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Principal Component Analysis in Bitter Gourd (*Momordica charantia* L.)

Vinod Jatav, D. K. Singh, N. K. Singh, A. Panchbhaiya

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Abstract The present investigation was carried out during summer. Twenty-four genotypes of bitter gourd were grown in randomized block design with three replications including two checks (Pant Karela-1 and Pant Karela-2) to assess genetic diversity through principal component analysis (PCA) and D^2 analysis. Out of 24 genotypes, PBIG-22 was found exceptionally unique and predominantly female (sub-gynoecious) with desirable agronomic traits. PCA showed that the first Eigen root had maximum of 26.83% variation of total variation, while the first six principal component axes together explained 84.05% variation. Clustering through D^2 analysis revealed maximum inter-cluster distance of 498.80 between clusters IV and V followed by cluster III and V (322.81), thus the genotypes grouped under cluster V, IV and III may yield maximum heterosis upon hybridization and also create wide variability including transgressive segregants in selfed generations.

Keywords Genetic divergence, PCA, D^2 analysis, Eigen root, Cluster distance.

Introduction

Bitter gourd (*Momordica charantia* L., 2n = 2x = 22) is one of the most important cucurbitaceous vegetable crop grown in India. It is known variously as bitter melon, bitter cucumber, african cucumber, karela, carrila, maiden apple and balsam pear. Its native home is tropical Asia particularly, east India and south China. Among the cucurbits, bitter gourd is considered a prized vegetable because of its high nutritive value, especially having ascorbic acid and iron. The 100 g edible fruit part constitutes 83.2% water, 10.5% carbohydrates, 0.2–1.0% fat, 0.5–1.0% minerals, 1.7% fiber, 2.1 g protein, 2 mg iron, 23 mg calcium, 96 mg vitamin C, 38 mg phosphorus, 171 mg potassium, 2.40 mg sodium, 0.19 mg cupper, 0.08 mg manganese, 0.46 mg zinc and 126 mg β carotene (Gopalan et al. 1993). Chang et al. (1996) reported that bitter gourd seeds contain 41–45% of essential oil of essential oil and it is ten times greater than the industrially important Tung oil in respect of oleostearic and stearic acid ratio. The fruits and seeds of bitter gourd possess cooling, appetitising, stomachic, antipyretic, carminative, antiheliminthic, aphrodisiac and vermifuge properties (Grover and Yadav 2004). Hypoglycemic glycoalkaloids viz., vicine present in seed (Dutta et al. 1981 and Handa et al. 1990) and charantin found in fruit (Lotlikar and Rao 1962). MAP-30, a basic protein that inhibits human immunodeficiency virus (HIV) is present in both seed and fruit (Lee et al. 1995).

Multivariate analysis of elite germplasm collections is a prerequisite for choosing promising genetically diverse lines for desirable traits (Mladenovic et al. 2012). Based on the genetic divergence the genotypes are assigned to specific heterotic groups to create segregating progenies with maximum genetic variability for further breeding purposes. Genetic diversity analysis is well exploited for transferring desirable genes from diverse genetic stock available in the gene pool for broadening the genetic base in

Vinod Jatav*, D. K. Singh, N. K. Singh, A. Panchbhaiya
Department of Vegetable Science, G. B. Pant University of Agriculture and Technology, Pantnagar 263145, Uttarakhand, India
e-mail: vinod.jatav@icar.gov.in
*Corresponding author

Table 1. List of genotypes used in present study.

