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GENETIC DIVERSITY IN BITTER GOURD (*MOMORDICA CHARANTIA* L.) UNDER COASTAL ECOSYSTEMS

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Abstract

A study on genetic divergence was carried out on 40 genotypes of bitter gourd. They were grouped into six clusters by the application of clustering technique. The cluster II consisted of maximum number of genotypes (19) followed by cluster II comprising 13 genotypes, while the clusters III and IV comprised of 3 genotypes each. Cluster V and VI were found to be mono-genotypic. The intra and inter-cluster divergence were computed. The intra-cluster divergence ranged from 0.00 to 43.68. Cluster IV showed maximum intra-cluster divergence of 43.68 followed by cluster II (41.32) and cluster I (38.85). Cluster V and VI had the minimum intra-cluster divergence of 0.00. The maximum inter-cluster divergence was found between cluster I and VI (88.84), while the minimum inter-cluster divergence was found between clusters II and IV (51.97). Cluster III recorded the highest mean value (2.22) for fruit yield per vine while cluster I registered the lowest mean value (0.71).

Key words : Genotypes, genetic divergence, D^2 analysis, yield, clusters, *Momordica charantia*.

Introduction

Bitter gourd (*Momordica charantia* L.) is one of the important nutritious vegetable belonging to the family Cucurbitaceae. The chromosome number is (2n = 22). The fruits are prepared for consumption in many ways and quite commonly used fried, boiled and stuffed forms. The bitter principle present in the fruit is momordicin, a bitter glucoside which decides the taste. It is liked by some and said to contain some medicinal properties. It is particularly used for the treatment of general fevers, malaria and diabetes. From nutritional point of view, bitter gourd can be considered as nutrition rich fruit vegetable. It contains considerable amount of water (83-92%), carbohydrates (4.0-10.5%), protein (1.5-2.0%), fat (0.2-1.0%), minerals (0.5-1.0%) and fiber (0.8-1.7 %). Ripe fruits are rich in vitamin A. Among all cucurbits vegetables bitter gourd contains the maximum amount of minerals and vitamins.

Bitter gourd is a monoecious cucurbit cultivated almost throughout the country during the warm season. It occupies the third position next to onion and okra in the export trade. Vegetable production in India is quite in the Indian diet (The recommended level is 300g for adult and 85g for children but the consumption is only 120g for adult). Therefore, it is necessary to increase production through appropriate methods. However, in spite of its importance, adaptability and export potential, the crop improvement programmes undertaken in this crop is very much less. The common approach of parent selection based on per se performance per se does not necessarily lead to successful results. The selection of best parents for hybridization has to be based upon the complete genetic information and esteemed prepotency of potential parents. Furthermost, plant breeders identify genotypes by evaluating phenotypes, an understanding about the heritability is an important step towards the successful selection of superior cultivars. Improvement in yield is normally attained through the exploitation of the genetically diverse parents in breeding programmes.

Bitter gourd is a highly cross-pollinated crop. It has wide range of genetic variability and the crop envisages ample scope of its improvement through heterosis breeding. Crop improvement through hybridization will be effective if the information on the genetic architecture of the experimental population is available. Knowledge

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of the combining ability and gene action responsible for important characters is also essential.

