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Genetic diversity analysis in bitter gourd (*Momordica charantia* L.) for yield and its attributing characters

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Abstract
Twenty four bitter gourd (*Momordica charantia* L.) genotypes were studied in a field experiment conducted at experimental field of College of Horticulture, Mudigere, during Summer 2017-18. The objective of the study was to estimate the genetic diversity among the genotypes for yield and its attributing characters. There was a significant difference among the genotypes for all the characters studied. Twenty four genotypes were grouped into five clusters, cluster I was the largest cluster having twenty genotypes and remaining clusters had only one genotype each. Fruit weight (31.16%) contributed maximum to the total genetic diversity among twenty four bitter gourd genotypes followed by flesh thickness (19.93%), node at which first female flower appear (11.59%). Intra cluster D^2 values ranged from 0.00 to 191.79. Among the five clusters, cluster I with twenty genotypes showed maximum intra cluster distance (D^2= 191.79). The clusters II, III, IV and V had no intra-cluster distance (D^2= 0.00) as they possessed single genotype in each cluster.

Keywords: Diversity, clusters and genotypes

Introduction
Bitter gourd is one of the highly nutritious and important vegetable among cucurbits grown throughout the country for its tender fruits. It belongs to the Family Cucurbitaceae and Genus Momordica. It is considered a prized vegetable because of its high nutritive values among the consumers especially due to its ascorbic acid and iron (Behera, 2004) [1] contents. Inspite having medicinal importance due attention was not given for the cultivation of bitter gourd, but recently the cultivation of bitter gourd has become increasingly popular, because of the growing awareness about the antidiabetic properties. Due to the efforts of many plant breeders several high yielding varieties and hybrids have been developed in the recent past. India is endowed with large amount of genetic diversity based on growth habit, maturity and various fruit characters including shape, size, colour and surface texture (Robinson and Decker-Walters, 1999) [8], by utilising this diversity marked improvement in yield potentiality and quality components has been achieved. The knowledge on genetic diversity is an important factor for heritable improvement in any crop and also helpful in selection of parents for successful breeding programme. Hence, the present study was aimed at ascertaining the nature and magnitude of genetic diversity among twenty four bitter gourd genotypes.

Materials and Methods
Twenty four bitter gourd genotypes were procured from different regions of Karnataka. The field experiment was conducted at Department of Crop Improvement and Biotechnology, College of Horticulture, Mudigere during summer 2017-18. The list of genotypes along with their place of collection was presented in Table 1. The experiment was laid out in a Randomized Block Design with three replications. The seedlings of all genotypes were transplanted with the spacing of 2 m between rows and 1.2 m between plants. The observations were recorded on five randomly selected plants on sixteen quantitative traits *viz.*, Vine length (m), Number of branches per vine, Internodal length (cm), Node at which first male flower appears, Node at which first female flower appears, Days to first male flower, Days to first female flower, Sex ratio, Number of fruits per vine, Fruit weight (g), Fruit length (cm), Fruit width (mm), Rind thickness (mm), Flesh thickness (mm), Fruit yield per vine (kg) and Fruit yield per plot (kg).

Table 1: Details of bitter gourd genotypes used in the study

Sl. No.	Germplasm	Source
1	Bidar local-1	Farmer's field
2	Chamrajpet local	Farmer's field
3	Belur local	Farmer's field
4	Kadur local	Farmer's field
5	Arka Harit	IIHR, Bengaluru
6	Chikmanglore local	Farmer's field
7	Dharwad local-1	Farmer's field
8	Bagalkot local	Bagalkot
9	Kolar local	Farmer's field
10	Hubli local	Farmer's field
11	Davangere local	Farmer's field
12	Chitradurga local-1	Farmer's field
13	Co-1	TNAU, Coimbatore
14	Shivamogga local-1	Farmer's field
15	Chitradurga local-2	Farmer's field
16	Dharwad local-2	Farmer's field
17	Hiriyur local-1	Farmer's field
18	Hiriyur local-2	Farmer's field
19	Javgal local	Farmer's field
20	Hassan local	Farmer's field
21	Pusa Do Mousami	IARI, New Delhi
22	HK-127	Kerala
23	Shivamogga local-2	Farmer's field
24	Bidar local -2	Farmer's field

Results and Discussion

Analysis of variance showed significant differences among the genotypes for all the characters studied provide considerable scope for selection. D^2 analysis proposed by Mahalanobis's (1936) [5] has been reported to be an effective tool to assess the genetic divergence. Such an analysis eventually helps to choose desirable parents for crop improvement programme, which results in the development of superior varieties and high yielding hybrids. Twenty four bitter gourd genotypes were evaluated for sixteen characters to study the divergence and the data obtained was subjected to D^2 analysis. Five clusters were constructed by using Tocher's method. These clusters were grouped irrespective of geographic divergence indicating no parallelism between geographic distribution and genetic diversity (Rasmi and Sreelathakumary, 2012) [7].

