Academic Journal of Plant Sciences 6 (2): 89-91, 2013
ISSN 1995-8986

DOI: 10.5829/idosi.ajps.2013.6.2.334

Genetic Divergence Studies in Bitter Gourd (*Momordica charantia* L.)

[1]*Bhagwat Singh,* [1]*Anoop Kumar Singh and* [2]*Shailesh Kumar*

[1]Department of Vegetable Science, [2]Department of Genetics and Plant Breeding,
Narendra Deva University of Agriculture and Technology,
Kumarganj, Faizabad, Uttar Pradesh, India, 224229

Abstract: A study was conducted during Zaid 2005, in Uttar Pradesh, India, to evaluate the nature and magnitude of genetic divergence in 30 bitter gourd genotypes. Results revealed the presence of wide genetic diversity. The genotypes were grouped into 6 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 6 clusters, maximum numbers of genotypes were found in cluster V, while clusters III was found to be mono-genotypic. Among the 12 quantitative characters studied, individual fruit weight constituted a maximum of 64.14% contribution to the divergence, followed by days to first female flower appearance. Ranking of genotypes based on intra-cluster mean performance for these characters which are major contributors of genetic diversity revealed its usulness in selecting parents for heterosis breeding.

Key words: 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 [1]. 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 M. macrocarpa*.

Inspite 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 of heterosis breeding has been recognized widely in many vegetable crops. However, the pre-requisite 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 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 30 bitter gourd genotypes were evaluated for the study of genetic divergence.

Corresponding Author: Bhagwat Singh, Department of Vegetable Science.

MATERIALS AND METHODS

Thirty genotypes of bitter gourd selected from the germplasm collection obtained from Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, Uttar Pradesh, India were grown in Randomized Block Design with three replications during *Zaid* 2005 at the Main Experimental Farm of Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, Uttar Pradesh, 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 50 cm respectively. Recommended 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, days to first harvest, 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% flowering and days to maturity. The data were subjected to multivariate analysis of genetic divergence using Mahalanobis D^2 statistic [3]. Grouping of entries was done by Tocher's method [6].

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed considerable amount of variability for the twelve traits studied suggesting ample scope to identify desirable genotypes. Based on the relative magnitude of D^2 values 30 genotypes were grouped into 6 different clusters (Table 1).

Grouping pattern showed no clear relationship between geographical diversity and genetically diversity. The cluster-V followed by cluster-IV and VI was the largest comprising thirteen and five 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 [4, 7]. Frequent exchange of breeding materials from one place to another and further selection may also

Table 1: Number and name of genotypes in different clusters.

Clusters	No. of Genotypes	Genotype
I	02	NDBT-86, NDBT-80
II	04	NDBT-76, NDBT-32, NDBT-28, NDBT-30
III	01	NDBT-77
IV	05	K. Sona, NDBT-12, NDBT-79, NDBT-26, NDBT-85
V	13	K. Baramasi, DVBTG-7, Priya, NDBT-21, NDBT-24, NDBT-25, NDBT-29, NDBT-34, NDBT-35, NDBT-24, NDBT-36, Pusa Do Mousami, NDBT-27
VI	05	DVBTG-5, PBIG-44, NDBT-33, Pusa Vishesh, NDBT-31

Table 2: Average Intra (Bold) and Inter Cluster Distance (D)

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	25.083	212.831	55.744	242.781	269.090	220.868
2 Cluster		71.454	337.005	625.318	145.067	502.185
3 Cluster			0.000	117.419	383.603	175.500
4 Cluster				127.011	691.012	263.807
5 Cluster					216.248	578.247
6 Cluster						383.713

Table 3: Cluster means for different characters in Bitter gourd

	Node 1st Male Flower Appearance	Node 1st Female Flower Appearance	Days 1st Male Flower Anthesis	Days 1st Female Flower Anthesis	Days to 1st harvest	Fruits Plant^{-1}	Fruit Diameter (cm)	Fruit Length (cm)	Average Fruit Weight (g)	Branches Plant^{-1}	Vine Length (m)	Yield Plant^{-1} (kg)
1 Cluster	10.625	14.090	53.465	59.465	76.250	16.030	6.000	13.885	55.365	18.290	1.840	1.195
2 Cluster	10.543	14.145	55.125	58.467	73.760	10.967	6.097	12.060	43.593	16.823	1.963	0.920
3 Cluster	9.000	15.250	51.130	57.670	72.930	15.480	5.080	16.500	59.330	17.130	2.630	0.860
4 Cluster	10.252	15.246	49.048	54.130	71.960	12.226	5.062	15.816	65.272	17.520	1.936	1.352
5 Cluster	9.878	15.164	54.185	58.514	74.207	13.160	6.022	14.636	43.264	18.902	2.069	1.002
6 Cluster	10.268	15.102	53.428	56.508	72.112	14.816	6.012	13.518	60.750	16.442	2.018	0.998

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, [8]. The intra cluster distance ranged from 0 to 383.71 and inter cluster distance (D) ranged from 55.74 to 337.00 (Table 2). Maximum inter cluster D-value was observed between cluster-IV and cluster-V (691.012) followed by cluster-IV and cluster-II (625.318). The average cluster means of 12 traits are presented in Table 3. Perusal of the table reveals that cluster-IV had the highest mean value for yield plant^{-1} (1.352 kg) and average fruit weight (17.52g).

It was found that number of average fruit weight contributed maximum to total divergence (64.14%) followed by days to first female flower appearance (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 (IV, V and VI) hold good promise for various hybridization based breeding programmes, genotypes from these clusters can be used for obtaining high heterotic response.

REFERENCES

1. Behera, T.K., 2004. Heterosis in bitter gourd. J. New Seeds, 6(2 and 3): 217-222.
2. Jagadev, P.N., K.M. Samal and D. Lanka, 1991. Genetic divergence in rape mustard. Ind. J. Genet. and Plant Breed., 51(4): 465-467.
3. Mahalanobis, P.C., 1936. Conference on the Generalized Distance in Statistia. Proceedings of National Instit. Sci., 50: 803-806.
4. Mahto, J.L., 1996. Genetic divergence and stability in Indian mustard under rainfed condition. J. Maharashtra Agric. Univ., 21(3): 334-337.
5. Murty, B.R. and V. Arunachalam, 1966. The nature of divergence in relation to breeding systems in some crop plants. Ind. J. Genet. and Plant Breed., 38: 375-379.
6. Rao, C.R., 1952. Advanced statistical methods in Biometrcal Research. John Wiey and Sons Inc, New York.
7. Shalini, T.S., R.A. Sheriff, R.S. Kulkarni and P. Venkataravan, 2000. Genetic divergence in Indian mustard. Mysore J. Agric. Sci., 34: 251-256.
8. Solanki, R.K., R.S. Tomar and M.D. Asha, 2006. Genetic divergence analysis in Indian mustard. J. Oilseeds Rese., 23(2): 156-158.