



Studies on Nature and Magnitude of Genetic Divergence in Bottle Gourd (*Lagenaria siceraria* Mol Standl.) using D² Analysis*

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ABSTRACT

An experiment was conducted to study the nature and magnitude of genetic divergence of twenty four bottle gourd genotypes obtained from NBPGR, Hyderabad along with one check variety i.e. Pusa Naveen sown in Randomized Block Design (RBD) with three replications during spring summer 2012. The genotypes were grouped into five different clusters using D² analysis. Cluster III possessed maximum number of genotypes (11) followed by the cluster IV (8). Maximum inter cluster distance was observed between cluster II and V and minimum between III and IV clusters. In case of intra cluster distance, the maximum distance was observed in cluster III and it was zero in solitary clusters like cluster II and V. Based on cluster mean, the genotypes of cluster II followed by cluster I recorded highest mean for yield per vine and other yield attributing traits. Selection of superior genotypes with desirable traits and with high genetic distance could be selected for hybridization programmes and recognition of best genotypes for different traits to produce new elite recombinants in bottle gourd.

Key words : Bottle gourd, Cluster, D² analysis, Genetic diversity.

Bottle gourd (*Lagenaria siceraria*, 2n=22) is one of the most important rainy and summer season cucurbit vegetable grown in India. It is a rich source of vitamin C, protein, potassium, sulphur and phosphorous and is good for people suffering from biliousness and indigestion (Thumburaj and Singh, 2003). Being a highly cross pollinated crop due to its monoecious and andromonecious nature (Swiander *et al.*, 1994) bottle gourd has wide genetic diversity.

It has originated in Africa and reached India through sea routes and has a tremendous potential for both domestic and export markets. However, no systematic information is available on the genetic amelioration of bottle gourd, especially on magnitude of genetic diversity. Multivariate analysis is a potent tool in divulging the divergence among the genotypes based on multiple characters. Mahalanobis (1936) generalized distance estimated by D² statistic has been generally used as an efficient tool in the quantitative estimation of genetic diversity for rational choice of potential parents in a breeding programme. Thus, an attempt has been made to assess the genetic diversity in twenty four genotypes of bottle gourd.

MATERIAL AND METHODS

The experimental material consists of 24 bottle gourd genotypes *viz.*, IC 249663, PSR 13300, PSR 13156, PSR 13290, RJR 27, PSR 13176, RJR 201, IC 446596, IC 249654, IC 249672, IC 249671, IC 249668, IC 446594, RJR 533, IC 249665, IC 249658, IC 249653, IC 446592, IC 249650, RJR 420, IC 249656, IC 256053 and NSJ 298 obtained from NBPGR, Hyderabad and along with one check variety i.e. Pusa Naveen, sown in randomized block design with three replications during spring summer of 2012 at College farm, Horticultural College and Research Institute, Dr. Y.S.R.Horticultural University, Venkataramanna gudem, Andhra Pradesh. The plants were spaced at 2x1 m maintaining six plants per plot. Recommended cultural practices were adopted to raise successful crop. Observations on tendrill length (cm), no. of primary branches per vine, total vine length (m), no. of nodes per vine, internodal length (cm), days to 1st male flower appearance, days to 1st female flower appearance, node at which 1st male flower appearance, node at which 1st female flower appearance, days to first fruit harvest, no. of fruits per vine, fruit weight (g), fruit length (cm),

fruit diameter (cm), fruit yield per vine (kg), total yield (t/ha), no. of seeds per fruit and 100 seed weight (g) for each genotype were recorded on five randomly selected plants.

Divergence between any two populations was obtained as sum of squares of difference in the transformed values of corresponding entries using D^2 statistic. Genetic diversity was worked out following Mahalanobis' (1936) generalized distance (D^2) extended to clustering in Ward's method.

