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Genetic divergence studies among different genotypes of bitter gourd (*Momordica charantia* L.)

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Abstract
A study was conducted during kharif 2019, in Uttar Pradesh, India, to evaluate the nature and magnitude of genetic divergence in 15 bitter gourd genotypes. Results revealed the presence of wide genetic diversity. The genotypes were grouped into 4 clusters based on Mahalanobis D2 statistics using Torcher's method. The clustering pattern of genotypes revealed that the genetic diversity was independent of the geographical diversity. Among the 4 clusters, maximum numbers of genotypes were found in cluster I, while clusters IV was found to be mono-genotypic. Among the 14 quantitative characters studied, number of fruits/plants constituted a maximum of 59.05% contribution to the divergence, followed by fruit yield (q/ha). 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, D^2

Introduction
Bitter gourd (*Momordica charantia* L.) is one of the important cucurbitaceous vegetables grown in India. Among the cucurbits, it is considered a prized vegetable because of its high nutritive value especially having ascorbic acid and iron. It is a large genus with many species of annual or perennial climbers of which *Momordica charantia L.* is widely cultivated. The crop is highly cross pollinated due to monoecy. Its native home is tropical Asia particularly, East India and south China. The somatic chromosome number of *Momordica charantia* is 2n=2x=22. Other species belonging to this genus are *M. dioca, M. cochinchinensis, M. balsamina, M. tuberosa, M. subangulata, M. denudata and* parents. *M. macrocarpa.*

In spite of the potential economic and medicinal importance of the crop, due attention has not been given towards a need based crop improvement programme. However, recently the cultivation of bitter gourd has become increasingly popular, because of the growing awareness of its antidiabetic property and nutritive value among consumers. Due to the efforts of many vegetable breeders marked improvement in yield has been achieved and a good number of new varieties and hybrids have been developed nevertheless, there is a long way to go with bitter gourd improvement work especially to get resistant source for pest and disease. Therefore, the improvement work should be focused on selection of genotypes for better yield, superior quality and resistant to biotic stresses.

The yield potential of bitter gourd in India is very low due to poor yielding varieties and high incidence of pests and diseases. One of the approaches to improve yield and quality is heterosis breeding. The importance heterosis breeding has been recognized widely in many vegetable crops. However, the pre-requisite of the heterosis breeding is the selection of the divergent.

Information on heterosis and genetic divergence analysis is inadequate in bitter gourd. The information about the nature and magnitude of genetic divergence is essential for selection of diverse parents which upon hybridization can result in productive hybrids. Evaluation of available germplasm assumes importance in this regard and is necessary.

Keeping foregoing points in view, a total of 15 bitter gourd genotypes were evaluated for the study of genetic divergence.

Materials and Methods

fifteen genotypes of bitter gourd selected from the germplasm collection obtained from IIVR Varanasi, IARI New Delhi and IIHR Bangalore were grown in Randomized Block Design with three replications during kharif 2019 at the Main Experimental Farm of Department of Horticulture, SHUATS, Prayagraj, UP, India Each replication consisted of a single row of 2.5 m for each entry with row-to-row and plant-to-plant spacing being 2 m and 1.5 m respectively agronomic practices were followed to raise a good crop. Five competitive plant were randomly selected in each entry for recording observation on node number of first male flower appearance, node number of first female flower appearance, days to anthesis of first male flower, days to anthesis of first female flower, number of male flowers, number of female flowers, average fruit weight (g), fruit diameter (cm), fruit length (cm), number of fruits plant -1, yield plant -1 (kg), number of branches plant-1 and vine length (m). However, observations were recorded on plot basis for days to 50% seedling emergence. The data were subjected to multivariate analysis of genetic divergence using Mahalanobis D2 statistic. Grouping of entries was done by Tocher's method.

Results and Discussion

The analysis of variance (ANOVA) revealed considerable amount of variability for the fourteen traits studied suggesting ample scope to identify desirable each genotypes. Based on the relative magnitude of D2 each values 15 genotypes were grouped into 4 different being 2 m.

Grouping pattern showed no clear relationship between geographical diversity and genetically diversity. The cluster-I followed by cluster-II and III was the largest comprising eight and four genotypes respectively. The result showed that geographical diversity was not necessarily a direct cause of genetic diversity. The geographical diversity has been disapproved to be an index of genetic diversity in several crops. Frequent exchange of breeding materials from one place to another and further selection may also be responsible for distribution of gene complex over distant locations. Thus, it is more appropriate to select genotypes for hybridization based on genetic diversity rather than geographical diversity. The intra cluster distance ranged from 0 to 640.01 and inter cluster distance (D) ranged from 924.01 to 3232.02 (Table 2). Maximum inter cluster D-value was observed between cluster-III and cluster-IV (3232.01) followed by cluster-I and cluster-III (2485.03). The average cluster means of 14 traits are presented in Table 3. Perusal of the table reveals that cluster-II had the highest mean value for yield plant 1 (2.07 kg).

It was found that number of fruit per plant contributed maximum to total divergence (59.05%) followed by fruit yield q/ha (17.01%). Node on first male flower appearance, vine length and yield Plant ¯1 followed by other traits had least contribution to the total divergence. So, from the present study, the diverse clusters (I and II) hold good promise for various hybridization based breeding programmes, genotypes from these clusters can be used for obtaining high heterotic response.

Table 1: Number and name of genotypes in different clusters

Clusters	No. of genotypes	Name of genotype
1. Cluster	8	IC-085611
		IC-085615
		IC-085614
		IC-085613
		IC-085610
		IC-085609
		IC-085617
		IC-085608
2. Cluster	4	Farmers Var
		Farmers Var
		IC-085616
		IC-085612
3. Cluster	2	Pusa Do Mousani
		Arka Harit
4. Cluster	1	Kashi Mayuri

Table 2: Average intra (Bold) and inter cluster distance (D)

Cluster distances	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	362.86	924.01	2485.03	1470.29
Cluster 2		640.01	1336.63	2083.81
Cluster 3			377.7	3232.02
Cluster 4				0

Table 3: Cluster means for different characters in bitter gourd

Cluster means	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Days to 50% seedling emergence	5.17	6.44	4.75	4.83
Vine length	4.83	6.21	3.12	2.83
No. of branches/plant	17.74	18.53	20.81	19.82
Days to 1st appearance of male flower	48.79	51.88	38.79	51.36
Days to 1st appearance of female flower	54.88	57.34	40.48	57.51
Node number at which 1st male flower appears	7.12	8.91	8.81	8.18
Node number at which 1st female flower appears	12.91	15.59	19.49	11.32
No. of male flowers	17.15	21.63	20.82	20.95
No. of female flowers	29.1	32.59	30.73	26.16
No. fruits per plant	29.29	31.85	21.65	31.29
Diameter of fruit(cm)	2.85	3.74	5.01	4.31
Fruit length(cm)	12.52	15.84	15.65	15.89
Avg fruit weight(g)	46.09	66.5	95.63	96.24
yield of marketable fruits per plant (kg/plant)	1.39	2.07	1.98	1.95
TSS of fruit (brix)	4.76	4.38	4.2	4.3
Vit. C of fruit (mg/100g)	73.88	77.95	84.94	89.28

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