

Genetic Divergence for Yield and Yield Attributes in Bitter Gourd (*Momordica charantia* L.)

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ABSTRACT: Twenty diverse genotypes were evaluated at Horticulture research centre of SVP university of Agriculture and Technology, Meerut during spring season, 2022. The experiment was laid out in Randomized block design with three replications. The analysis of variance revealed significant among all the genotypes for all the characters under study. Mahalanobis D2 statistics revealed that a considerable genetic diversity was found among genotypes. Twenty genotypes of bitter gourd were formed in five clusters. The cluster I comprised highest 13 genotypes, Cluster II comprised 3 genotypes, Cluster V comprised 2 genotypes, cluster III and cluster IV comprised 1 genotype each respectively. The maximum intra-cluster distance was recorded in cluster II, cluster V, cluster I, cluster III and cluster IV with minimum intra-cluster distance, suggested that the genotypes of cluster II are more heterogeneous whereas, genotype of cluster II are comparatively homogenous based on intra-cluster distance. The maximum inter-cluster distance was recorded in cluster IV and cluster III whereas, the minimum inter-cluster distance was observed in cluster II and cluster I.

Keywords: Genetic Diversity, Bitter gourd, Yield and Cluster analysis.

INTRODUCTION

Bitter gourd [*Momordica charantia* L. (2n=2x=22)] belongs to the family Cucurbitaceae. It is also known as bitter melon, balsam pear, pare, or karela. Bitter gourd is of old-world origin and is a native of tropical Asia, particularly in the Indo Burma region. It is widely grown in India, Indonesia, Malaysia, China and tropical Africa. In India, it is estimated to cover 101 thousand ha whereas India produces around 1174 million tonnes with an average yield of 11.90 tonnes/ha of bitter gourd (NHB 2020-21). The *Momordica* genus contains roughly 60 species, with *Momordica charantia* L. being the most extensively grown. It is a monoecious crop that receives a lot of cross-pollination, and the majority of the commercially significant features show a lot of diversity. Fruit's form, size, and colour are where variation is most noticeable (Tyagi *et al.*, 2017).

The bitter gourd has a long history of use as a food and medicine. It is a potent plant that is rich in nutrients and made up of a wide variety of advantageous substances. These include phytochemicals, vitamins, minerals, and

antioxidants, all of which help explain its extraordinary adaptability in the treatment of a variety of diseases. The fruits are rich in folate (vitamin B9), vitamins B1, B2, and B3, vitamin C, vitamin A, vitamin E, and vitamin E. The high antioxidant capabilities of bitter melon, which are partly owing to the phenols, flavonoids, isoflavones, terpenes, anthroquinones, and glucosinolates that give it a bitter taste.

Consumption of vegetables has been increased owing to their high content of bioactive compounds like ascorbic acid, phenolic acids, carotenoids, flavonoids, proteins, minerals and dietary fibers while insufficient source of sugar. Among various vegetables bitter gourd is one of most nutritionally rich and plentiful medicinal properties of vegetable around the world (Islam *et al.*, 2011). The fruits, seeds, leaves, vines and roots of bitter gourd have been used as food and remedy from various types of diseases (Islam *et al.*, 2011). and has an important role in human diet for maintaining sound health. The seeds of bitter gourd are also rich source of protein and oil. Bitter gourd consumption has

tremendously increased day by day not only for their nutritional value but also their therapeutic value. Bitter gourd exhibited good sources of catechin, gallic acid, gentisic acid, chlorogenic acid and saponin compounds. Horax *et al.*, (2005) also revealed that bitter gourd also potential sources of antioxidant that would be used in food system.

Genetic diversity provides the raw material for evolution by natural selection (Fisher, 1930). The widespread evidence for evolution by natural selection in nature confirms the presence of genetic variation for traits that influence fitness (Endler, 1986), and a straightforward corollary is that individual genotypes must vary in ecologically important ways. However, the simple presence of heritable trait variation does not mean that different levels of genetic diversity will have predictable ecological consequences. For example, by allowing for increases in fitness, genetic diversity can

increase the population growth rate, but only if the population is not regulated by other factors and is experiencing directional selection (Fisher, 1930).

MATERIAL AND METHODS

An experiment named “Studies on Genetic Variability for yield and its components traits in Bitter Gourd (*Momordica charantia*)” was carried out during 2022 with three replications at the Horticulture Research Centre of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.). Total 20 genotypes of bitter gourd were collected from NBPGR, New Delhi. The collections were made from different source of supply comprising indigenous and exotic means of collections. The details of collected genotypes with source of supply are presented in Table 1.