Materials and Methods

The present experiment was carried out at the Shivapuri, Cuddalore, Tamil Nadu, India. The forty bitter gourd genotypes which were collected from different agro-climatic regions of India were used for the experiment and summarized as MC 1 to MC 40. The experiment was laid out in a randomized block design with 3 replications of each genotype. Pits of 30 cm × 30 cm × 30 cm size at 1.5 × 1.5 m spacing were dug diameter and 30 cm depth were taken and then basins were formed. In each pit, five seeds were sown. Sowing was done in such a way that in each replication there was a single row of five plants per accession. The cultural and management practices were adopted according to the package of practices recommended by Tamil nadu Agricultural University. The observation were recorded by selecting five random plants for 14 quantitative traits along with 2 qualitative traits. D^2 is the sum squares of difference between any two populations for each of the uncorrelated variables (ys) obtained by transforming correlated variables (xs) through pivotal condensation method. The square root of these D^2 values gives the general distance between the two populations. The significance of the D^2 values between any two populations is determined by taking D^2 values as the calculated value of X^2 for P degrees of freedom, where P is the number of characters considered. Based on degree of divergence (D^2 values) between any two genotypes, grouping of genotypes was done by using Tocher's method (Singh *et al*., 1977). In this method, the populations are arranged in order of their relative distances (D^2 values) from each other and a table is formed. Mahalanobis (1936) developed this model to determine divergence among, populations in terms of generalized group distance.

Results and Discussion

All the 40 genotypes were grouped into six clusters by the application of clustering technique. The constituents of different clusters are presented in table 1. The clusters II consisted of the maximum number of genotype (19) followed by cluster I comprising of 13 genotypes, while the clusters III and IV had 3 genotypes each. Cluster V and VI comprising one genotype. Therefore, genotypes originating at the same place might have developed different architectures. Likewise, genotypes at different places may possess similar characteristics. Thus, genetic diversity was the outcome of several factors along with a factor of geographical diversity. A similar trend of clustering pattern of diversification of genotypes based on origin was reported by Kumari *et al*. (2017), Angadi and Mulge (2018), Maurya *et al*. (2018) and Jatav *et al*. (2019). The intra and inter-cluster distance were computed and were presented in table 2. The intra-cluster distance ranged from 0.00 to 43.68. Cluster IV showed the maximum intra-cluster distance of 43.68 followed by cluster II (41.32) and cluster I (38.85). Cluster V and VI had the minimum intra-cluster distance 0.00 followed by cluster III (32.83). The maximum inter-cluster distance was found between cluster I and VI (88.84), while the minimum inter-cluster distance was found between clusters II and IV (51.97). Minimum inter-cluster distance was noticed between cluster II and IV, which explains that the genotypes in these cluster would have been evolved by similar evolutionary procedures even though their origin was different. Maximum inter-cluster distance was noticed between cluster I and VI (table 2). This wider distance indicated that the hybridization among the genotypes between these clusters would produce successful hybrids and desirable segregants in further generations. The lower intra-cluster distance was noticed in cluster V and VI which shows the closeness of genotypes included in the cluster, while the highest intra-cluster distance was recorded by the cluster IV. The limited gene exchange between the genotypes of the cluster may be the reason for the highest intra-cluster distance. Further selection for diverse characters could be a reason for such as high intra-cluster divergence. In addition to the general feature of variation and divergence indicated, this study also provides the information as of the potent character that contributes to the divergence. The most important trait found to cause maximum genetic divergence is sex ratio (29.23%), ascorbic acid content (19.62%), days to first female flower (12.05%) and days to first fruit harvest (8.59%). Maurya *et al*. (2018), Tyagi *et al*. (2017), Singh *et al*. (2014), Singh *et al*. (2013) contributed that sex ratio, ascorbic acid content, days to first female flower and days to first fruit harvest was a major character that caused genetic divergence.

Computing the cluster mean values, it was found that, the cluster III showed high values for ten of the characters *viz*, days to first male flower, node number of first female flower, node number of first male flower, vine length, days to first fruit harvest, fruit length, fruit girth, average fruit weight, seeds per fruits and fruit yield per vine. Interestingly, it is noticed that the genotype MC 13 from the same cluster III contributed for the characters *viz*., vine length, days to first fruit harvest, fruit girth, average fruit weight and fruit yield per vine. Hence, this genotype may serve as an ideal plant for hybridization programme

Table 1 : Clustering pattern of 40 genotypes on the basis of Mahalanobis D^2 statistics.

