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Studies on genetic divergence in bitter gourd (*Momordica charantia* L.)

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Abstract

The experiment was conducted during the spring-summer season, 2017 in Eastern Uttar Pradesh, to evaluate the nature and magnitude of genetic divergence among the thirty genotypes of bitter gourd were carried out by using Mahalanobis D^2 statistics. Thirty genotypes were grouped into 6 different non-overlapping clusters. Cluster III had the highest number of genotypes (8) followed by cluster II (7), cluster V (6), cluster IV (5) and cluster I, VI (2) whereas cluster I and VI had only two genotypes. The highest intra-cluster distance was observed for cluster VI recorded for (123.61) followed by cluster V (91.85), cluster I (69.08) and cluster II (62.75), cluster IV (47.92). The maximum inter-cluster distance observed between cluster III to cluster VI (231.577), which suggested that members of these two clusters are genetically very diverse to each other. The inter-cluster values between cluster II to cluster VI (222.683), cluster II to cluster V (220.722), cluster V to cluster VI (205.629), cluster I to cluster VI (187.421), cluster III to cluster V (148.762), cluster II to cluster IV (134.414) and cluster I to cluster V (133.185) were very high. The minimum inter-cluster distance was recorded in cluster I to IV (91.813) and cluster IV to V (104.356). Highest inter-cluster distances recorded indicated between two cluster pairs greater genetic divergence between the genotypes of those clusters, whereas, lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. The intra-cluster means for twelve characters in bitter gourd. Among 12 characters studied, average fruit weight (g) contributed maximum (27.82%) towards genetic divergence followed by fruit yield/plant (18.39%) and fruit length (12.64%) in bitter gourd. Ranking of genotypes based on intra-cluster mean performance for these characters which are major contributors of genetic diversity revealed its usefulness in selecting parents for heterosis breeding.

Keywords: Genetic divergence, bitter gourd, *Momordica charantia* L.

1. Introduction

Bitter gourd (*Momordica charantia* L.; $2n=2x=22$) is a commercial and medicinal vegetable, belongs to the family Cucurbitaceae and is an annual as well as perennial climber. Diverse morphological characters of *M. Charantia* provide a relatively broad phenotypic species-variation. The enlightenment about the nature and magnitude of genetic divergence is a need for selection of diverse parents which upon hybridization can result in productive hybrids. Although this crop has potential medicinal and economic values, there are only a few reports are available of multivariate analysis in bitter gourd (Singh *et al.*, 2013; Dey *et al.*, 2007) [8, 2]. Fruits and seeds of bitter gourd have essential medicinal properties which are very using our health conscious such as anti-HIV, anti-leukemic, anti-inflammatory, antimicrobial, anti-ulcer, antitumor and last but not the least the important anti-diabetic property. A various statistics tools are available for divergence analysis, among them only Mahalanobis's D^2 statistics is highly acceptable for determining the degree of divergence between populations and the relative contribution of several components to the total divergence and isolation of most appropriate parents. Heterosis communication and genetic divergence analysis are inadequate in bitter gourd. Therefore, this research was carried out to observe the nature and magnitude of genetic divergence among thirty genotypes of bitter gourd through diverse geographical origin and distribution.

Material and Methods

Thirty genotypes (including Pusa Do Mausami as check variety) of bitter gourd having diverse origin were evaluated at Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, during the spring-summer season, 2017.

The experiment was laid out in a randomized block design with three replications in individual plot size (3m x 2m). The distance maintained between row to row and plant to plant was 2m and 0.50m, respectively. Five plants were randomly selected from each plot in each replication. Recommend cultural practices and plant protection measures were followed to raise a healthy crop. Data were recorded on various parameters (Table 3). The data recorded on each character of different genotypes were statistically analyzed. The genetic divergence was estimated using D2 statistics of Mahalanobis (1928) [4]. The intra and inter-cluster distance were calculated according to Tocher's method envisaged by Rao (1952) [6].

Results and Discussion

There were significant differences among the genotypes for all the characters under this investigation indicated a considerable amount of genetic variability among 30 genotypes including one check variety (Pusa Do Mausmi). Based on D² values all the genotypes of bitter melon were grouped in six distinct non-overlapping clusters using Mahalanobis D² statistics. Thirty genotypes were grouped into 6 different non-overlapping clusters. Cluster III had the highest number of genotypes (8) followed by cluster II (7), cluster V (6), cluster IV (5) and cluster I, VI (2) whereas cluster I and VI had only two genotypes. (Table 1) The genotypes within the same cluster although formed specific cluster but were collected from different places. The clustering pattern of the genotypes revealed that the genotypes collected from the same place did not form a single cluster. This indicates that geographic diversity is not always related to genetic diversity. Similar results had been also reported by Islam *et al.*, 2010 [3]; Singh *et al.*, 2014 [9] in bitter melon. Intracluster distances were smaller than inter-cluster distances, show a considerable amount of genetic diversity among the genotypes studied.

The highest intra-cluster distance was observed for cluster VI recorded for (123.61) followed by cluster V (91.85), cluster I (69.08) and cluster II (62.75), cluster IV (47.92). The maximum inter-cluster distance observed between cluster III

to cluster VI (231.577), which suggested that members of these two clusters are genetically very diverse to each other. The inter-cluster values between cluster II to cluster VI (222.683), cluster II to cluster V (220.722), cluster V to cluster VI (205.629), cluster I to cluster VI (187.421), cluster III to cluster V (148.762), cluster II to cluster IV (134.414) and cluster I to cluster V (133.185) were very high. (Table 2), similar observations were also reported by Resmi *et al.*, 2012 [5], Devmore *et al.*, 2007 [1]; Dey *et al.*, 2007 [2].