Table 1: List of Genotypes Used in The Experimental Trial.

Sr. No.	Number of Genotypes	Source
1.	Pusa Aushadhi	NBPGR, New Delhi
2.	Pusa-do-mausami	NBPGR, New Delhi
3.	Pusa Rasdar	NBPGR, New Delhi
4.	Pusa Poorvi	NBPGR, New Delhi
5.	Pusa Vishesh	NBPGR, New Delhi
6.	Pusa Hybrid-2	NBPGR, New Delhi
7.	TCR-271 1C85647	NBPGR, New Delhi
8.	TCR-290 1C66023	NBPGR, New Delhi
9.	TCR-333 1C470535	NBPGR, New Delhi
10.	TCR-331 1C505638	NBPGR, New Delhi
11.	TCR-337 1C113876	NBPGR, New Delhi
12.	TCR-358 1C505630	NBPGR, New Delhi
13.	TCR-344 1C505640	NBPGR, New Delhi
14.	TCR-289 1C65972	NBPGR, New Delhi
15.	TCR-356 1C505621	NBPGR, New Delhi
16.	TCR-336 1C505637	NBPGR, New Delhi
17.	TCR-334 1C505629	NBPGR, New Delhi
18.	TCR-349 1C470546	NBPGR, New Delhi
19.	TCR-359 1C470553	NBPGR, New Delhi
20.	TCR-276A 1C85649A	NBPGR, New Delhi

RESULTS

A. Estimation of Genetic Divergence

The studies of genetic divergence among 20 genotypes of bitter gourd were carried out by using Mahalanobis D² statistics.

B. Cluster Mean

The cluster mean for sixteen different characters under study have been presented in Table 2. The result revealed that the days to germination were recorded highest mean value for cluster III (10.58) followed by cluster IV (9.58), cluster II (9.06), cluster I (8.41) and lowest in cluster V (7.12). The result revealed that node number to first male flower was recorded highest mean value for cluster III (17.50) followed by cluster IV (10.50), cluster II (10.25), cluster I (9.83) and lowest in cluster V (7.58). The result revealed that node number to first female flower was recorded highest mean value for cluster III (20.25) followed by cluster IV (13.75), cluster II (12.28), cluster I (12.03) and lowest in cluster V (9.96). The result revealed that days to first male flower was recorded highest mean value for cluster II

(41.69) followed by cluster IV (39.92), cluster III (39.42), cluster I (37.64) and lowest in cluster V (36.21). The result revealed that days to first female flower was recorded highest mean value for cluster. The result revealed that days to first male flower was recorded highest mean value for cluster II (45.50) followed by cluster IV (43.33), cluster III (42.17), cluster I (41.13) and lowest in cluster V (38.79). The result revealed that number of primary branches per plant was recorded highest mean value for cluster IV (11.92) followed by cluster I (11.62), cluster II (11.58), cluster III (9.79) and lowest in cluster III (9.42). The result revealed that number of leaves per plant was recorded highest mean value for cluster IV (47.67) followed by cluster II (44.83), cluster III (42.42), cluster I (40.24) and lowest in cluster V (32.29). The result revealed that vine length was recorded highest mean value for cluster IV (2.95) followed by cluster II (2.66), cluster I (2.41), cluster V (2.09) and lowest in cluster III (2.04). The result revealed that days to first fruit harvest was recorded highest mean value for cluster II (54.33) followed by cluster I (53.38), cluster

IV (52.83), cluster III (50.92) and lowest in cluster V (50.50). The result revealed that fruit length was recorded highest mean value for cluster II (12.90) followed by cluster IV (12.38), cluster I (10.39), cluster V (8.03) and lowest in cluster III (4.54). The result revealed that fruit diameter was recorded highest mean value for cluster IV (4.88) followed by cluster V (4.60), cluster II (4.42), cluster I (3.75) and lowest in cluster III (1.08). The result revealed that number of fruits per plant was recorded highest mean value for cluster III (34.92) followed by cluster IV (33.50), cluster I (28.76), cluster V (22.29) and lowest in cluster II (16.42). The result revealed that average fruit weight was recorded highest mean value for cluster IV (63.25) followed by cluster II (57.97), cluster I (52.15), cluster V (49.92) and lowest in cluster III (16.58). The result revealed that TSS was recorded highest mean value for cluster II (5.00) followed by cluster III (4.90), cluster IV (4.10), cluster I (4.09) and lowest in cluster V (4.08). The result revealed that fruit yield per plot was recorded highest mean value for cluster IV (1.83) followed by cluster I (1.18), cluster II (0.90), cluster V (0.88) and lowest in cluster III (0.54). The result revealed that fruit yield per hectare was recorded highest mean value for cluster IV (19.93) followed by cluster I (13.11), cluster II (9.83), cluster V (9.70) and lowest in cluster III (6.00).