Grouping of bitter gourd genotypes

By usingTocher's method given by Rao (1952), 24 genotypes were grouped into five clusters by treating estimated D^2 values as the square of the generalized distance (Figure 1). Cluster I was the largest cluster having twenty genotypes and remaining clusters had only one genotype each, they indicate their independent identity and various unique characters possessed by them (Table 2).

Table 2: Clustering pattern of bitter gourd genotypes

Cluster No.	No. of genotypes	Genotypes name
Cluster I	20	Bidar local-1, Chamrajpet local, Kadur local, Pusa Do Mousami, Chikmanglore local, Dharwad local-1, Bagalkot local, Kolar local, Davangere local, Chitradurga local-1, Co-1, Chitradurga local-2, Dharwad local-2, Hiriyur local-1, Hiriyur local-2, Javgal local, Hassan local, HK-127, Shivamogga local-2 and Bidar local-2.
Cluster II	1	Arka Harit
Cluster III	1	Belur local
Cluster IV	1	Hubli local
Cluster V	1	Shivmogga local-1

Percent contribution of different traits towards total divergence

The relative contribution of different traits for genetic divergence (D^2) is given in the Table 3. Fruit weight (31.16%) contributed maximum to the total genetic diversity among twenty four bitter gourd genotypes followed by flesh thickness (19.93%), node at which first female flower appear (11.59%), rind thickness (10.87%), fruit width (5.80%), number of fruits per vine (5.43%), sex ratio (4.71%), fruit length (3.26%), days to first female flower (2.90%), internodal length (2.54%) and days to first female flower (1.81%). However traits like vine length, number of branches per vine, node at which first male flower appear, fruit yield per vine and fruit yield per plot had no substantial contribution to total divergence.

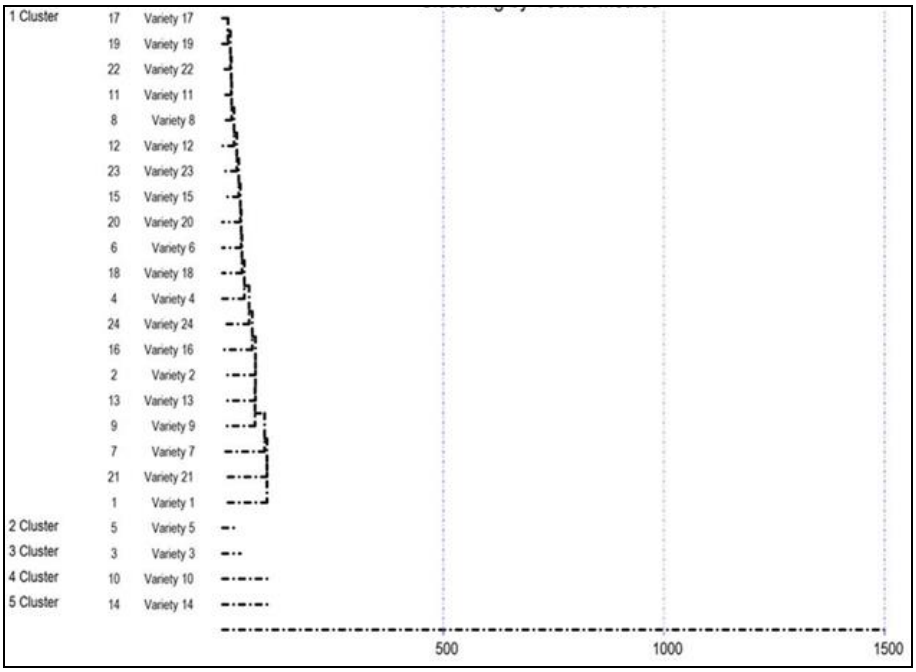

Fig 1: Dendrogram showing the genetic diversity among 24 genotypes of bitter gourd

Table 3: Percent contribution of different characters to the total divergence among Bitter gourd genotypes

Sl. no.	Source of variation / characters	Times ranked 1st	% Contribution
1	Vine length (m)	0	0
2	Number of branches/plant	0	0
3	Internodal length (cm)	7	2.54
4	Node at which first male flower appears	0	0
5	Node at which first female flower appears	32	11.59
6	Days to first male flower	5	1.81
7	Days to first female flower	8	2.90
8	Sex ratio	13	4.71
9	Number of fruits per plant	15	5.43
10	Fruit weight (g)	86	31.16
11	Fruit length (cm)	9	3.26
12	Fruit width (mm)	16	5.80
13	Rind thickness (mm)	30	10.87
14	Flesh thickness (mm)	55	19.93
15	Fruit yield per plant (kg)	0	0
16	Fruit yield per plot (kg)	0	0

