



GENETIC DIVERGENCE STUDIES IN BOTTLE GOURD [*LAGENARIA SICERARIA* (MOL.) STANDL.]

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Abstract

An experiment was carried out to analyze genetic diversity for yield and its contributing traits in 31 bottle gourd genotypes at Research cum Instructional Farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), India; during *Kharif* 2014. The cluster analysis grouped all 31 bottle gourd genotypes into 5 major clusters based on D^2 value. Extreme genetic divergence was estimated among clusters. Maximum number of genotypes were grouped into cluster V included ten genotypes, whereas, cluster II included eight genotypes. The cluster I had six genotypes, which is followed by cluster IV and cluster III had only three genotypes in each cluster. Fruit length, fruit girth and average fruit weight contributes maximum towards genetic divergence.

Key words : Bottle gourd, cluster, divergence, genotypes and yield.

Introduction

Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.], locally known as Lauki is an important home garden vegetable. It is a fast growing crop, native to India. India is endowed with the wealth of bottle gourd germplasm, comprising of both wild and cultivated species. Continuous cultivation of cross-pollinated crop, large variation in vegetative and fruit characters has occurred and created huge genetic diversity. It is grown in both rainy and summer seasons and its fruits are available in the market throughout the year. Bottle gourd is the largest produced cucurbitaceous vegetables in the world preferred in both urban and rural population. Bottle gourd is a rich source of minerals and vitamins. In Chhattisgarh, no comprehensive systematic research has been done in this crop. The yield potentiality of this crop needs to be improved through an effective breeding programme. Studies on the variations of yield and yield contributing characters are of great importance before planning a breeding program.

Genetic diversity analysis among elite germplasm is prerequisite for choosing promising genetic diverse lines for desirable traits and to reveal genetic distinctness among genotypes (Ali *et al.*, 2008). Assessment of genetic diversity in germplasm collections imposes the

categorization of accessions and useful in assigning genotypes to specific heterotic groups to create segregating progenies with maximum genetic variability for further breeding purposes. Looking to the above present study, we classify the genotypic set based on multivariate analysis for generating more heterotic cross combinations and finally superior useful hybrids.

Materials and Methods

The study was carried out during *Kharif* season (2014) at Research cum Instructional farm, IGKV, Raipur (C.G.), India. The experiment comprised of thirty one genotypes of bottle gourd collected from different region of southern Chhattisgarh. The experiment was laid out in a randomized block design with three replications at 3.0 × 1.0 m row to row and plant to plant spacing. All the recommended cultural practices were adopted to raise a healthy crop. Data were recorded on five randomly selected plants with respect to characters *viz.*, days to 50% flowering, number of branches per plant, node number of first female flower appears, node number of first female flower appears, days to fruit set, days to first fruit harvest, number of fruits per plant, fruit length (cm), fruit girth (cm), average fruit weight (g), total soluble solid (%), 100 seed weight, fruit yield per plot, duration of crop (sowing to last harvest). The data obtained on

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Table 1 : Composition of clusters in bottle gourd genotypes.

Cluster Number	Number of genotypes included	Name of genotypes
I	6	IBG-5, IBG-6, IBG-12, IBG-14, IBG-24, IBG-27
II	8	IBG-4, IBG-19, IBG-20, IBG-21, IBG-23, IBG-26, IBG-29, IBG-30
III	2	IBG-13, IBG-31.
IV	5	IBG-1, IBG-2, IBG-3, IBG-15, IBG-22.
V	10	IBG-7, IBG-8, IBG-9, IBG-10, IBG-11, IBG-16, IBG-17, IBG-18, IBG-25, IBG-28.

Table 2 : Intra (bold) and Inter cluster distance values in bottle gourd genotypes.

Cluster number	I	II	III	IV	V
I	1.854				
II	3.809	2.611			
III	5.348	5.483	2.095		
IV	3.889	2.737	5.554	2.215	
V	2.997	4.284	5.379	4.045	3.441

above 14 characters was used for cluster analysis and investigated to select the parents for hybridization using Mahalanobis (1936) D^2 statistics. The genotypes were grouped into different clusters by Tocher's method (Rao, 1952). The population was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D^2 was fixed by taking the maximum D^2 values between any two populations in the first row of the table where D^2 values were arranged in increasing order of magnitude.

Results and Discussion

The analysis of variance revealed significant differences among bottle gourd genotypes for all characters suggesting considerable genetic variability in the population. Using the estimated D^2 values as squares of generalized distance, all genotypes were grouped into 5 clusters (table 1). Maximum number of genotypes were grouped into cluster V (IBG-7, IBG-8, IBG-9, IBG-10, IBG-11, IBG-16, IBG-17, IBG-18, IBG-25, IBG-28) included ten genotypes, whereas, cluster II (IBG-4, IBG-19, IBG-20, IBG-21, IBG-23, IBG-26, IBG-29, IBG-30) included eight genotypes. The cluster I had (IBG-5, IBG-6, IBG-12, IBG-14, IBG-24, IBG-27) six genotypes, which is followed by cluster IV (IBG-1, IBG-2, IBG-3, IBG-15, IBG-22) and cluster III (IBG-13, IBG-31) had three

genotypes in each. The pattern of clustering indicated that there was no association between geographic distribution of genotypes and genetic divergence as the same group consisted of genotypes from diverse locations and the genotypes of same source fell into different groups also.