C. Intra and Inter-Cluster Distance

The average intra and inter-cluster distance have been presented in Table 3. The result was recorded maximum intra-cluster distance in case of cluster II (2.754) followed by cluster V (2.736), cluster I (1.912), cluster III (0.013) and cluster IV with minimum intra-cluster (0.002), suggested that the genotypes of cluster II are more heterogeneous whereas, genotype of cluster II are comparatively homogenous based on intra-cluster distance and maximum inter-cluster distance (12.33) was recorded in case of cluster IV and cluster III. Whereas, the minimum inter-cluster distance (4.749) was observed in cluster II and cluster I.

D. Cluster Pattern

The cluster patterns of the 20 genotypes were grouped into 5 different non-overlapping clusters on the basis of genetic diversity by Tocher's methods presented in Table 4. The cluster I comprise highest 13 genotypes viz, Pusa Aushadhi, TCR-271 1C85647, TCR-290 1C66023, TCR-333 1C470535, TCR-337 1C113876, TCR-358 1C505630, TCR-344 1C505640, TCR-289 1C65972, TCR-336 1C505637, TCR-334 1C505629, TCR-349 1C470546, TCR-359 1C470553 and TCR-276A 1C85649A. Cluster II comprised 3 genotypes viz, Pusa do Mausami, Pusa Vishesh and Pusa Hybrid-2. Cluster V comprised 2 genotypes viz, Pusa Rasdar and TCR-356 1C505621. Whereas, the minimum genotypes comprised in cluster III and cluster IV viz., Pusa Poorvi and TCR-331 1C505638 respectively.

E. Contribution %

The contribution of various characters under study toward the expression of genetic divergence as presented in Table 5. The result showed that days to first female flower had maximum contribution (9.75) followed by number of primary branches per plant (8.44), fruit yield per hectare (8.22), days to germination (7.90), vine length (7.32), days to first fruit harvest (6.58), node number to first male flower (6.57), node number to first female flower (6.32), days to first male flower (6.20), TSS (6.06), number of leaves per plant (5.86), fruit length (5.33), average fruit weight (4.55), number of fruits per plant (4.26), fruit diameter (3.60) and lowest contribution of fruit yield per plot (3.05).

DISCUSSION

The problem of plant classification and plant selection and the utility of discriminate function for the purpose has been greatly emphasized (Fisher, 1936; Smith, 1936). Among the available statistical methods, principle component analysis, multiple range tests, inter specific correlation and regression analysis were used to classify genus brassica (Murty and Arunachalam 1966). A comparison of these methods with large number of characters has revealed the superiority and consistency of D2 analysis, conical and factor analysis which complementary to each other.

In the present study 20 genotypes of bitter gourd were subjected to D2 analysis using 16 component characters. According to D2 analysis, there were five clusters formed. According to the clustering pattern, there was enough divergence to allow for the development of unique character. The clustering pattern provided evidence that spatial variety was not a reliable indicator of genetic diversity. In light of this, Mahalanobis D2 analysis of quantitative traits is a potent technique for assessing genetic divergence among the material chosen, even from the same geographic region.

The cluster pattern of the 20 genotypes were grouped into 5 different non-overlapping clusters on the basis of genetic diversity by Tocher's methods presented in Table 4. Cluster I comprise highest 13 genotypes viz, Pusa Aushadhi, TCR-271 1C85647, TCR-290 1C66023, TCR-333 1C470535, TCR-337 1C113876, TCR-358 1C505630, TCR-344 1C505640, TCR-289 1C65972, TCR-336 1C505637, TCR-334 1C505629, TCR-349 1C470546, TCR-359 1C470553 and TCR-276A 1C85649A. Cluster II comprised 3 genotypes viz, Pusa do Mausami, Pusa Vishesh and Pusa Hybrid-2. Cluster V comprised 2 genotypes viz, Pusa Rasdar and TCR-356 1C505621. Whereas, the minimum genotypes comprised in cluster III and cluster IV viz., Pusa Poorvi and TCR-331 1C505638 respectively. The point of view has been supported by Singh *et al.* (2018); Singh *et al.* (2014); Tyagi *et al.* (2017); Jatav *et al.* (2019); Singh *et al.* (2020).