Sl. No.	Accession	Source/Availability	Sl. No.	Accession	Source /Availability
1	PBIG-2	GBPUA&T, Pantnagar	13	PBIG-22	GBPUA&T Pantnagar
2	PBIG-4	GBPUA&T, Pantnagar	14	PBIG-28	GBPUA&T, Pantnagar
3	PBIG-5	GBPUA&T, Pantnagar	15	PBIG-56	GBPUA&T, Pantnagar
4	PBIG-8	GBPUA&T, Pantnagar	16	PDM (Pusa Do Mausmi)	IARI, New Delhi
5	PBIG-9	GBPUA&T, Pantnagar	17	NDBT-5	NDUAT, Faizabad
6	PBIG-10	GBPUA&T, Pantnagar	18	MC-84	KAU, Kerala (Maintained at GBPUA&T, Pantnagar)
7	PBIG-11	GBPUA&T, Pantnagar	19	US-33	U.S. Agriseeds, Telangana (Maintained at GBPUA& T, Pantnagar)
8	PBIG-12	GBPUA&T, Pantnagar	20	PCPGR NO.-1561	NBPGR, New Delhi
9	PBIG-13	GBPUA&T, Pantnagar	21	GP 2011/1183	NBPGR, New Delhi
10	PBIG-14	GBPUA&T, Pantnagar	22	GP-2011-08	NBPGR, New Delhi
11	PBIG-15	GBPUA&T, Pantnagar	23	Pant Karela-1	GBPUA&T, Pantnagar
12	PBIG-16	GBPUA&T, Pantnagar	24	Pant Karela-2	GBPUA&T, Pantnagar

crops with narrow genetic base. 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. However, despite the potential medicinal and economic values, there are only few reports of multivariate analysis in Indian bitter gourd genotypes (Dey et al. 2007, Shankar et al. 2009 and Singh et al. 2014). In view of this, the present study was conducted 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

Twenty-four germplasm including two checks, i.e. Pant Karela-1 and Pant Karela-2 of bitter gourd (*Momordica charantia* L.) were evaluated for genetic diversity during February–June, 2014 at Vegetable Research Center (VRC), G.B. Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar (Uttarakhand). VRC, Pantnagar is situated in the foot hills of Shivalik range of Himalayas in the narrow belt called Tarai. Geographically, it is situated at an altitude of 243.84 m above mean sea level, and between 29° North latitude and 79.3° East longitude. The climate of Pantnagar is humid subtropical. The monsoon starts in the month of June and often remains active up to September. The summer is humid dry and hot whereas, winters are cool. Sometimes frost may occur occasionally. Light rains occur during winter season too.

The experiment was conducted in randomized complete block design with three replications to assess the performance of 24 bitter gourd genotypes (Table 1). The crop was planted in 9 m long row, spaced 2.0 m apart, whereas 60 cm plant to plant spacing was maintained. All the recommended agronomic package and practices and protective measures were followed to raise a good crop. The data recorded on 19 quantitative characters, namely days to first male flower, days to first female flower, number of node to first male flower, number of node to first female flower, days to first harvest, number of fruits per plant, average fruit weight, fruit length, fruit diameter, number of seed cavity per fruit, length of seed cavity, main vine length, number of primary branches per vine, length of internodes, number of seeds per fruit, weight of seed per fruit, seed index, fruit yield per plant and fruit yield per hectare. Data of five plants from each genotype was averaged replication wise and mean data was used for statistical analysis. Cluster and PC analysis of 24 bitter gourd genotypes based on yield and its 19 component traits to assess the magnitude of genetic variation were performed by using statistical software Widostat Version 9.2 from indostat services. Clustering pattern among 24 bitter gourd genotypes exhibiting dendrogram was assessed by using Tocher's method (Fig. 1). Average intra (diagonal) and inter-cluster distance was estimated by using Tocher's method represent-

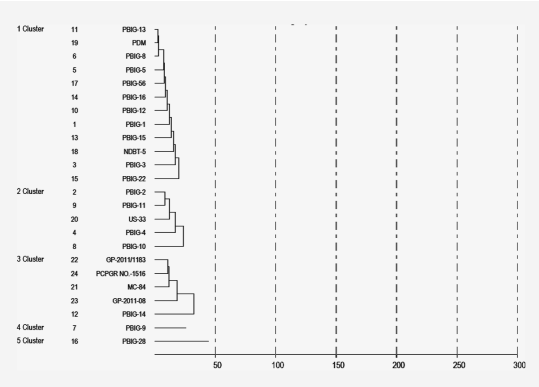

Fig. 1. Clustering pattern of different genotypes by Tocher's method.

ing Euclidean distances considering yield and its ten contributing traits in bitter gourd genotypes.

