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Assessment of Genetic Diversity in Culinary Melon (*Cucumis melo* var *conomon*) under Rainfed Condition

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A B S T R A C T

A field experiment was conducted at College of Horticulture, Sirsi during late *kharif* 2017 to study the nature and magnitude of genetic diversity of 40 culinary melon genotypes. Based on D^2 analysis, the genotypes were grouped into seven different clusters, where the cluster I possessed maximum number (28) of genotypes followed by the cluster II (5), V (3), and rest are solitary. The maximum inter-cluster distance was observed between the cluster IV and cluster VI (D^2=645.83) followed by cluster III and cluster VI (D^2=641.23) and minimum in cluster III and IV (D^2=34.81). The Number of female flowers (25.13%) contributed maximum towards expression of genetic divergence followed by seed weight per fruit (17.95%) and least by number of nodes at 30 DAS (0.13%). Considering cluster mean, the genotypes of cluster IV could be selected for yield per plant and average fruit weight.

Introduction

Culinary melon or Oriental pickling melon (*Cucumis melo* var. *conomon*) is one among the melon group vegetables belongs to Cucurbitaceae family with a diploid chromosome number 2n=2x=24. It is also called as golden melon or culinary melon in English. In Karnataka it is called by local names as Sambar southe, Mogge kayi or Mangalore south. It is an ideal summer vegetable crop mainly growing for fresh vegetable as well as for pickling and cooking purpose (Gondi *et al.*, 2016).

The fruits are used in the preparations of an array of traditional vegetarian dishes like chutney, curry, sambar and pickles. The fruits

possess cooling properties and are used as a skin moisturizer and as a digestive agent. It is a highly cross pollinated and usually monoecious in nature, preferring warm weather and bright sunlight for its better growth and development. Kerala, South Karnataka, Andhra Pradesh and Tamil Nadu are the major oriental pickling melon growing states in India.

Being less known crop to the world, crop improvement efforts in pickling melon are limited. Hence, in the successful crop improvement programme especially, exploit heterosis depends upon the selection of diverse parents. The D^2 analysis was proposed by Mahalanobis (1936) has been reported to be an effective tool to assess the genetic diversity. Such an analysis eventually helps to choose desirable parents for recombination breeding and thus results in the development of superior varieties. Improvement on yield and quality achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Selection of parents identified on the basis of diversity analysis would be more promising for a hybridization programme. Several methods are available, out of which D^2 statistic (Rao, 1952) is a unique method for disseminating populations considering a set of parameters together rather than deciding from indices based upon morphological similarities, eco-geographical diversity and phylogenetic relationship. Keeping these points in view, to select parents genetically diverse and economically desirable genotypes for exploitation of heterosis in hybrids with aimed at improving fruit yield of pickling melon.

Material and Methods

The present study carried out at College of Horticulture Sirsi, Karnataka during late *Kharif* 2017. The 40 genotypes were assessed in a field experiment under a randomized block design with two replications. Observations recorded for vine length at 30 and 60 DAS, number of nodes at 30 and 60 DAS, number of male flowers, number of female flowers, fruit length, fruit width, average fruit weight, number of fruits per vine, fruit yield per vine, flesh thickness, seed cavity diameter and seed weight per fruits. Genetic diversity among 40 oriental pickling melon genotypes were assessed by using Mahalanobis D^2 analysis (1936) and the 40 genotypes were grouped in various clusters according to Tocher's method as suggested by Rao (1952). The statistical analysis was carried out using software program WINDOSTAT.

Results and Discussion

Mahalonobis generalized distance (D^2) occupies a unique place in plant breeding. It is a very sensitive tool for measuring genetic divergence based on traits in selection of parents for hybridization to exploit heterosis. The multivariate analysis using Mahalanobis D^2 statistics, which measures the forces of differentiation at intra and inter cluster levels a valuable tool in obtaining quantitative estimates of divergence.

In the present investigation, the genetic diversity was studied to know the existing genetic diversity among 40 genotypes for 14 characters. The diversity was determined by using Mahalanobis D^2 statistics. It also helped to know the relative distances between these genotypes for the characters under study. The results based on the D^2 values indicated that there was adequate diversity noticed among the genotypes.

Relative contribution of different plant traits towards divergence

The relative contribution of different quantitative characters towards expression of genetic divergence was calculated and

presented in a Table 1. The Number of female flowers contributed maximum towards expression of genetic divergence, followed by seed weight per fruit, vine length at 60 DAS, seed cavity diameter, number of male flowers, vine length at 30 DAS, flesh thickness, number of fruits per vine, fruit width, fruit width, average fruit weight, fruit length and number of nodes at 60 DAS.