S. no.	Cluster	No. of genotypes	Genotypes
1	I	13	MC 24,MC 36, MC 26, MC 21, MC 29, MC 3, MC 19, MC 33, MC 27, MC 10, MC 23, MC 32, MC 9
2	II	19	MC 8, MC 39, MC 38, MC 5, MC 25, MC 40, MC 31, MC 4, MC 30, MC 7, MC 37, MC 11, MC 2, MC 22, MC 12, MC 35, MC 17, MC 6, MC 15
3	III	3	MC 1, MC 13, MC 20
4	IV	3	MC 18, MC 16, MC 28
5	V	1	MC 14
6	VI	1	MC 34

Table 2 : Intra and Inter cluster distance between genotypes of bitter gourd.

Cluster	I	II	III	IV	V	VI
I	1509.07**(38.85)**	3394.51**(58.26)**	7402.86**(86.04)**	4941.27**(70.29)**	7809.08**(88.37)**	7892.37**(88.84)**
II		1706.98**(41.32)**	3152.40**(56.15)**	2700.91**(51.97)**	3092.94**(55.61)**	3551.84**(59.60)**
III			1077.89**(32.83)**	6110.38**(78.17)**	2787.28**(52.79)**	2972.54**(54.52)**
IV				1908.32**(43.68)**	3721.71**(61.01)**	4590.94**(67.76)**
V					**(0.00)**	3468.31**(58.89)**
VI						**(0.00)**

Values in parenthesis indicates D value, Bold value indicates intra cluster distance

Table 3 : Cluster mean of 40 bitter gourd genotypes for various characters.

Characters	Clusters					
	I	II	III	IV	V	VI
Days to first male flower	43.80	39.32	34.37	42.46	38.31	35.43
Days to first female flower	53.67	48.87	43.79	52.03	40.24	43.60
Node number of first male flower	9.48	7.92	6.37	8.90	9.37	6.43
Node number of first female flower	17.52	15.87	13.15	17.40	13.50	13.36
Sex ratio	16.46	30.66	39.81	32.74	34.26	46.24
Vine length (m)	2.73	3.66	4.76	3.45	4.62	3.22
No. of primary branches per vine	10.00	12.29	15.18	10.48	16.50	14.50
Days to first fruit harvest	73.00	65.89	57.10	69.41	58.28	79.06
Fruit length (cm)	14.11	14.22	18.33	9.21	10.59	13.42
Fruit girth (cm)	11.65	10.83	14.14	8.12	8.33	10.35
Average fruit weight (g)	77.47	79.00	107.68	47.41	65.44	63.44
Number of fruits per vine	8.56	15.40	20.30	20.94	25.53	21.23
Seeds per fruit	14.62	13.17	19.13	8.31	8.33	12.28
TSS (Brix°)	5.20	4.91	5.21	4.80	3.21	6.28
Ascorbic acid content (mg/100g)	67.69	65.91	86.72	49.50	71.24	87.45
Fruit yield per vine (kg)	0.71	1.27	2.22	1.22	1.88	1.42

for improving the vine length, days to first fruit harvest, fruit girth, average fruit weight and fruit yield per vine. Similarly, the genotype MC 1 from cluster III had contributed for fruit length, seeds per fruit and ascorbic acid and node number of first male flower. The genotype MC 14 which falls under cluster V had contributed for the earliest female flowering and also observed more number of fruits and primary branches per vine. The genotype 24 which falls under cluster I has minimum sex ratio (male flowers for one female flower). The genotype MC 30 of cluster II possessed the earliest node of female flower while genotype 36 of cluster VI had maximum content of TSS. Among the six parents selected for hybridization programme, they fell into different divergent

clusters. MC 1 and MC 13 belongs to cluster III, while MC 14, MC 24 MC 30, MC 34 belongs to cluster V, I, II and VI, respectively. Thus from the present study the genotypes MC 1 and MC 13, MC 14, MC 24, MC 30 and MC 34 were identified as suitable parents for hybridization programme to develop superior varieties in bitter gourd.

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