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Studies on genetic divergence in sponge gourd (*Luffa cylindrica* L. Roem.)

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Abstract

The experiment was conducted during the spring-summer season, 2017 in Eastern Uttar Pradesh, to evaluate the nature and magnitude of genetic divergence among the thirty genotypes of bitter gourd were carried out by using Mahalanobis D^2 statistics. Thirty genotypes were grouped into 7 different non-overlapping clusters. The highest number of genotypes was presented in cluster III which contained 9 entries followed by cluster V which contains 8 entries, cluster VI which contained 5 entries, cluster I which contained 4 entries, cluster IV which contained 3 entries and cluster II possess 1 entries respectively. Highest estimates of genetic advance in per cent of mean was recorded for vine length (80.31%), node number to anthesis of first staminate flower (66.23%), number of fruits per plant (45.65%), total fruit yield/plant (38.42%). Moderate genetic advance in per cent of mean was estimated in number of primary branches per plant (37.86%), node number to anthesis of first staminate flower (37.65%), fruit length (37.40%), number of nodes per vine (35.35%), average fruit weight (31.68%), fruit diameter (29.79%) whereas days to anthesis of first pistillate flower (26.12%), days to anthesis of first pistillate flower (23.80%), days to first fruit harvest (21.58%) showed low genetic advance in per cent of mean. Vine length contributed maximum towards genetic diversity (26.67%), followed by fruits per plant (25.75 %), days to anthesis of first pistillate flower (13.69%), average fruit weight (9.43%), number of primary branches per plant (8.51%), node number to anthesis of first staminate flower (7.36%), fruit length (4.37%) and total marketable fruit yield per plant in sponge gourd.

Keywords: genetic divergence and sponge gourd

Introduction

Luffa [*Luffa cylindrica* L. (Roem) Syn. *L. aegyptica* Mill.] commonly called as sponge gourd, Loofah, vegetable sponge or dish cloth gourd, is a member of family Cucurbitaceae having diploid chromosome number $2n=2x=26$. It originated in subtropical Asian region particularly India (Kalloo, 1993) [2]. Sponge gourd is an annual cucurbit plant produces fruits containing a fibrous vascular system with various vines and cylindrical tenangled fruit. Leaves are deltoid to nearly orbicular exteriorly, but pointed at the apex and usually three to seven lobed with dentate margin (Whitaker and Davis, 1962) [6]. Sponge gourd is monoecious crop with branches tendrils. Flowers are yellow and showy having five petals. The inflorescence of staminate flowers is on raceme, while the pistillate flowers are solitary and have short to long peduncle. It is commonly grown for its tender marketable green fruits for vegetable purpose as well as for sponge of mature fruits which is used for scrubbing of body skin and utensil purposes. Fruits are rich in Iron Vitamin A and C. It has certain medicinal uses. The cooked fruit are easily digestible and very appetizing therefore it is recommended to the patients suffering from malaria or other seasonal fevers.

Luffa (*Luffa cylindrica* (L.) MJ. Roem syn. *L. aegyptica* Mill.) commonly called as sponge gourd, loofah, vegetable sponge or dish cloth. It is one of the most important cucurbits grown extensively throughout the tropical and sub-tropical regions of the country and world, The crop belongs to the family Cucurbitaceae which includes about 118 genera and 855 species. Its unripe tender fruits are popular and well known culinary in India with good nutritive value and high yield potentials. The tender fruits are rich in carbohydrates, vitamin A, vitamin C and iron.

Material and Methods

Thirty genotypes (including Pusa Chikni as check variety) of sponge gourd having diverse origin were evaluated at Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, during the spring-summer season, 2017.