RESULTS AND DISCUSSION

Genetic divergence among the genotypes of bottle gourd was studied through Mahalanobis' D^2 analysis. Clustering based on the studied traits separated the genotypes into five clusters (Table 1.) on the basis of their genetic similarity so that genotypes within a cluster had smaller D^2 value among themselves than those belonging to different clusters. Cluster III consisted of maximum number of genotypes (11) followed by cluster IV (8) while cluster I had three genotypes whereas clusters II and V were solitary clusters.

The intra cluster D^2 values ranged from 0.000 to 160.201 and maximum distance was

reported in cluster III (160.201) followed by cluster I (142.207). The solitary clusters II and V had no intra cluster distance (zero). The inter cluster D^2 values varied from 239.737 to 3966.505 and maximum genetic divergence existed between clusters II and V (3966.505) followed by cluster I and V (2198.979) indicating wider genetic diversity among the genotypes included in these groups (Table 2 & Fig 1). Selection of parents for hybridization programme from cluster combinations of II & V and I & V, which showed higher inter cluster distance would help in achieving novel recombinants. The minimum genetic divergence registered between clusters III and IV (239.737) suggested that genotypes of these clusters had closeness among themselves.

Medium inter-cluster distances were observed between the cluster I and III, I and IV, IV and V, III and V. The crosses involving parents belonging to medium divergent clusters may also exhibit significant and positive heterosis (Karim *et al.*, 2001 and Mian and Bhal, 1989). In the present study, inter cluster distance was always higher than intra-cluster distance and similar results were earlier reported by Sidhu and Gautom (1985) in

Table 1. Clustering pattern of 24 bottle gourd genotypes by Ward's method.

Cluster	No. of genotypes	Genotypes
I	3	IC 249663, IC 249672, IC 446594
II	1	IC 249671
III	11	PSR 13300, RJR 201, RJR 27, IC 249658, IC 249656, PSR 13176, RJR 420, IC 249653, IC 249668, IC 256053, PSR 13156
IV	8	PSR 13290, IC 249654, RJR 533, IC 249665, IC 446592, IC 249650, NSJ 298, Pusa Naveen
V	1	IC 446596

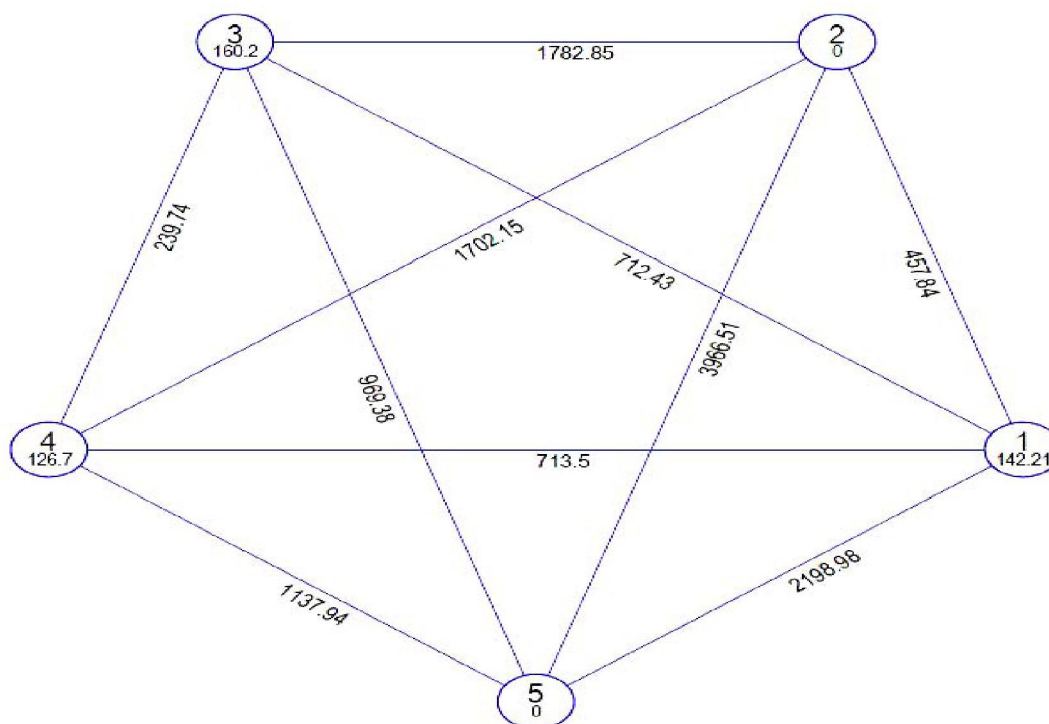
Table 2. Average intra and inter-cluster D^2 values for five clusters in 24 genotypes of Bottle gourd.

