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Genetic divergence studies in sponge gourd genotypes

Shailesh Singh, VB Singh and Nidhi Tyagi

Shailesh Singh
Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, Uttar Pradesh, India

VB Singh
Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, Uttar Pradesh, India

Nidhi Tyagi
Department of Vegetable Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India

Correspondence
Nidhi Tyagi
Department of Vegetable Science, Dr. Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India

Abstract

The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful sponge gourd breeding programme. Genetic divergence analysis, using Mahalanobis's D^2 statistic, grouped all the genotypes into six clusters. Cluster III had nine genotypes. The intra-cluster value was maximum in cluster VI and minimum in cluster II. The maximum inter cluster distance average D^2 value was observed between cluster I and cluster IV indicating wide range of genetic diversity between these two clusters. Thus the genetically diverged genotypes could be used as parent in hybridization program for getting desirable segregants. The lowest inter cluster divergence was observed between cluster III and IV. Cluster I showed maximum desirable mean values for node number to anthesis of first pistillate flower, days to anthesis of first staminate flower, days to anthesis of first pistillate flower, days to first fruit harvest, number of fruits per plant and average fruit yield per plant (kg), while cluster VI revealed the highest mean vales for vine length (m), number of nodes per vine, number of primary branches per plant and fruit length (cm). Genotypes much in use of the above mentioned characters both in cluster I and VI would offer a good scope of improvement of the crop through rational selection for hybrid breeding program. The characters like average fruit yield per plant (41.27%) followed by number of fruits per plant and node number to anthesis first staminate flower each (11.38%) contributed maximum to genetic divergence and hence played a major role in improvement of sponge gourd.

Keywords: Sponge gourd, genetic diversity, cluster analysis

Introduction

Genetic diversity is an important factor for heritable improvement in any crop and the knowledge of genetic diversity, its nature and degree of variability would be useful for selecting desirable parents from available germplasm for a successful breeding programme. Sponge gourd is a cultivated annual climber and monoecious vegetable belonging to cucurbitaceace family. Sponge gourd is a tropical and sub-tropical plant which requires warm temperature. It is widely and easily cultivated in India. The tender fruit is used as vegetable which is easily digestible and increase appetite when consumed (Okusanya *et al*., 1981) [12]. Besides being a vegetable, the mature, dry fruit consists of a hard shell surrounding a stiff, dense network of cellulose fibers (sponge) which is a good source of fiber used in industries for filter and cleaning the motor car, glass wares, kitchen utensil, bath and body bathing accessories (Shah *et al*., 1980; Oboh and Aluyor, 2009) [16, 11]. Sponge gourd is a highly nutritive vegetable and contains moisture of 93.2 g, protein 1.2 g, fat 0.20 g, carbohydrate 2.9 g, vitamins (thiamin 0.02 mg, riboflavin 0.06 mg, niacin 0.4 mg and carotene 120 mg), minerals (calcium 36 mg, phosphorus 19 mg and ferrous 1.1 mg) and fibers 0.20 g per 100 g of edible portion (Gopalan *et al*., 1999) [3].

Continuous breeding efforts for high yield have resulted in contraction of genetic variability in natural population of crop species. To optimize and conserve the germplasm for plant breeding and other activities, studies on genetic diversity is important (Uddin and Boerner, 2008) [19]. Germplasm improvement and genetic diversity is a key to reliable and sustainable production of the food crops. For effective evaluation and utilization of germplasm, measure of extent of available genetic diversity is of utmost importance (Zubair *et al*., 2007) [20]. Genetic diversity of crop plants determines their potential for improved efficiency and hence their use in breeding, which eventually may result in enhanced food production. Genetic divergence analysis provides basis for the selection of diverse parents to yield more heterotic effect and generate wide spectrum of variability during segregation and recombination of genes at heterozygous polygenic blocks (Khan *et al*., 2014) [7]. The use of D^2 statistics is an important strategy for germplasm classification and study of genetic relationships among genotypes. Towards this end, in the present study, Mahalanobis's D^2 statistic was used to quantify the extent of divergence among twenty eight sponge gourd genotypes with respect to thirteen quantitative traits. This exercise would help to identify the putative parents and design appropriate crossing plan to obtain high heterotic effect and recovery of transgressive segregants (Bhatt, 1973) [2].