The experiment was lay out in a randomized block design with three replications in individual plot size (3m x 2.5m). The distance maintained between row to row and plant to plant was 2.5

m and 0.50m, respectively. Five plants were randomly selected from each plot in each replication. Recommend cultural practices and plant protection measures were followed to raise a healthy crop. Data were recorded on various parameters (Table 3). The data recorded on each character of different genotypes were statistically analyzed. The genetic divergence was estimated using D² statistics of Mahalanobis (1928) [3]. The intra and inter-cluster distance were calculated according to Tocher's method envisaged by Rao (1952)

Results and Discussion

There were significant differences among the genotypes for all the characters under this investigation indicated a considerable amount of genetic variability among 30 genotypes including one check variety (Pusa Chikni). Based on D² values all the genotypes of sponge gourd were grouped in six distinct non-overlapping clusters using Mahalanobis D² statistics. Thirty genotypes were grouped into 7 different non-overlapping clusters. The highest number of genotypes was presented in cluster III which contained 9 entries followed by cluster V which contains 8 entries, cluster VI which contained 5 entries, cluster I which contained 4 entries, cluster IV which contained 3 entries and cluster II possess 1 entries respectively. The genotypes within the same cluster although formed specific cluster but were collected from different places. The clustering pattern of the genotypes revealed that the genotypes collected from the same place did not form a single cluster. This indicates that geographic diversity is not always related to genetic diversity. Similar results had been also reported by Islam *et al.*, 2010 [1]; Singh *et al.*, 2014 [5] in sponge gourd. Intra-cluster distances were smaller than inter-cluster distances, show a considerable amount of genetic diversity among the genotypes studied.

The maximum intra-cluster distance observed in case of cluster II (330.49) followed by cluster VI (171.57) and cluster I (169.51), cluster III (153.00) while the minimum intra-

cluster distance showed by cluster IV (140.65) and cluster V (60.89).

The maximum inter-cluster distance was found between II and V (1084.584) followed by cluster II and IV (935.013), cluster II and VI (672.807), cluster II and III (486.229), cluster I and II (343.181). The minimum inter-cluster D² were recorded in case of cluster IV and V (238.581), cluster I and III (318.022), cluster IV to VI (367.142), cluster I and IV (463.759).

A perusal of showed that the cluster means for different traits indicated considerable differences between the clusters. Cluster VI showed the maximum mean value for node number to anthesis of first staminate flower (12.67), node number to anthesis of first pistillate flower (15.43), days to anthesis of first staminate flower (45.60), days to anthesis of first pistillate flower (50.40). Cluster V showed the maximum mean value for days to first marketable fruit harvest (68.50), cluster VII showed the maximum mean value for vine length (8.93), number of nodes per vine (74.36), cluster III showed the maximum mean value for number of primary branches per plant (6.27), cluster VI showed the maximum mean value for fruit length (38.93), cluster IV showed the maximum mean value for fruit diameter (4.46), cluster V showed the maximum mean value for number of fruits per plant (32.26), Cluster IV showed the maximum mean value for average fruit weight (191.33) and cluster VII showed the maximum mean value for total marketable fruit yield (3.40).

Vine length contributed maximum towards genetic diversity (26.67%), followed by fruits per plant (25.75 %), days to anthesis of first pistillate flower (13.69%), average fruit weight (9.43%), number of primary branches per plant (8.51%), node number to anthesis of first staminate flower (7.36%), fruit length (4.37%) and total marketable fruit yield per plant in sponge gourd. Ranking of genotypes based on intra-cluster mean performance for these characters which are major contributors of genetic diversity revealed its usefulness in selecting parents for heterosis breeding.