The negligible amount of contributed by number of nodes at 30 DAS, number of nodes at 60 DAS and fruit yield per vine.

Clustering of oriental pickling melon genotypes

Clustering of oriental pickling melon genotypes was done by adopting the method suggested by Tocher (Rao, 1952). The genotypes were grouped into seven clusters by treating estimated D^2 values as the squares of generalized distances.

The distribution pattern of entries into various clusters is given in Table 2. Cluster I is the largest having twenty eight genotypes, five in cluster III and three in clusters V where as the clusters III, IV and VII contained a solitary genotype. Intra and inter cluster average D^2 values are presented in Table 3.

Among the 08 clusters, cluster V showed maximum intra cluster diversity (D^2=112.36) fallowed by cluster I (D^2=73.72) and Cluster III (D^2=61.77). But other clusters had no intra cluster distance (D^2=0.000) as it possessed single genotype.

The inter cluster average D^2 value was maximum (D^2=645.83) between cluster IV and cluster VI closely followed by cluster III and cluster VI (D^2=641.23), cluster VI and cluster VII (D^2= 625.20), cluster V and cluster VI (D^2=502.41), cluster I and cluster VI (D^2=430.19),cluster II and cluster VII (D^2=278.79), cluster II and cluster III (D^2=260.43) cluster II and cluster IV (D^2=252.43), cluster II and cluster V (D^2=229.72) clearly denotes the genotypes found in any of these pairs of clusters were highly divergent, can be utilized for hybridization programme to exploit heterosis in hybrids.

Szamosi *et al.*, (2010) found heterosis by crossing between the genotypes with higher inter cluster distance.

The inter cluster D^2 value was least between cluster III and IV (D^2=34.81) fallowed by cluster III and V (D^2=98.68) and cluster III and cluster VII (D^2= 124.77). This clearly indicated that clusters III, IV, V and VII were close to each other.

Mean performance for characters in clusters

The mean values of 14 characters for 7 clusters are summarized in Table 4. Highest cluster mean for vine length at 30 DAS was recorded in cluster VI (154.00) fallowed by cluster II (126.59), cluster I (109.37) and least was recorded in cluster IV (94.50).

Highest cluster mean for vine length at 60 DAS was observed in cluster VI (240.17) fallowed by cluster II (199.26) cluster VII (170.17) and least was observed in cluster III (133.34).

For the parameter number of nodes at 30 DAS, highest cluster mean was recorded in cluster VI (22.34) fallowed by cluster V (21.44), cluster II (18.47) and least was recorded in cluster IV (12.50).

Highest cluster mean for number of nodes at 60 DAS was recorded in cluster V (29.61) fallowed by cluster VI (29.31), cluster IV (28.34) and least was recorded in cluster III (26.00).

Table.1 Contribution of different characters towards genetic divergence in oriental pickling melon

(N=40)

Sl.No.	Character	No. of times ranked first	Percent contribution
1.	Number of nodes at 30 DAS	1	0.13%
2.	Number of nodes at 60 DAS	8	1.03%
3.	Vine length at 30 DAS (cm)	41	5.26%
4.	Vine length at 60 DAS (cm)	118	15.13%
5.	Number of male flowers	62	7.95%
6.	Number of female flowers	204	25.16%
7.	Fruit length (cm)	9	1.15%
8.	Fruit width (cm)	18	2.31%
9.	Average fruit weight (g)	15	1.92%
10.	Number of fruits per vine	21	2.69%
11.	Fruit yield per vine (kg)	6	0.77%
12.	Flesh thickness (cm)	38	4.87%
13.	Seed cavity diameter (cm)	99	12.69%
14.	Seed weight per fruits (g)	140	17.95%

Table.2 Categorization of 40 genotypes of oriental pickling melon into different clusters

Cluster number	Number of genotypes	Genotypes
Cluster I	28	Manabagi-1, Manabagi-2, Manabgi-3, Salkani-1, Siddapur-1, Siddapur-2, Local-2, Local-4, Local-5, Local-6, Soubhagya, Mudicode, M-1, M-2, M-3, M-4,SS-1, SS-3, SS-4, SS-5, SS-6, SS-7, SS-9, SS-11, SS-15, SS-16, IIHR- 381 and Sirsi Local-3
Cluster II	05	SS-8, SS-12, SS-13, SS-14 and L-4
Cluster III	1	Manabagi-4
Cluster IV	1	Local-3
Cluster V	3	Salkani-2, SS-2 and SS-10
Cluster VI	1	Local-1
Cluster VII	1	IIHR-386