Materials and Methods

The experimental materials consisted of 28 genotypes of sponge gourd including check variety Pusa Chikini was laid in Randomized Complete Block Design with three replications during *Summer* season, 2015 at Main Experiment Station (Vegetable Research Farm), Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, India (26.47° North latitude and 82.12° East longitudes at an altitude of 113 m above the mean sea level). The plot size was of 3m × 2.5m with row to row spacing of 2.5m and plant to plant spacing of 0.50m. All the recommended package of practices was followed to raise a healthy crop. The observations were recorded on five randomly selected plants from each genotype in each replication for the characters viz., node number to anthesis of first staminate flower, node number to anthesis of first pistillate flower, days to anthesis of first staminate flower, days to anthesis of first pistillate flower, days to first fruit harvest, vine length (m), number of nodes per vine, number of primary branches per plant, fruit length (cm), fruit diameter (cm), number of fruits per plant, average fruit weight (g) and average fruit yield per plant (kg). The D^2 statistic (Mahalanobis, 1936) [9] was used to assess genotype genetic divergence for quantitative traits. Grouping of populations was performed using Tocher's method as described by Rao (1952) [14].

Results and Discussion

Genetic diversity arises due to geographical separation or due to genetic barriers to crossability (Murty and Arunachalam, 1966) [10]. The analysis of genetic divergence among the 28 genotypes of sponge gourd was carried out using Mahalanobis D^2 statistics. Based on D^2 value 28 genotypes of sponge gourd were grouped into six distinct non-overlapping clusters (Table 1) as per Tocher's method. The grouping pattern of genotypes was random, indicating geographical diversity and genetic divergence was unrelated (Rasul *et al*., 2004) [15]. The cluster III had maximum number of genotypes (9) followed by Cluster I and V comprised 5 genotypes each. Cluster VI comprised 4 whereas, cluster IV comprised 3 genotypes and cluster II comprised 2 genotypes. 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) [4], Singh *et al*. (2014) [17] and Tyagi *et al*. (2018) [18] in bitter gourd.

The estimates of intra and inter-cluster distances represented by D^2 values are given in Table 2. The intra- cluster D^2 values ranged from cluster II (60.03) to cluster VI (184.75). Among the six clusters, the intra- cluster distance was maximum in cluster VI (184.75) followed by cluster I (151.65), cluster III (129.12) and cluster (111.87) while, the minimum intra-cluster distance was observed in cluster II (60.03) followed by cluster IV (66.15). Similar opinions were also exhibited by Quamruzzaman *et al*. (2008) [13] in ridge gourd and Khule *et al.* (2012) [8] in sponge gourd. In general inter- clusters were higher than intra- cluster distance which indicated that diverse genotypes/ parents could be selected from the two clusters with higher D^2 values. The maximum inter-cluster distance was observed between cluster I and cluster V (669.54), followed by cluster II and cluster V (650.65), cluster II and cluster IV (646.42), cluster I and cluster IV (441.49), cluster II and cluster VI (399.53) were very high, which suggested that genotypes of these two clusters are genetically very diverse to each other. The minimum inter-cluster D^2 values were recorded in case of cluster III and cluster IV (178.24). Kalloo *et al*. (1980) [6] stated that crosses between selected varieties from widely separated clusters were most likely to give desirable recombinants. 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. These results are in agreement with the previous workers (Kabir *et al*., 2009 in pointed gourd and Tyagi *et al*., 2018 in bitter gourd) [5, 18].