Table 1: Clustering pattern of 30 genotypes on the basis of Mahalanobis D² statistics

| Cluster number | No. of genotypes | Genotypes |
|----------------|------------------|---|
| I | 4 | NDSG-1, NDSG-5, NDSG-8, NDSG-13 |
| II | 1 | NDSG-10 |
| III | 9 | NDSG-7, NDSG-9, NDSG-11, NDSG-12, NDSG-15, NDSG-16, NDSG-22, NDSG-26, NDSG-28 |
| IV | 3 | NDSG-14, NDSG-20, NDSG-23 |
| V | 8 | NDSG-2, NDSG-4, NDSG-6, NDSG-18, NDSG-19, NDSG-21, NDSG-24, NDSG-25 |
| VI | 5 | NDSG-3, NDSG-17, NDSG-27, NDSG-29, PusaChikni |

Table 2: Average of intra- and inter- clusters D² values for six clusters

| Clusters Number | I | II | III | IV | V | VI |
|-----------------|--------|---------|---------|---------|----------|---------|
| I | 169.51 | 343.181 | 318.022 | 463.759 | 580.915 | 478.341 |
| II | | 330.49 | 486.229 | 935.013 | 1084.584 | 672.807 |
| III | | | 153.003 | 567.28 | 433.252 | 531.827 |
| IV | | | | 140.654 | 238.581 | 367.142 |
| V | | | | | 60.89 | 411.373 |
| VI | | | | | | 171.577 |

Table 3: Intra-cluster group means for 13 characters in sponge 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 | Day to First Marketable Fruit harvest | Vine Length (m) | No. of Nodes Per Vine | No. of Primary Branches per plant | Fruit Length (cm) | Fruit Diameter (cm) | No. of Fruits Per Plant | AverageFruit Weight (g) | Fruit Yield Per Plant (kg) |
|----------|---|--|--|---|---------------------------------------|-----------------|-----------------------|-----------------------------------|-------------------|---------------------|-------------------------|-------------------------|----------------------------|
| I | 4.583 | 8.961 | 35.706 | 36.033 | 48.233 | 3.500 | 47.994 | 5.144 | 22.367 | 4.022 | 17.778 | 136.672 | 2.114 |
| II | 6.517 | 11.889 | 41.606 | 47.931 | 60.386 | 6.264 | 57.233 | 5.264 | 24.833 | 3.311 | 20.961 | 159.867 | 2.904 |
| III | 7.488 | 11.800 | 41.975 | 44.583 | 57.092 | 3.196 | 43.579 | 6.279 | 23.892 | 3.725 | 19.667 | 157.483 | 2.654 |
| IV | 4.233 | 7.133 | 35.233 | 44.467 | 63.367 | 8.133 | 65.200 | 5.233 | 31.267 | 4.467 | 16.867 | 191.133 | 2.706 |
| V | 8.667 | 11.200 | 41.333 | 47.300 | 68.500 | 7.100 | 64.667 | 6.133 | 21.167 | 2.533 | 32.267 | 106.400 | 3.122 |
| VI | 12.267 | 15.433 | 45.600 | 50.400 | 66.467 | 5.800 | 53.200 | 4.633 | 38.933 | 2.933 | 23.267 | 142.767 | 2.828 |
| VII | 10.867 | 10.800 | 46.167 | 49.900 | 61.300 | 8.933 | 74.367 | 5.133 | 30.267 | 3.567 | 20.233 | 187.467 | 3.409 |

Table 4: Per cent contribution in 13 characters towards total genetic divergence in sponge gourd

| S. No. | Source | Contribution % |
|--------|--|----------------|
| 1 | Node No.to Anthesis of First staminate flower | 7.36 |
| 2 | Node No.to Anthesis of First pistillate flower | 1.38 |
| 3 | Days to Anthesis of First staminate flower | 0.23 |
| 4 | Days to Anthesis of First pistillate flower | 13.79 |
| 5 | Day to First Marketable Fruit harvest | 0.01 |
| 6 | Vine Length (m) | 26.67 |
| 7 | No. of Nodes Per Vine | 0.01 |
| 8 | No. of Primary Branches per plant | 8.51 |
| 9 | Fruit Length (cm) | 4.37 |
| 10 | Fruit Diameter (cm) | 0.92 |
| 11 | No. of Fruits Per Plant | 25.75 |
| 12 | Average Fruit Weight (g) | 9.43 |
| 13 | Fruit Yield Per Plant (kg) | 1.61 |

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