Clusters	I	II	III	IV	V
I	142.207	457.837	712.427	713.503	2198.979
II		0.000	1782.849	1702.149	3966.505
III			160.201	239.737	969.380
IV				126.704	1137.935
V					0.000

Table 3. Mean values of clusters for different characters in 24 genotypes of Bottle gourd (Ward's method).

Character	Cluster				
	I	II	III	IV	V
Tendrill length (cm)	28.18	36.40	25.73	25.50	19.03
Nodes per vine	123.99	144.73	114.04	117.82	79.73
Number of primary branches per vine	15.83	20.50	12.78	12.75	8.17
Total vine length (m)	12.74	16.36	10.65	11.54	7.70
Internodal length (cm)	10.25	11.34	9.37	9.80	9.17
Days to 1 st male flower appearance	68.53	66.86	75.19	58.98	50.18
Days to 1 st female flower appearance	83.58	80.91	89.78	84.28	67.79
Node at which 1 st male flower appearance	37.67	27.51	36.19	27.36	24.67
Node at which 1 st female flower appearance	51.74	40.74	53.28	46.47	41.84
Days to first harvest	104.55	102.50	108.76	102.29	75.43
Number of fruits per vine	6.26	9.13	4.12	4.88	10.45
Fruit weight (g)	1707.29	1841.49	1203.40	1397.55	197.55
Fruit length (cm)	20.91	20.77	37.97	44.05	13.75
Fruit diameter (cm)	16.45	18.04	7.45	7.96	6.28
Yield per vine (kg)	10.74	16.77	4.80	6.80	2.09
Total yield (t/ha)	26.86	41.92	12.01	16.99	5.23
Number of seeds per fruit	347.54	729.63	204.84	212.93	155.84
100 seed weight (g)	15.07	18.22	9.88	13.82	6.54

Fig. 1. Mean inter and intra cluster distances of bottle gourd genotypes.



watermelon and Khatun *et al.* (2010) in snake gourd.

Mean performance of different clusters for eighteen characters presented in table 3 revealed that the mean values of cluster varied in magnitude for all the traits under study. Cluster II showed highest mean for tendril length, no. of nodes per vine, no. of primary branches per vine, total vine length, internodal length, node at which 1st female flower appearance, fruit weight, fruit diameter, no. of seeds per fruit and 100 seed weight. Cluster V exhibited the minimum no. of days to 1st male and female flower appearance, node at which 1st male flower appearance and days to first fruit harvest. Fruit length was maximum in cluster IV. The most important economic trait, yield per vine was maximum in cluster II (16.77 kg) followed by cluster I (10.74 kg) and cluster IV (6.80 kg).

The clustering pattern could be utilized in choosing parents for cross combinations likely to generate the highest possible variability for various economic characters. Hence, in the present study a convergent improvement can be suggested between the genotypes of the cluster II & V followed by cluster II & III to develop high yielding novel recombinants. The genotypes of highly divergent clusters may also be utilized in a diallel or line \times tester fashion for effective exploitation of heterosis.

Conclusion

Based on genetic divergence study using Mahalanobis' D² statistic, the 24 genotypes differed significantly for all the characters under study and were grouped into five clusters on the basis of

genetic similarities. Genotypes IC 249671(cluster II) and genotypes IC 446596 (cluster V) and genotypes IC 249663, IC 249672 and IC 446594 (cluster III) exhibited high genetic diversity, so crosses between these genotypes are likely to produce new recombinants with desired traits.

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