Results and Discussion

Cluster analysis by Tocher's method was done to study divergence in 24 genotypes in respect of various economic traits. The genotypes were grouped into clusters. Cluster number I had highest number (12) of genotypes (viz., PBIG-13, PDM, PBIG-8, PBIG-5, PBIG-56, PBIG-16, PBIG-12, PBIG-1, PBIG-15, NDBT-5, PBIG-3 and PBIG-22) followed by cluster number II and III (5 each) then cluster IV and V (1 each). Distribution of genotypes in each cluster is presented in Table 2.

Maximum inter-cluster distance was calculated between cluster IV and V (498.807) followed by cluster III and V (322.814), cluster I and V (228.385), cluster II and IV (219.074), cluster II and V (187.665), cluster III and IV (170.542), and cluster II and III (157.031), however, minimum distance was found between inter-cluster, cluster I and II (81.147) followed by cluster I and II (87.893) and I and IV (114.919). The maximum intra-cluster distance was noted in cluster III (75.125) followed by cluster II (61.947) and cluster I (40.470), while minimum intra-cluster distance was recorded in cluster IV and cluster V (0.000). The averages inter and intra-cluster distances have been presented in Table 3. Cluster dendrogram and Mahalanobis distance depicted in Fig. 1 and Fig. 2, respectively. Result showed that the inter-cluster distance greater than intra-cluster distance in all cases. This findings are agreement with Islam et al. (2010) and Khosa and Dhatt (2015). The grouping of genotypes in clusters reflects the relative divergence of clusters and allows a convenient selection group of genotypes with their overall phenotypic similarity for hybridization program facilitating better exploitation of germplasm. Generally crosses involving parents belonging to most divergent clusters are expected to give maximum heterosis and create wide variability in genetic architecture. However, for a practical plant breeder, the objective is not only obtaining high heterosis but also to achieve high level of production with the shortest possible time. In the present study, the maximum distances existed between cluster IV and V (498.807). Considering group distances and other agronomic performance, the inter-genotypic crosses between the members of cluster V with that of cluster IV would exhibit high heterosis and is also likely to produce new recombinants with desired traits. Therefore, more emphasis should be given on cluster V and IV in selecting inbreds for crossing in

Table 2. Distributing pattern of 24 genotypes of bitter gourd into five clusters.

Cluster number	Number of genotypes	Genotype included
I	12	PBIG-13, PDM, PBIG-8, PBIG-5, PBIG-56, PBIG-16, PBIG-12, PBIG-1, PBIG-15, NDBT-5, PBIG-3 & PBIG-22
II	5	PBIG-2, PBIG-11, US-33, PBIG-4 & PBIG-10
III	5	GP-2011//1183, PCPGR NO.-1516, MC-84, GP-2011-08 & PBIG-14
IV	1	PBIG-9
V	1	PBIG-28

Table 3. Inter and intra-cluster distances. The intra cluster distances are shown in parentheses.

Cluster	I	II	III	IV	V
I	(40.470)	81.147	87.893	114.919	228.385
II	81.147	(61.947)	157.031	219.074	187.665
III	87.893	157.031	(75.125)	170.542	322.814
IV	114.919	219.074	170.542	(0.000)	498.807
V	228.385	187.665	322.814	498.807	(0.000)

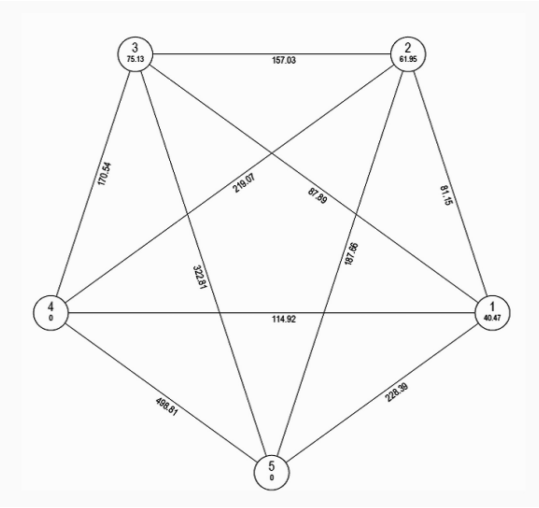

Fig. 2. Mahalanobis Euclidean distance through Tocher's method.