The minimum inter-cluster distance was recorded in cluster I to IV (91.813) and cluster IV to V (104.356). Highest inter-cluster distances recorded indicated between two cluster pairs greater genetic divergence between the genotypes of those clusters, whereas, lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other.

A perusal of (Table-3) revealed that cluster I had shown minimum mean values for node number to anthesis of first staminate flower, node number to anthesis of first pistillate flower, days to anthesis of the first staminate flower. Cluster II had shown minimum mean values for average fruit weight. Cluster III had shown minimum mean values for fruit length, no. of fruits per plant. Cluster V showed maximum mean values for no. of nodes per vine, vine length, fruit yield per plant. Cluster VI had shown maximum mean values for days to anthesis of first pistillate flower, days to first fruit harvest and fruit diameter. Cluster IV showed maximum mean values for days to anthesis first staminate flower, fruit diameter, fruit yield per plant. Cluster III showed maximum mean value for vine length and average fruits weight. Cluster I showed maximum mean value for fruit length. The intra-cluster means for twelve characters in bitter melon. Among 12 characters studied, average fruit weight (g) contributed maximum (27.82%) towards genetic divergence followed by fruit yield/plant (18.39%) and fruit length (12.64%) in bitter melon. Ranking of genotypes based on intra-cluster mean performance for these characters which are major contributors of genetic diversity revealed its usefulness in selecting parents for heterosis breeding.

Table 1: Clustering pattern of 30 genotypes on the basis of Mahalanobis D² statistics

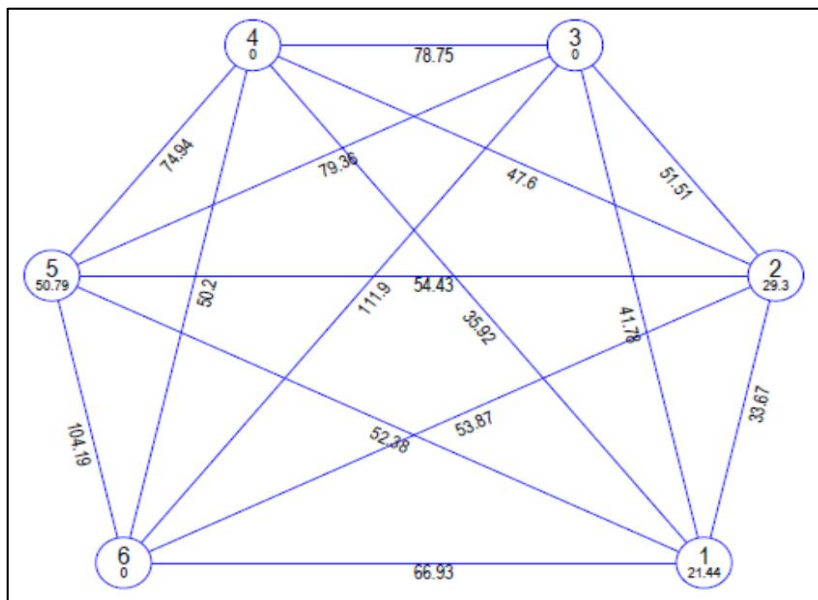
Cluster number	No. of genotypes	Genotypes
I	2	NDBT-11, NDBT-16
II	7	NDBT-3 NDBT-5, NDBT-6, NDBT-10, NDBT-14, NDBT-15, NDBT-16
III	8	NDBT-1, NDBT-17, NDBT-18, NDBT-20, NDBT-21, NDBT-26, NDBT-29, NDBT-30
IV	5	NDBT-2, NDBT-9, NDBT-12, NDBT-13, NDBT-19
V	6	NDBT-4, NDBT-7, NDBT-8 NDBT-24, NDBT-25, NDBT-28
VI	2	NDBT-27, NDBT-22

Table 2: Average of intra and inter- clusters D² values for six clusters

Cluster number	I	II	III	IV	V	VI
I	69.082	105.153	131.138	91.813	133.185	187.421
II		62.758	121.405	134.414	220.722	222.683
III			43.597	112.748	148.762	231.577
IV				47.929	104.356	116.980
V					91.855	205.629
VI						123.618

Table 3: Intra-cluster group means for twelve characters in bitter gourd

Clusters	Node No. of 1st Staminate Flower Appearance	Node No. of 1st Pistillate Flower Appearance	Days to Anthesis of 1st Staminate Flower Appearance	Days to Anthesis of 1st Pistillate Flower	Days to 1st Fruit harvest	No. of Nodes Per Vine.	Vine Length (m)	Fruit Length (cm)	Fruit Diameter (cm)	No. of Fruits Per Plant	Average Fruit Weight (gm)	Marketable Fruit Yield/Plant (kg)
I	8.330	11.913	40.553	45.233	59.687	52.760	2.577	17.717	3.690	23.230	103.570	2.070
II	10.264	13.341	41.864	46.867	60.895	54.715	3.079	16.087	3.749	23.779	75.356	1.478
III	9.867	14.100	41.700	46.900	60.700	62.567	3.533	11.000	3.300	17.400	123.367	1.756
IV	9.133	13.200	44.267	51.233	63.067	47.733	2.633	16.267	4.067	32.400	91.700	2.620
V	10.392	14.900	42.683	51.583	64.375	46.650	1.892	15.858	3.775	20.767	87.925	1.474
VI	10.833	13.200	41.933	45.133	56.100	65.933	2.800	15.800	2.800	34.400	58.333	1.786

**Fig 1:** Diagram showing intra and inter-cluster distances of 30 genotypes in the Bitter gourd

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