The average inter and intra cluster distances among the five clusters are presented in table 2. Maximum inter cluster distance was observed between cluster III and IV (5.554) followed by cluster III and II (5.483), cluster III and V (5.379), cluster III and I (5.348). The minimum inter-cluster distance was recorded in between cluster IV and cluster II (2.737) followed by cluster V and I (2.997). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. The maximum intra cluster distance was observed in cluster V (3.441) closely followed by cluster II (2.611) indicating maximum diversity within these clusters. Genotypes from distant clusters could be exploited in hybrid development programmes due to their wide genetic distance. These results are in general agreement with the findings of Islam (2004), Singh *et al.* (2007) and Bhardwaj *et al.* (2013).

The contribution of each character to divergence is presented in table 3. The result showed that fruit length contributes highest (23.87%) towards divergence followed by fruit girth (23.44%), average fruit weight (23.44%) and node number of first female flower appears (18.06%). Whereas, fruit yield per plot (9.46%), days to fruit set (0.86%) and 100 seed weight (0.86) contribute lowest to divergence. This contribution is an important consideration for the purpose of further selection and choice of parents for hybridisation. The results of the present study was close agreement with findings of Islam (2004) who reported that primary branches per plant, fruit length and weight, number of fruits and yield per plant contributed the most of the total genetic divergence and Mladenovic *et al.* (2012).

The mean performance for different clusters of genotypes for yield and its components are presented in table 4. Cluster V expressed highest mean value fruit length, number of fruit per plant, 100 seed weight, duration of crop and fruit yield per plot and lowest mean value for node number of first male flower appears. Cluster IV showed highest mean performance for average fruit weight. The better genotypes can be selected for most of characters on the basis of mean performance in the cluster.

Table 3 : Contribution of character's towards divergence in bottle gourd genotypes.

Characters	Days to 50% flowering	No. of branches per plant	Node no. of first female flower	Node no. of first male flower	Days to fruit set	Days to 1st fruit harvest	Fruit length (cm)	Fruit girth (cm)	Avg. fruit weight (g)	No. of fruits per plant	T.S.S	100 seed weight	Fruit yield/plot (kg)	Duration of crop (sowing to last harvest)	Total
Number times appearing first time	0	0	84	0	4	0	111	109	109	0	0	4	44	0	465
Percent contribution	0	0	18.06	0	0.86	0	23.87	23.44	23.44	0	0	0.86	9.46	0	100

Table 4 : Mean performance of genotypes in individual cluster for yield and its components in bottle gourd genotypes.

Character	Days to 50% flowering	No. of branches per plant	Node no. of first female flower appears	Node no. of first male flower appears	Days to fruit set	Days to first fruit harvest	Fruit length (cm)	Fruit girth (cm)	Avg. fruit weight (gm)	No. of fruits per plant	T.S.S	100 seed weight	Duration of crop (sowing to last harvest)	Fruit yield/plot (kg)	Total
I	6	47.33	12.89	46.61	37.00	55.17	67.83	23.78	40.94	941.67	9.50	3.06	19.17	154.61	57.17
II	8	63.00	12.17	40.42	38.71	71.75	83.12	29.96	37.77	700.00	7.12	3.49	19.25	155.67	51.88
III	2	52.00	17.83	52.17	49.83	61.00	74.00	32.50	30.50	1066.67	5.50	5.50	5.50	152.33	55.00
IV	5	63.60	16.73	51.73	40.67	72.00	82.80	24.33	37.53	1196.67	9.93	2.60	18.47	154.27	47.20
V	10	49.80	16.20	53.23	28.10	58.40	69.50	36.30	25.87	1140.33	11.20	3.22	19.83	156.52	62.70

Table 5 : Desirable bottle gourd genotypes based on cluster mean performance.

Cluster Chracters	I	II	III	IV	V
1	IBG-14	IBG-26	IBG-13	IBG-3	IBG-11
2	IBG-16	IBG-4	IBG-31	IBG-15	IBG-28
3	IBG-5	IBG-23	IBG-13	IBG-22	IBG-8
4	IBG-5	IBG-29	IBG-13	IBG-2	IBG-10
5	IBG-12	IBG-21	IBG-13	IBG-3	IBG-10
6	IBG-14	IBG-21	IBG-13	IBG-3	IBG-8
7	IBG-24	IBG-29	IBG-31	IBG-2	IBG-7
8	IBG-24	IBG-21	IBG-13	IBG- local	IBG-11
9	IBG-5	IBG-20	IBG-31	IBG-3	IBG-11
10	IBG-14	IBG-26	IBG-31	IBG-15	IBG-11
11	IBG-6	IBG-29	IBG-31	IBG-22	IBG-11
12	IBG-14	IBG-19	IBG-31	IBG-2	IBG-28
13	IBG-14	IBG-21	IBG-31	IBG- local	IBG-11
14	IBG-6	IBG-4	IBG-31	IBG-22	IBG-8

1. Days to 50% flowering 2. Number of branches per plant 3. Node number of first female flower appears 4. Node number of first male flower appears. 5. Days to fruit set 6. Days to first fruit harvest 7. Fruit length (cm) 8. Fruit girth (cm) 9. Average fruit weight (g) 10. Number of fruits per plant 11. T.S.S (%) 12.100 seed weight 13. Fruit yield/plot (kg) 14. Duration of crop (Sowing to last harvest).

The best genotypes, which had chosen for different characters are presented in table 5. In this study, group constellation showed that cluster V (IBG-7, IBG-8, IBG-9, IBG-10, IBG-11, IBG-16, IBG-17, IBG-18, IBG-25 and IBG-28) included genotypes with most of the superior traits hence these genotypes could be directly selected and utilised on the basis of the observations recorded on a diverse group of bottle gourd genotypes, it may be concluded that hybridization between genotypes of diverse clusters may help in developing better genotype/varieties for fruit yield in bottle gourd for Chhattisgarh plains.

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