Table.3 Average inter (above diagonal) and Intra cluster (diagonal) Distances (D^2) for 7 clusters in oriental pickling melon

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**73.72**	142.33	133.69	113.08	193.06	430.19	**200.04**
Cluster II		**61.77**	260.43	252.43	229.72	146.50	**278.79**
Cluster III			**0.00**	34.81	98.68	641.23	**124.77**
Cluster IV				**0.00**	129.58	645.83	**174.06**
Cluster V					**112.36**	502.41	**174.75**
Cluster VI						**0.00**	**625.20**
Cluster VII							**0.00**

Table.4 The mean values of 14 characters for 7Clusters formed by 40 genotypes of oriental pickling melon

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Vine length at 30 DAS (cm)	109.37	126.59	109.13	94.50	105.85	154.00	102.50
Vine length at 60 DAS (cm)	158.73	199.26	133.34	144.50	164.40	240.17	172.17
Number of nodes at 30 DAS	17.72	18.47	16	12.5	21.44	22.34	14.83
Number of nodes at 60 DAS	26.68	28.87	26	28.34	29.61	29.34	26.17
Number of male flowers	28.92	32.91	42.72	19.66	37.2	31.17	95.83
Number of female flowers	2.51	2.87	3.00	1.35	2.45	2.84	7.34
Average fruit weight (Kg)	0.81	0.81	0.98	1.42	0.62	0.94	0.29
Fruit length (cm)	21.37	23.43	24.04	25.75	19.98	22.59	14.42
Fruit width (cm)	15.19	16.51	17.94	18.69	12.61	17.27	9.57
Number of fruits per vine	1.63	1.77	1.84	1.09	1.33	1.84	5.34
Fruit yield per vine (Kg)	1.32	1.40	1.26	1.64	0.98	1.36	1.54
Flesh thickness (cm)	3.17	3.37	3.65	3.45	3.30	3.55	1.80
Seed cavity diameter (cm)	5.38	5.23	3.68	4.18	4.60	5.68	3.18
Seed weight per fruits (g)	8.39	10.53	8.60	10.74	8.02	12.15	11.45

Highest cluster mean was recorded in cluster VII (95.83) fallowed by cluster III (42.72), cluster V (37.2) and least was recorded in cluster IV (19.66) for number of male flowers. Highest cluster mean for number of female flowers was noticed in cluster VII (7.34) fallowed by cluster III (3.00), cluster (II) and least was noticed in cluster IV (1.35).

Highest cluster mean for number of fruits per vine was recorded in cluster VII (7.34) fallowed by cluster VI (1.84), cluster III (1.84) and least was recorded in cluster IV (1.09). Highest cluster mean for fruit yield per vine was noticed in cluster IV (1.60) fallowed by cluster VII (1.54), cluster II (1.40) and least was noticed in cluster V (0.98).

Highest cluster mean for average fruit weight was noticed in cluster IV (1.42) fallowed by cluster III (0.98), cluster VI (0.94) and least was noticed in cluster VII (0.29). Highest cluster mean for fruit length was noticed in cluster IV (25.75) fallowed by cluster III (24.04) and least was noticed in cluster VII (14.42). Highest cluster mean for fruit width was noticed in cluster IV (18.69) fallowed by cluster III (17.94), cluster VI (17.94) and least was noticed in cluster VII (9.57).

For the parameter flesh thickness, highest cluster mean was recorded in cluster III (3.65) fallowed by cluster VI (3.55), cluster IV (3.45) and least was recorded in cluster VII (1.80). Highest cluster mean for seed cavity diameter was noticed in cluster VI (5.68) fallowed by cluster I (5.38), cluster II (5.23) and least was noticed in cluster VII (3.18). Highest cluster mean for seed weight per fruit was noticed in cluster VI (12.15) fallowed by cluster VI (11.45), cluster IV (10.74) and least was noticed in cluster V (8.02).

Based on D^2 analysis, the genotypes were grouped into seven different clusters, where the cluster I possessed maximum number (28) of genotypes. The Number of female flowers contributed maximum towards expression of genetic divergence followed by seed weight per fruit. The genotypes of cluster IV could be

selected for yield per plant and average fruit weight. Crosses can be attempted between genotypes belonging to cluster IV and cluster VI, cluster III and cluster VI, cluster VI and cluster VII, cluster V and cluster VI to get heterotic effect with higher fruit yield.

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