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Short Communication

Genetic divergence study in bottle gourd (*Lagenaria siceraria* Molina Standl.)

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Bottle gourd is one of the most important cucurbitaceous crops and is a rich source of potassium, vitamin C, protein, sulphur, fat and phosphorous. The experimental material consisted 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 which were sown in randomized block design with three replications during spring summer of 2012 at Horticultural College and Research Institute, Dr. Y.S.R.Horticultural University, Venkataramannagudem, Andhra Pradesh. Row to row and plant to plant spacings were maintained at 2m and 1m, respectively in 6m × 4m plot. Six plants were maintained in each plot for recording the observations. Recommended cultural practices were adopted for proper growth and stand of crop. Observations on tendril 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 appears, node at which 1st female flower appears, 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 from five randomly selected plants per replication. 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.

Genetic divergence among the genotypes of bottle gourd was studied through Mahalanobis' D^2analysis. 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, the remaining clusters II and V were solitary clusters. The intra cluster D^2 values ranged from 0.000 to 160.201, where maximum distance was reported in cluster III (160.201) followed by cluster I (142.207). The 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 was 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. It is mentioned that 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 this experiment, intercluster distance was always higher than intra-cluster distance. Sidhu and Gautom (1985) in watermelon and Khatun *et al.,* (2010) in snake gourd also found similar

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Table 1. Clustering pattern of 24 genotypes of bottle gourd 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
Tendril 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 1st male flower appearance	68.53	66.86	75.19	58.98	50.18
Days to 1st female flower appearance	83.58	80.91	89.78	84.28	67.79
Node at which 1st male flower appearance	37.67	27.51	36.19	27.36	24.67
Node at which 1st 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

result in watermelon. Mean performance of different clusters for eighteen characters were shown in the Table 3 revealed that the mean values of cluster varied in magnitude for all the traits under this 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 appears, 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 appears and days to first fruit harvest. Fruit length was maximum in cluster IV. The most important economic trait, yield per vine was maximum for cluster II (16.77 kg) followed by cluster I (10.74 kg) and cluster IV (6.80 kg). 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 × tester fashion for effective exploitation of heterosis.

Conclusion

Genetic divergence using Mahalanobis' D^2 statistic was studied in 23 bottle gourd genotypes. The genotypes differed significantly for all the characters under studied and were grouped into five clusters on the basis of genetic similarities. Genotype IC 249671(cluster II), and genotype IC 446596 (cluster V) and genotypes IC 249663, IC 249672 and IC 446594 (cluster III) show a lot of genetic diversity, so crosses between these genotypes are likely to produce new recombinants with desired traits.

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