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Genetic divergence analysis by morphological descriptors among bitter gourd (*momordica charantia* l.) Accessions for yield related traits

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Abstract

A field experiment was subjected to genetic divergence analysis of Bitter gourd (*Momordica charantia* L.) accessions for yield related traits. The experiment was comprised of 30 accessions including two check varieties (P. Vishesh and Pusa Do Mausami), laid out in Randomized Block Design with three replications at Main Experiment Station, Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.), India. These genotypes were grouped into 6 different non-overlapping clusters. Cluster III had highest number of genotypes (9) followed by cluster VI (8). The different clusters showed considerable differences in intra-cluster group means for all the traits. Maximum intra cluster distance was recorded with cluster VI (105.70) followed by cluster III (103.348). The maximum inter-cluster distance observed between cluster II to cluster VI (558.00) followed by cluster II to cluster V (405.33) which suggested that members of these clusters are genetically very diverse to each other and can be used for heterosis and recombinant breeding programme. The proportionate contribution of avg. fruit weight and fruit length towards genetic divergence was 35.40% and 18.85%, respectively. Major cluster in divergence analysis contained genotypes of heterogeneous origin, thereby, indicating no parallelism between genetic and geographic diversity. Therefore, crosses between members of clusters separated by high inter cluster distance are likely to produces desirable segregates.

Key words: Genetic divergence, Yield, cluster, Heterogeneous, Bitter gourd (*Momordica charantia* L.).

Introduction

Bitter gourd (*Momordica charantia* L.), which belongs to family Cucurbitaceae, is an important vegetable mainly valued for its nutritional and medicinal properties (Jadhav *et al.*, 2009). The origin of this crop is probably India with secondary centre of diversity in China (Grubben, 1977). Bitter gourd is widely cultivated and distributed in Malaysia, China, India, tropical Africa and North and South America (Singh *et al.,* 2014). It is considered one having medicinal properties and with a compound named 'Charantin' present in the bitter gourd is useful to reduce blood sugar for diabetic patients (Dhillon *et al.*, 2005). It is also rich in vitamins and carbohydrates. Bitter gourd has been used for centuries in the ancient traditional medicine of India, China, Africa, and Latin America (Rahman *et al.*, 2011). Bitter gourd fruits also possess anti-oxidant, anti-microbial, anti-viral, anticancer and anti-diabetic activities (Chen *et al.*, 2003; Grover and Yadav, 2004).

The crop is highly cross pollinated due to monoecy and the diploid chromosome number is 2n=2x=22, in which a large amount of variation has been observed for most of the economically important traits in the land races cultivars. Inspite of the potential economic and medicinal importance of the crop, due attention has not been given towards a need based crop improvement programme (Dey *et al*., 2007 and Singh *et al*., 2013). Therefore, the improvement work should be focused on selection of genotypes for better yield, superior quality and

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resistant to biotic stresses. In general, crop improvement involves the strategies to enhance the yield potentiality and quality components. The yield potential of bitter gourd in India is very low due to poor yielding varieties and high incidence of pests and diseases. Improvement in yield is normally attained through exploitation of the genetically diverse parents in breeding programmes. Genetic divergence among parents is essential since the crossing programme involving genetically diverse parents is likely to produce high heterotic effects and also more variability could be expected in the segregating generations.

Genetic diversity between genotypes indicates the differences in gene frequencies. Cluster analysis and PC (principal component) analysis are the important genetic diversity measuring tools employed for exhibiting relative genetic differences among the genotype collection of various crop species. For identifying such diverse parents for crossing, multivariate analysis using Mahalanobis D^2 statistic (1936) has been used in several crops. This is a valuable tool to study genetic divergence at inter varietal and sub-species level in classifying the crop plants. In view of this an investigation was carried out to classify a set of bitter gourd genotypes based on multivariate analysis that may be used for generating more heterotic cross combinations and finally superior useful hybrids.

Materials And Methods

The present study was carried out to assess genetic divergence analysis of 30 accessions of bitter gourd including two check varieties, *i.e.* P. Vishesh and PDM. The experiment was laid out in a Randomized Block Design with three replications at Main Experimental Farm of Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh (India). The experiment site had sandy loam soil, low in organic carbon and N, medium in P and K and slightly alkaline having pH=8.0. The genotypes of bitter gourd selected from the germplasm collection obtained from the Department of Horticulture (Vegetable Science), N.D.U.A.T., Ayodhya. Each genotype of bitter gourd was planted in 2.5 m for long row, spaced 2.0 m. apart where, 50 cm. plant to plant spacing was maintained. Recommended agronomic practices and protective measures were followed to raise a good crop.

