3.50	61.83	95.50	0.98	0.73	1.72	5.31	0.22	2.80

Characters:

- C₁: Node number to first staminate flowers, C₂: Node number to first pistillate flowers,
C₃: Days to anthesis of first staminate flowers, C₄: Days to anthesis of first pistillate flowers,
C₅: Days to first fruit harvest, C₆: Vine length (m),
C₇: Fruit length (cm), C₈: Nodes per plant,
C₉: Number of branches per plant, C₁₀: Number of seeds per fruit,
C₁₁: Fruit diameter (cm), C₁₂: Number of fruits per plant,
C₁₃: Seeds weight per fruit (g), C₁₄: Average fruit weight (g),
C₁₅: Ascorbic acid (mg/100g), C₁₆: Reducing sugar (%),
C₁₇: Non-reducing sugar (%), C₁₈: Total sugars (%),
C₁₉: Total soluble solids (T.S.S.)⁰Brix, C₂₀: Titratable acidity (%) and
C₂₁: Marketable fruit yield per plant (kg).

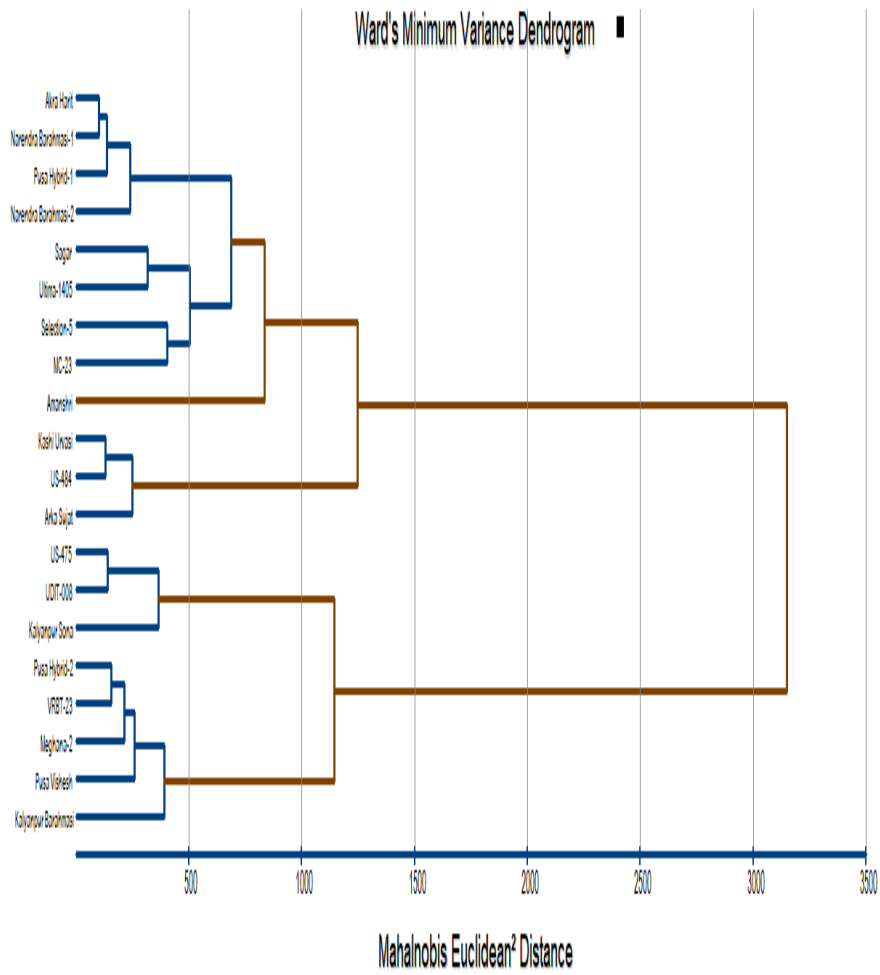


Fig 1. Clustering pattern

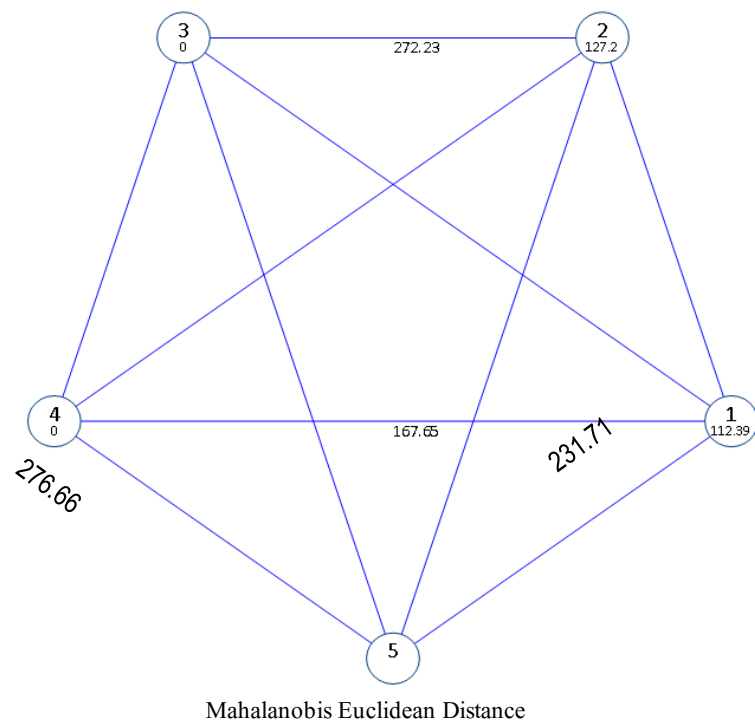


Fig 2. Average intra and inter clusters distance by Tocher Method