The intra-cluster means for thirteen characters in sponge gourd (Table 3) showed that cluster means for different traits indicated considerable differences between the clusters. Cluster I showed desirable mean values for node number to anthesis of first pistillate flower, days to anthesis of first staminate flower, days to anthesis of first pistillate flower, days to first fruit harvest, number of fruits per plant and average fruit yield plant. Cluster IV showed minimum mean value for node number to anthesis of first staminate flower but in desirable direction and maximum mean value for fruit diameter, While, cluster VI showed maximum mean values for vine length, number of nodes per vine, number of primary branches per plant and fruit length; cluster V showed maximum mean value for average fruit weight. Overall conclusion is that, to develop early varieties with higher yield, selection of genotypes from Cluster I could be effective as, it showed early maturity, good morphological traits and higher fruit yield. Whereas, to breed good varieties with improve morphological traits which linked to yield, selection from cluster VI will prove to be highly useful. Similar results have been reported by Quamruzzaman *et al*. (2008) [13] in ridge gourd and Tyagi *et al*., (2018) [18] in bitter gourd.

An assessment of relative maximum contribution of 13 characters towards total genetic divergence (Table 3) was recorded in average fruit yield per plant (41.27%), followed by node number to anthesis of first staminate flower (11.38%) and number of fruits per plant (11.38%) indicating the possibility for selection of these characters while, lowest per cent contribution was observed for days to anthesis of first staminate flower (0.26%), number of primary branches per plant (1.85%) and fruit diameter (3.70%). Our results are in accordance with the findings of Singh *et al.* (2014) [17] in bitter gourd. Therefore, crossing of the genotypes from the cluster I and cluster VI and remaining genotypes in other clusters could be effective for the best utilization of heterosis for different economic traits and isolation of transgressive segregants with respect to the same in sponge gourd improvement program.

Table 1: Cluster classification of 28 genotypes of sponge gourd

Clusters	Number of genotypes	Genotypes
I	5	NDSG-1, NDSG-21, NDSG-6, NDSG-12, NDSG-24
II	2	NDSG11, NDSG-16
III	9	NDSG-2, NDSG-4, NDSG-10, Pusa Chikini (c), NDSG-13, NDSG-22, NDSG-5, NDSG-23, NDSG-3
IV	3	NDSG-8, NDSG-19, NDSG-27
V	5	NDSG-7, NDSG-31, NDSG-15, NDSG-26, NDSG-30
VI	4	NDSG-28, NDSG-34, NDSG-17, NDSG-9

Table 2: Intra-and inter-cluster distances of 28 genotypes of sponge gourd

Clusters	I	II	III	IV	V	VI
I	151.65	256.25	246.26	441.49	669.54	385.07
II		60.03	325.77	646.42	650.65	399.53
III			129.12	178.24	327.82	256.22
IV				66.15	201.91	254.79
V					111.87	236.33
VI						184.75

*Bold diagonal values indicate intra cluster distance, rest of the values show the inter cluster distances.

Table 3: Cluster means and percent contribution of the total genetic divergence for 13 characters in sponge gourd

Clusters	Node number to anthesis of first staminate flower	Node number to anthesis of first pistillate flower	Days to anthesis of first staminate flower	Days to anthesis of first pistillate flower	Days to first fruit harvest	Vine length (m)	Number of nodes per vine	Number of primary branches per plant	Fruit length (cm)	Fruit diameter (cm)	Number of fruits per plant	Average fruit weight (g)	Average fruit yield per plant (kg)
I	4.993	7.973	34.013	36.213	48.460	2.727	43.747	5.087	23.160	3.333	23.493	132.927	2.730
II	8.000	13.900	45.117	47.500	60.317	2.150	35.783	4.517	22.850	3.667	21.483	136.883	2.543
III	4.519	9.304	37.026	39.707	52.437	2.526	39.304	4.685	20.104	3.789	16.337	149.978	1.989
IV	3.622	8.067	36.622	38.667	51.422	3.167	50.867	4.689	21.533	3.933	12.544	158.467	1.578
V	6.880	11.593	44.647	46.687	59.113	3.527	50.593	6.287	24.547	3.660	10.607	175.647	1.470
VI	6.183	11.442	39.083	44.992	57.117	3.625	53.633	6.975	25.667	3.642	17.233	132.375	1.999
Per cent contribution (%)	11.38	5.29	0.26	0.00	0.00	5.03	4.23	1.85	8.20	3.70	11.38	7.41	41.27

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