Data Recording and statistical analysis

The observations were recorded on eleven traits viz. node number to anthesis of first staminate flower, node number to anthesis of first pistillate flower, days to anthesis of first staminate flower, days to anthesis of first pistillate flower, days of first fruit harvest, vine length (m), fruit length (cm), fruit diameter (cm), number of fruit per plant, average fruit weight (g) and marketable fruit yield per plant (kg). The observations were recorded from five randomly selected plants and subjected to statistical analysis. Cluster and PC analysis of 30 bitter gourd genotypes based on yield and its ten component traits to assess the magnitude of genetic variation was performed by using statistical software Windostat version 8.6 from Indostat services. Clustering pattern among 30 bitter gourd genotypes was assessed by using Tocher's method. Average intra and inter-cluster distance was estimated by using Tocher's method representing $Elucidean^2$ distance considering yield and its ten contributing traits in bitter gourd (Table 2). Cluster mean value and its deviation from grand mean value for each corresponding contributing traits has been presented in Table 3.

Result And Discussion

The studies 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 (Table 1). Cluster III had highest number of genotypes (9) followed by cluster VI (8), cluster I (5), cluster II and IV (3) whereas cluster V had only two genotypes. This indicated presence of considerable genetic diversity in the germplasm collections. Major cluster in divergence analysis contained genotypes of heterogeneous origin, thereby, indicating no parallelism between genetic and

geographic diversity. Therefore, the choice of suitable diverse parent selected on the basis of genetic divergence analysis would be more rewarding than the choice made on the basis of geographic diversity. This finding is in agreement with the report of (Day *et al.,* 2007; Sundaram and Vadivel, 2007; Shashikanth *et al*., 2010; Pedapati *et al*., 2014**)** advocating lack of definite relationship between genetic and geographic diversity.

The estimates of intra and inter-cluster distances represented by D^2 values are given in Table 2. Maximum intra cluster distance in cluster VI recorded for (105.70) followed by cluster III (103.348), cluster IV (86.564) and cluster V (70.30). The maximum inter-cluster distance observed between cluster II to cluster VI (558.00) followed by cluster II to cluster V (405.33), cluster V to cluster VI (385.710), cluster II to cluster IV (322.740), cluster IV to cluster VI (321.543), cluster II to cluster III (292.294) and cluster III to cluster IV (261.765) were very high. While the lowest inter-cluster distance was observed between cluster I to IV (135.74), cluster IV to V (144.98), cluster I to III (153.89) and cluster I to VI (186.41). Highest inter cluster distances recorded between two cluster pairs, indicated 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. Thus the crossing between the genotypes belonging to cluster pairs separated by very high inter-cluster distance may be exploited through combination breeding, while crosses between genotypes belonging to clusters separated by low inter-cluster distances are unlikely to through promising recombinant in the segregating generations. These results are in accordance with the findings of Kumar *et al*. (2010); Meena and Bahadur (2013) and Pedapati *et al*. (2014).

The Cluster means for different eleven traits in bitter gourd indicated considerable differences between the clusters in Table 3. The perusal of data depicted that minimum mean values for earliness characters recorded with cluster IV *viz.,* node number to anthesis of first pistillate flower (10.33), days to anthesis of first pistillate flower (45.90) and days to first fruit harvest (53.73) followed by cluster I *viz*., node number to anthesis of first staminate flower (7.17), node number to anthesis of first pistillate flower (12.05), days to anthesis of first pistillate flower (46.89) and days to first fruit harvest (58.61), whereas cluster II recorded minimum values for node number to anthesis of first staminate flower (8.20), node number to anthesis of first pistillate flower (12.36), days to anthesis of first staminate flower (42.47), days to anthesis of first pistillate flower (47.76) and days to first fruit harvest (59.15). It suggests that if breeding program is aimed at earliness, then members of these clusters can be used (Meena and Bahadur, 2013).