Table 4: Intra (diagonal) and inter cluster distance (D^2) among different bitter gourd genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	191.79	311.99	287.72	736.17	433.67
Cluster II	311.99	0.00	453.36	960.71	546.54
Cluster III	287.72	453.36	0.00	689.52	456.78
Cluster IV	736.17	960.71	689.52	0.00	841.54
Cluster V	433.67	456.54	456.78	841.54	0.00

The inter cluster distance average D^2 value was maximum (D^2= 960.71) between cluster II and cluster IV having one genotype each followed by cluster IV and cluster V (D^2=841.54) having one genotype each, cluster I and cluster IV (D^2=736.17), cluster III and cluster IV(D^2=689.52), cluster II and cluster V(D^2=546.54), cluster III and cluster V(D^2=456.78), cluster II and cluster III (D^2=453.36), cluster I and cluster V (433.67), cluster I and cluster II (311.99), cluster I and cluster III (D^2=287.72),this clearly suggested that the genotypes found in any of these clusters were highly divergent. Similar results were also reported by Ghosh *et al*. (2015) [2] and Laxuman *et al*. (2012) [4].

Mean performance for all the characters in different clusters

Cluster mean for 24 genotypes are summarized in Table 5.

The highest mean for vine length was observed in the cluster IV (3.09 m) followed by cluster I (2.37m). The lowest cluster mean was observed in the cluster III (2.03m). The highest cluster mean was recorded in cluster IV (6.67) followed by cluster I (6.52) and the least was recorded in the cluster V (5.50) for number of branches per vine. The highest cluster mean was recorded in cluster IV (7.73 cm) followed by cluster I (7.61 cm) and the least was recorded in the cluster II (5.64 cm) for internodal length. Similar results are obtained by Kale *et al.* (2002) [3] in pumpkin.

The highest cluster mean for the node at which first male flower appears was observed in the cluster V (10.60) followed by cluster I (10.13). The lowest mean was observed in the cluster II and cluster III (6.40). The highest cluster mean was observed for the cluster V (16.67) followed by cluster I (14.51). The lowest cluster mean was observed for the cluster II (8.40) for node at which first female flower appears.

The highest cluster mean for days to first male flower was observed in the cluster V (34.63) followed by cluster III (31.53).

The lowest mean was observed in the cluster IV (22.60). The highest cluster mean was observed for the cluster V (40.03) followed by cluster III (39.67). The lowest cluster mean was observed for the cluster IV (28.00) for days to first female flower.

The lowest cluster mean for sex ratio was observed for the cluster IV (5.78). The highest cluster mean was observed for the cluster III (10.70), followed by cluster V (9.47). The highest cluster mean for number of fruits per vine was observed in the cluster V (25.21) followed by cluster I (17.09). The lowest mean was observed in the cluster III (10.17).

The highest cluster mean for fruit weight was observed in the cluster IV (167.93 g) followed by cluster III (94.21 g). The lowest mean was observed in the cluster II (44.94 g). The lowest cluster mean for fruit length was observed for the cluster I (11.57 cm). The highest cluster mean was observed for the cluster IV (26.17 cm), followed by cluster V (20.50 cm). The highest cluster mean for fruit widthobserved for the cluster IV (53.90 mm) followed by cluster II (53.48 mm). The lowest cluster mean was observed for the cluster V (23.53 mm).

Highest cluster mean for rind thickness was recorded in cluster V (18.41 mm) followed by cluster IV (11.13 mm) and the least was recorded in cluster I (6.89 mm). The highest cluster mean was recorded in cluster II (41.87 mm) followed by cluster IV (30.03 mm) and the lowest was recorded in the cluster V (19.30 mm) for flesh thickness.

The highest cluster mean for fruit yield per vine was observed in the cluster IV (2.86 kg) followed by cluster V (1.90 kg). The lowest mean was observed in the cluster II (1.06 kg). The highest cluster mean was observed for the cluster IV (18.90kg) followed by cluster V (13.26 kg). The lowest cluster mean was observed for the cluster II (7.43 kg) for fruit yield per plot.

Conclusion

Genetic diversity is largely contributed by fruit weight, flesh thickness, node at which first female flower appear and rind thickness. Thus, these characters may be given high emphasis while selecting lines for hybridization programme to generate large variability and it will provide immense scope for improvement of yield through selection. Divergence study revealed that, highest inter cluster mean for fruit yield per vine was observed between cluster II and cluster IV. Hence, the crosses between the genotypes of these clusters can be tried for improvement of yield.

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