



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; 7(4): 757-759
Received: 08-05-2018
Accepted: 13-06-2018

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Genetic divergence studies in bitter gourd (*Momordica charantia* L.)

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Abstract

A study was conducted during kharif 2013, in Karnataka, India to evaluate the nature and magnitude of genetic divergence in 55 bitter gourd genotypes. Results revealed the presence of wide genetic diversity. The genotypes were grouped into 10 clusters based on Mahalanobis D^2 statistics using Tocher's method. The clustering pattern of genotypes revealed that the genetic diversity was independent of the geographical diversity. Among the 10 clusters maximum number of genotypes were found in cluster I. Among the 19 quantitative characters studied rind thickness contributed a maximum of 35.01 % contribution to the divergence followed by fruit yield per vine. 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 an important commercial cucurbit belonging to the family Cucurbitaceae, genus *Momordica*. The crop is extensively grown in China, Japan, South East Asia, tropical Africa and South America. In India, Karnataka, Maharashtra, Tamil Nadu and Kerala are the major bitter gourd growing states. In spite of the potential economic and medicinal importance of the crop, due attention was not 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 the antidiabetic property and nutritive value of the crop among the consumers.

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. The yield potential of bitter gourd in India is very low due to poor yielding varieties and high incidence of pest and diseases. One of the approaches to improve yield and quality is heterosis breeding. The importance of heterosis breeding has been recognized widely in many vegetable crops. However, the prerequisite of the heterosis breeding is the selection of the divergent parents. 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 the selection of diverse parents which upon hybridization can result in productive hybrids, evaluation of available germplasm assumes importance in regard and necessary. Keeping foregoing points in view, a total of 55 bitter gourd genotypes were evaluated for the study of genetic divergence.

Material and Methods

In the present study fifty five bitter gourd genotypes from Kittur Rani Channamma College of Horticulture, Arabhavi were used for genetic divergence studies. The genotypes grown in Randomized Block Design with two replications during kharif 2013 at the main experimental fields of Department of Vegetable Science, KRCCH Arabhavi. Each replication consisted of a single row of 2.5 m for each entry with row-row and plant-plant spacing being 1.5 m and 0.9 m respectively. Recommended agronomic practices were followed to raise a crop. Five competitive plants were randomly selected in each entry for recording observation on vine length, number of branches, days to first male flowering, days to first female flowering, nodes upto first female flowering, days to first harvesting, days from fruit set to maturity, sex ratio, number of fruits per vine, average fruit weight, fruit length, fruit girth, fruit yield per vine, fruit yield per plot, fruit yield per hectare, rind thickness and flesh thickness.

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Results and Discussion

The analysis of variance (ANOVA) revealed considerable amount of variability for the 19 traits studied suggesting

ample scope to identify desirable genotypes. Based on the relative magnitude of D^2 values of 55 genotypes were grouped into 10 clusters. (Table 1).

Table 1: Clustering pattern of 55 genotypes of bitter gourd based on D^2 values

Cluster number	Number of genotypes	Genotypes included
I	33	Preeti, Solan Hara, Nuda Tittu, Nanjanagood Local, TCR-162, TCR-334, TCR-250, Ankalagi Local-1, Ankalagi Local-2, Sunadholi Local-1, Sunadholi Local-2, IC-44433, IC-45338, K-1, K-2, k-3, K-4, Arka Harit, Co-1, Coimbatore Long, Sungrow White Long, Pannuruthi, Chidambaram Small, KRCCH 241-1, KRCCH 241-2, KRCCH 241-3, KRCCH 241-4, KRCCH 241-5, KRCCH 241-6, KRCCH 241-7, KRCCH 241-8, KRCCH 243-1, KRCCH 243-2
II	2	KRCCH 245-6, KRCCH 247-2
III	2	KRCCH 245-5, KRCCH 247-4
IV	2	KRCCH 243-4, KRCCH 243-7
V	2	KRCCH 243-8, KRCCH 247-8
VI	2	KRCCH 243-5, KRCCH 245-3
VII	2	KRCCH 247-1, KRCCH 247-7
VIII	2	KRCCH 245-2, KRCCH 245-4
IX	2	KRCCH 245-1, KRCCH 245-8
X	6	KRCCH 243-3, KRCCH 243-6, KRCCH 245-7, KRCCH 247-3, KRCCH 247-5, KRCCH 247-6