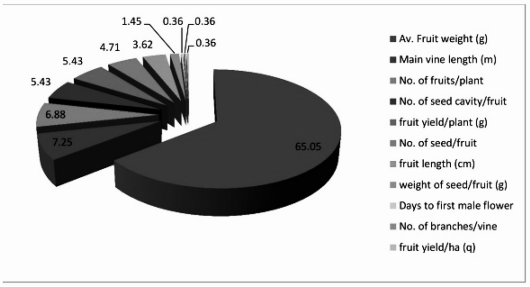

Fig. 3. Contribution (%) of characters towards divergence.

bitter gourd hybridization programs.

The selection and choice of parents mainly depends upon contribution of characters towards divergence. The present study resulted that average fruit weight (65.05%) contributed maximum to the total genetic diversity among the genotypes followed by, main vine length (7.25%), number of fruits per plant (6.88%), number of seed cavity per fruit (5.43%), fruit yield per plant (5.43%), number of seeds per fruit (4.71%), fruit length (3.62%), weight of seed per fruit (1.45%), days to first male flower (0.36%), number of branches per vine (0.36%) and fruit yield per hectare (0.36%). Contribution (%) of characters towards divergence dipicted in Fig. 3. Therefore, average fruit

Table 4. Values of Latent roots (Eigen values) for PC of different characters.

Parameters	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Eigen value (Root)	5.098	4.363	2.795	1.676	1.076	0.963
Explained variation (%)	26.830	22.962	14.712	8.821	5.662	5.068
Cumulative explained variation (%)	26.830	49.792	64.504	73.325	78.987	84.055
Trait			Eigen vectors			
Days to first male flower	0.263	0.152	0.310	0.060	0.274	0.005
Days to first female flower	0.329	0.017	– 0.275	0.130	– 0.182	0.110
Number of node to first male flower	0.329	0.178	– 0.094	0.089	0.113	0.355
Number of node to first female flower	0.103	– 0.045	– 0.380	– 0.432	– 0.043	0.250
Days to first harvest	0.148	0.336	0.090	0.003	0.281	0.168
Number of fruits per plant	–0.281	0.178	0.203	– 0.227	– 0.229	0.216
Average fruit weight (g)	– 0.005	– 0.352	0.126	– 0.359	0.049	0.257
Fruit length (cm)	0.356	– 0.108	0.043	– 0.068	0.128	– 0.355
Fruit diameter (cm)	– 0.311	0.103	– 0.178	0.012	0.147	0.446
Number of seed cavity per fruit	– 0.367	– 0.008	– 0.174	0.069	0.068	– 0.088
Length of seed cavity (cm)	– 0.247	0.175	– 0.224	0.268	0.320	– 0.084
Main vine length (m)	– 0.182	– 0.276	0.322	– 0.118	0.103	– 0.273
Number of branches per vine	0.211	0.146	– 0.169	– 0.299	– 0.477	– 0.204
Internodal length (cm)	0.085	–0.104	0.390	– 0.063	– 0.018	0.387
Number of seeds per fruit	0.032	–0.437	– 0.053	– 0.105	0.053	– 0.104
Weight of seed per fruit (g)	– 0.013	–0.389	– 0.031	0.341	– 0.245	0.123
Seed index (g)	0.141	–0.173	0.149	0.529	– 0.334	0.157
Fruit yield per plant (g)	0.266	–0.266	0.037	– 0.057	0.367	0.050
Fruit yield per ha (q)	– 0.082	0.264	0.429	– 0.069	– 0.224	0.003