Table 2: Cluster Mean of Different Genotype of Bitter Gourd (*Momordica charantia* L.).

Clusters		Days to Germination	Node no. to first Male flower	Node to number first Female flower	Days to first male flower	Days to first female flower	Number of primary branches per plant	Number of leaves per plant	Vine length (m)	Days to first fruit harvest	Fruit length (cm)	Fruit diameter (cm)	Number of fruits per plant	Average fruit weight	TSS (Brix°)	Fruit yield per plot(kg)	Fruit yield/ha(q)
I	Mean	8.41	9.83	12.03	37.64	41.13	11.62	40.24	2.41	53.38	10.39	3.75	28.76	52.15	4.09	1.18	13.11
	SE±	0.54	1.20	1.07	1.08	1.34	0.26	0.90	0.12	1.29	1.80	0.26	3.02	4.97	0.37	0.06	0.73
II	Mean	9.06	10.25	12.28	41.69	45.50	11.58	44.83	2.66	54.33	12.90	4.42	16.42	57.97	5.00	0.90	9.83
	SE±	0.49	1.64	1.06	2.11	1.94	0.08	4.08	0.18	5.40	1.56	0.47	1.64	4.75	0.15	0.10	1.19
III	Mean	10.58	17.50	20.25	39.42	42.17	9.42	42.42	2.04	50.92	4.54	1.08	34.92	16.58	4.90	0.54	6.00
	SE±	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IV	Mean	9.58	10.50	13.75	39.92	43.33	11.92	47.67	2.95	52.83	12.38	4.88	33.50	63.25	4.10	1.83	19.93
	SE±	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
V	Mean	7.12	7.58	9.96	36.21	38.79	9.79	32.29	2.09	50.50	8.03	4.60	22.29	49.92	4.08	0.88	9.70
	SE±	0.53	0.12	2.06	0.77	0.18	0.29	3.36	0.06	0.59	0.54	1.77	7.72	15.56	1.18	0.07	0.63

Table 3: Average Inter and Intra Cluster(D² Value) Distances in 20 Genotypes of Bitter Gourd (*Momordica charantia* L.).

Clusters	I	II	III	IV	V
I	1.912				
II	4.749	2.754			
III	9.343	10.099	0.013		
IV	5.502	6.565	12.233	0.002	
V	4.982	7.513	10.309	9.652	2.736

Table 4: Number of Genotypes in each Cluster on the Basis of Mahalanobis D² Statistics.

Clusters	No. of Genotypes	Genotypes
I	13	Pusa Aushadhi, TCR-271 1C85647, TCR-290 1C66023, TCR-333 1C470535, TCR-337 1C113876, TCR-358 1C505630, TCR-344 1C505640, TCR-289 1C65972, TCR-336 1C505637, TCR-334 1C505629, TCR-349 1C470546, TCR-359 1C470553 and TCR-276A 1C85649A
II	3	Pusa Do Mausami, Pusa Vishesh and Pusa Hybrid-2
III	1	Pusa Poorvi
IV	1	TCR-331 1C505638
V	2	Pusa Rasdar and TCR-356 1C505621

Table 5: Contribution of Various Characters Toward Genetic Divergence.

Sr. No.	Characters	Contribution %
1.	Days to Germination	7.90
2.	Node Number to First Male Flower	6.57
3.	Node Number to First Female Flower	6.32
4.	Days to First Male Flower	6.20
5.	Days to First Female Flower	9.75
6.	Number of Primary Branches /Plants	8.44
7.	Number of Leaves Per Plant	5.86
8.	Vine Length(M)	7.32
9.	Days to First Fruit Harvest	6.58
10.	Fruit Length (Cm)	5.33
11.	Fruit Diameter (Cm)	3.60
12.	Number of Fruits Per Plant	4.26
13.	Average Fruit Weight	4.55
14.	TSS (°Brix)	6.06
15.	Fruit Yield Per Plot	3.05
16.	Fruit Yield/Ha	8.22