The means of the clusters for yield and related traits (Table 4) depicted that Cluster V showed maximum mean values for fruit length (21.63), vine length (2.57) and for average fruit weight (124.36), followed by Cluster I for fruit length (19.95), fruit diameter (3.73), vine length (2.38), no. of fruits/plant (22.19) and average fruit weight (111.46), while it was maximum for fruit yield/plant (2.11). Cluster II showed maximum mean value for fruit diameter (3.86) and Cluster VI showed maximum mean value for no. of fruits/plant (30.27). The top ranking clusters for total yield per plant were clusters I (2.11), cluster V and VI (1.91) and IV (1.82) which indicates that the accessions included in these clusters could effectively be used for the crop improvement program for increasing yield (Ara *et al.,* 2009; Prashanth *et al.*, 2008 and Singh *et al.,* 2013)**.**

The present study found that out of the eleven yield and its component traits, ten major traits contributed 100 per cent towards genetic divergence. It is evident from the table-4 that Average fruit weight contributed maximum towards genetic diversity (35.40%), followed by fruit length (18.85 %), node number of anthesis of first staminate flower (16.78) and number of fruit per plant (13.10). Similar studies of (Singh *et al.*, 2013 and Laxuman, 2005) have also reported maximum contribution of fruit weight towards genetic divergence in bitter ground genotype. Therefore, fruit weight and fruit length would be the important parameter for selecting divergent genotypes.

Conclusion

The overall review of the result obtained by genetic diversity study in present investigation revealed that the crosses between the entries separated by the large inter-cluster distance with high cluster mean values for one or other

character to be improved. For future experiment, traits contributing maximum to genetic diversity such as fruit weight and length should be given top priority as selection parameters and diverse genotypes identified in the present study may be utilized for attempting heterotic cross combination and developing hybrid varieties.

Table 1: Clustering pattern of 30 genotypes on the basis of Mahalanobis D^2 statistics

Cluster number	No. of genotypes	Genotypes
I	5	NDBT-8, NDBT-11, NDBT-15, NDBT-53, NDBT-56,
II	3	NDBT-16, NDBT-38, NDBT-58
III	9	NDBT-1, NDBT-6, NDBT-10, NDBT-12, NDBT-18, NDBT-23, NDBT-37, NDBT-54, P. Vishesh©
IV	3	NDBT-17, NDBT-29, NDBT-50
V	2	NDBT-57, NDBT-61
VI	8	NDBT-3, NDBT-5, NDBT-21, NDBT-30, NDBT-41, NDBT-55, NDBT-59, PDM ©

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

Clusters	Node no. to anthesis of first staminate flower	Node no. to anthesis of first pistillate flower	Days to anthesis of first staminate flower	Days to anthesis of first pistillate flower	Days to first fruit harvest	Fruit length (cm)	Fruit diameter (cm)	Vine length (m)	No. of fruit/ plant	Average fruit weight (g)	Fruit yield/ plant (kg)
I	7.17	12.05	43.46	46.89	58.61	19.95	3.73	2.38	22.19	111.46	2.11
II	8.20	12.36	42.47	47.76	59.15	16.08	3.86	2.12	19.02	101.51	1.55
III	10.05	15.27	44.78	49.46	60.66	16.41	3.73	1.90	14.24	106.03	1.25
IV	8.67	10.33	43.00	45.90	53.73	9.27	3.70	1.91	21.43	91.07	1.82
V	14.34	17.23	47.34	51.07	63.77	21.63	3.45	2.57	17.71	124.36	1.91
VI	11.00	16.20	43.73	51.17	61.43	9.23	3.57	1.64	30.27	71.90	1.91

Table 2: Average of intra- and inter- clusters D^2 values for six clusters.

Cluster number	I	II	III	IV	V	VI
I	**51.51**	204.84	153.89	135.74	236.83	186.41
II		**0.00**	292.29	322.74	405.33	558.00
III			**103.35**	261.76	229.17	212.23
IV				**86.56**	144.98	321.54

V					**70.31**	385.71
VI						**105.71**

Table 4: Per cent contribution in eleven characters towards total genetic divergence in bitter gourd.

S. No.	Characters	Per cent contribution
1.	Node no. to anthesis of first staminate flower	16.78
2.	Node no. to anthesis of first pistillate flower	1.15
3.	Days to anthesis of first staminate flower	0.92
4.	Days to anthesis of first pistillate flower	0.00
5.	Days to first fruit harvest	2.07
6.	Fruit length (cm)	18.85
7.	Fruit diameter (cm)	2.07
8.	Vine length (m)	5.75
9.	Number of fruit / plant	13.10
10.	Average fruit weight (g)	35.40
11.	Fruit yield /plant(kg)	3.91

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