Grouping pattern showed no clear relationship between geographical diversity and genetical diversity. The cluster I was largest comprising thirty three genotypes followed by cluster X comprising six genotypes respectively. The geographical diversity has been disapproved to be index of genetic diversity in several vegetable crops. The intra cluster distance ranged from 39.783 to 4283.999 and inter cluster

distance ranged from 86.851 to 2456.816. Maximum inter cluster D value was observed between cluster I and cluster X ($D^2=2456.816$) followed by cluster VIII and X ($D^2=2418.245$), cluster III and X ($D^2=2363.647$). The average cluster means of 19 traits are presented in Table 2. Perusal of the table reveals that cluster-I had highest mean value for yield per vine (7.00 kg) and average fruit weight (61.750 g).

Table 2: Average intra and inter-cluster D^2 values along with their 'D' values (in parenthesis) of 10 clusters for 19 characters formed by 55 genotypes of bitter gourd

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	563.882 (23.746)	436.776 (20.899)	375.023 (19.366)	342.941 (18.519)	384.417 (19.607)	359.350 (18.957)	353.721 (18.807)	584.140 (24.169)	472.944 (21.747)	2456.816 (49.566)
II		39.783 (6.307)	358.954 (18.946)	309.232 (17.585)	277.798 (16.667)	328.684 (18.130)	249.176 (15.785)	365.504 (24.169)	297.567 (21.747)	2200.587 (49.566)
III			48.987 (6.999)	86.851 (9.319)	98.617 (9.931)	101.444 (10.072)	210.762 (14.518)	372.691 (19.305)	342.120 (18.496)	2363.647 (48.617)
IV				51.812 (7.198)	158.201 (12.578)	109.642 (10.471)	107.136 (10.351)	351.783 (18.756)	326.030 (18.056)	2193.527 (46.835)
V					74.510 (8.632)	143.372 (11.974)	266.533 (16.326)	263.863 (16.244)	202.383 (14.226)	2322.758 (48.195)
VI						99.293 (9.965)	149.009 (12.207)	431.733 (22.665)	240.575 (17.800)	2321.376 (46.703)
VII							127.871 (11.308)	513.707 (22.665)	316.828 (17.800)	2181.146 (46.703)
VIII								174.979 (13.228)	390.212 (19.754)	2418.245 (49.176)
IX									280.204 (16.739)	2309.722 (48.060)
X										4283.999 (65.452)

Bold and diagonal values indicates the intra cluster distances

It was observed that rind thickness contributed maximum to total genetic divergence (35.01 %) followed by fruit yield per vine (14.14 %), fruit yield per plot (14.07 %), sex ratio (10.03 %) and fruit yield per hectare (9.26 %) (Table 3). So, from the

present study it is revealed that the diverse clusters (I, X and VIII) hold good promise for various hybridization based breeding programmes, genotypes from these clusters can be used for obtaining heterotic response.

Table 3: Relative per cent contribution of different characters to the total divergence in bitter gourd

Sl. No.	Character	No. of times ranked first	Per cent contribution
1.	Vine length at 45 DAS	0	0
2.	Vine length at 90 DAS	0	0
3.	Number of branches at 90 DAS	34	2.2896
4.	Days to first male flowering	1	0.0673
5.	Days to first female flowering	6	0.4040
6.	Nodes up to first female flowering	0	0

7.	Days to first harvesting	46	3.0976
8.	Days from fruit set to maturity	2	0.1347
9.	Sex ratio	149	10.0337
10.	Number of fruits per vine	6	0.4040
11.	Average fruit weight	4	0.2694
12.	Fruit length	51	3.4343
13.	Fruit girth	99	6.6667
14.	Fruit yield per vine	213	14.1434
15.	Fruit yield per plot	209	14.0741
16.	Fruit yield per hectare	145	9.2643
17.	Rind thickness	510	35.0168
18.	Flesh thickness	6	0.4040
19.	Ascorbic acid	4	0.2694
Total		1485	100

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