The average intra and inter-cluster distance have been presented in Table 3. The result was recorded maximum intra-cluster distance in case of cluster II (2.754) followed by cluster V (2.736), cluster I (1.912), cluster III (0.013) and cluster IV with minimum intra-cluster (0.002), suggested that the genotypes of cluster II are more heterogeneous whereas, genotype of cluster II are comparatively homogenous based on intra-cluster distance and maximum inter-cluster distance (12.33) was recorded in case of cluster IV and cluster III. Whereas, the minimum inter-cluster distance (4.749) was observed in cluster II and cluster I. Similar results

were also earlier reported by Behera *et al.* (2008); Shankar *et al.* (2009); Singh and Kandasamy (2020); Prasanth *et al.* (2020). Crosses that imply a parent's membership in the majority of divergence clusters should exhibit the highest levels of heterosis and a wide range of genetic architecture. Therefore, crosses between the genetically diverse genotypes of clusters I and II may be used to create high heterosis populations, segregate, and also to create hybrid bitter gourds based on the genetic diversity and superiority with respect to any of the traits the genotype may be identified.

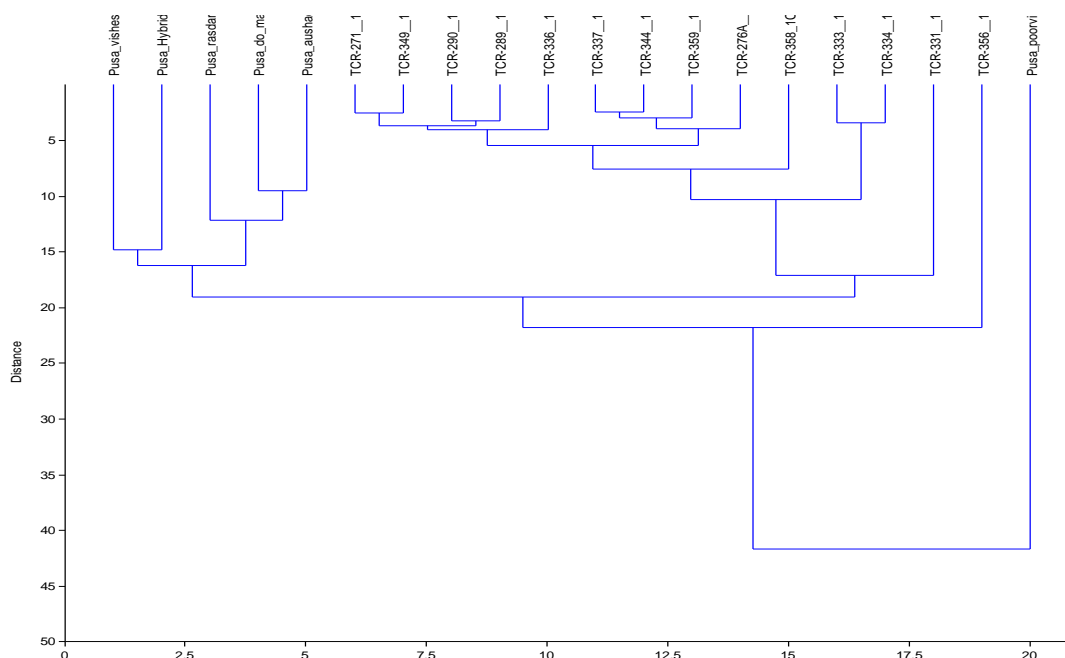


Fig. 1. Dendrogram Showing Diversity of Tomato Genotypes Generated using Mahalanobis D² Cluster Analysis.

CONCLUSIONS

Mahalanobis D² statistics on genetic divergence showed that a significant amount of genetic diversity was observed. There are five separate genetic clusters

formed from 20 genotypes. The cluster I (13 genotype) were the maximum number of genotype and minimum in cluster III and cluster IV (1 genotype) respectively. Based on the D² value in respect to the values for the

distances between and within clusters. Cluster II had the highest intra-cluster distance, which indicates that its genotype is more heterogeneous than cluster II's genotype, which is comparatively homogeneous based on intra-cluster distance. Cluster II was followed by cluster V, cluster I, cluster III, and cluster IV with intra-cluster distance. Clusters IV and III had the greatest inter-cluster distances that were seen. The smallest inter-cluster distance, however, was found in clusters II and I. As can be seen from the modest variance of D2 values, the genotype of the cluster does not differ greatly with respect to their relative genetics.

FUTURE SCOPE

Genetic divergence for yield and yield attributes in bitter gourd is promising, driven by advancements in genomics, breeding techniques, and interdisciplinary collaborations. These efforts can result in the development of high-yielding bitter gourd varieties with improved agronomic traits, nutritional quality, and resilience to biotic and abiotic stresses.

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Conflict of Interest. None.

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