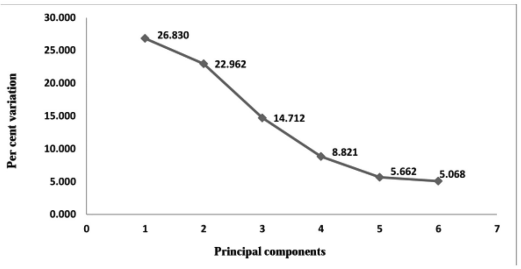

Fig. 4. Latent roots (Eigen values) for PC of different characters.

weight would be the more important characters for selecting divergent genotypes in breeding program. Similarly, high contribution towards the divergence was reported by average fruit weight (Singh et al. 2013), average fruit weight, fruit length (Singh et al. 2014), days to first male flower, number of branches per vine, fruit yield per plant, weight of seed per fruit (Kundu et al. 2012).

The principal component analysis of 24 bitter gourd genotypes based on correlation matrix of yield and yield contributing traits yielded the 6 Eigen roots or Eigen values. Eigen roots along with percentage of variation explained by each Eigen roots have beenpresented in Table 4. Principal component analysis revealed highest Eigen value (5.09) of first principal axis. The Eigen root of first principal component was accounted approximately 26.830% of the total variation followed by second to sixth components which accounted 22.962, 14.712, 8.821, 5.662 and 5.068% of total variation presented among genotypes, respectively. Latent roots (Eigen values) for PC of different characters are depicted in Fig. 4. The first six PC axes explained 84.055% of the variations, suggesting first six principal axes are adequate to explain the variation in reduced dimension. These were interpreted as relative weight of the variables in each component. The important variables are those which have high positive or negative relative weight values. The first principal component had high positive weight to fruit length (0.356) followed by number of node to first male flower (0.329) and days to first female flower (0.329), while high negative weight to number of seed cavity per fruit (–0.367) followed by fruit diameter (–0.311) and number of fruits per plant (–0.281). The second principal component had high positive weight to days to firsty harvest and fruit yield per ha, while high negative weight to number of seeds per fruit and weight of seed per fruit. The third principal component exhibited high positive weight to fruit yield per ha and internodal length, while negatively associated with number of node to first female and days to first female flower. The fourth principal component had high positive weight to seed index and weight of seed per fruit, while showing negative association with number of node to first female flower and average fruit weight. The fifth principal component contained high positive weight to fruit yield per plant and length of seed cavity. However, exhibited high negative weight to number of branches per and seed index. The sixth principal component exhibited high positive weight to fruit diameter and internodal length, while exhibited negative weight to fruit length and main vine length. The results presented here are in conformity with the findings of Sanwal et al. (2008), Singh et al. (2008), Singhal et al. (2010), Choudhary et al. (2011), Rabbani et al. (2012) and Singh et al. (2014). Out of 24 genotypes, PBIG-22 was found exceptionally unique and predominantly female (sub-gynoecious) with desirable agronomic traits having a 1:5.5 ratio of male and female flowers with highest fruit yield per plant (2.32 kg), yield per hectare (193.52 q), vine length (3.30 m), high number of fruits per plant (33.00), fruit length (12.33 cm), fruit diameter (3.73 cm), fruit weight (68.89 g), number of branches per vine (9.00), lower number of node at which first female flower emerged (8.57) and days taken to first harvest (63.06). We have been able to maintain this novel line with a very high proportion of pistillate flowers through sib-mating. Development of sub-gynoecious lines with high proportions of pistillate flowers will help in the development of hybrids with very high proportion of pistillate flowers with better agronomic traits which will ultimately yield high. Hence, the identified sub-gynoecious line can be conserved and utilized for further bitter gourd improvement program.

It was concluded from the principal component analysis that important variables in bitter gourd genotype with respect to agronomic and yield contributing traits were number of primary branches, main vine length, days to first female flower anthesis,

number of node number to first female flower, days to first harvesting, fruit length, fruit diameter, length of seed cavity, number of fruits per plant, average fruit weight and fruit yield per plant. The above variables might be taken into consideration for effective selection of parents during hybridization program.

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