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Research Article

Genetic divergence studies in muskmelon (*Cucumis melo* L.)

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Abstract
Thirty five muskmelon (*Cucumis melo* L.) genotypes were evaluated in a randomized block design with two replications to check its genetic diversity. Based on D^2 analysis these genotypes were grouped in to 11 clusters. Out of eleven clusters, cluster I was the largest, comprising of seven genotypes. Among 21 characters studied, fruit yield per vine (24.54 %) contributed maximum towards expression of genetic divergence followed by beta carotene (23.53%), fruit fly infestation (18.49%), total sugars (6.72%), sex ratio (6.39%) and seed yield per fruit (5.21%). Maximum intra cluster distance was found in the cluster VII followed by XI, X and I. The genotypes in the most divergent clusters VI and VIII could be used for hybridization programme to develop best performing hybrids.

Key words
Clustering and Genetic Divergence; Muskmelon.

Introduction

Cucumis melo L. commonly called as muskmelon or cantaloupe is a member of the family *Cucurbitaceae*. Asia has been indicated as the centre of origin of the melon plant (John *et al.*, 2013). This crop is very popular in developed countries where the per capita calorie consumption is high. It is grown worldwide mainly for fresh market consumption. The fruits are used for both salad and table purpose. It is gaining importance due to its short duration, high nutritive, medicinal and industrial values. It is highly relished because of its sweet and musky flavor.

In India there are several muskmelon cultivars and varieties grown extensively in hot and dry areas of Uttar Pradesh, Punjab, Rajasthan, Madhya Pradesh, Bihar and Karnataka on an area of 47,000 ha with production of 962,000 MT. In Tamil Nadu, it is mostly grown in Coimbatore, Thiruvannamalai and Theni districts which covers an area of 750 ha with production of 12,930 MT (Saxena *et al.*, 2017).

Though muskmelon is most nutritious, its productivity is very low as compared to other vegetable fruits in India. This certainly indicates that there is a great scope for improving the productivity by using suitable varieties and hybrids.

A logical way to start any breeding program is to collect precise information on the nature and degree of genetic divergence that would help the plant breeder in choosing the right type of parents for purposeful hybridization in heterosis breeding (Patel *et al.*, 1989). Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). D^2 statistic proposed by Mahalanobis (1936) has been generally used as an efficient tool in the quantitative estimation of genetic diversity for a rational choice of potential parent in a breeding programme. The main aim of this research is to assess the genetic diversity among the collected germplasm and to identify the diverse parents for use in further genetic study.

Materials and Methods

The present study was carried out at the College Orchard, Department of Vegetable Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore during 2017-18. The experimental materials comprised of thirty five indigenous genotypes of muskmelon collected from IIVR, Varanasi, PAU, Ludhiana and TNAU, Coimbatore. The genotypes were assessed in

a field experiment under a randomized block design with two replications. All the recommended agronomic package of practices was followed. Five plants at random were taken from each plot for recording the observations on twenty one characters of the study. Analysis of variance exhibited significant differences among the genotypes for all the 21 characters, *viz.*, vine length (cm), number of primary branches per vine, days to appearance of first staminate flower, days to appearance of first pistillate flower, node number of first staminate flower, node number of first pistillate flower, days to first fruit harvest, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of fruits per vine, pulp thickness (cm), rind thickness (mm), seed yield per fruit (g), sex ratio, fruit yield per vine (kg), TSS (˚brix), total sugars (%), ascorbic acid (mg $100g^{-1}$), beta carotene (mg $100g^{-1}$) and fruit fly infestation (%). Thus, it indicated, considerable amount of genetic variability among 35 genotypes. Mean across two replications were calculated for each traits. Multivariate analysis was done utilizing Mahalanobis D^2 statistic (Mahalanobis, 1936) and the genotypes were grouped into different clusters following Tocher's method.

Results and Discussion

On the basis of D^2 values, the 35 genotypes were grouped into 11 highly divergent clusters. The cluster divergence was proved by the high inter-cluster (37544.53) and low intra cluster (3517.72) D^2 values in Table 1. Among them, cluster I was found to be the largest containing 7 genotypes followed by cluster VII with 5 genotypes and cluster III with 4 genotypes. The cluster IV, X and XI contained 3 genotypes in each and rest of the clusters had 2 genotypes in each. The above results indicated that there is no parallelism between genetic divergence and geographical divergence of genotypes as genotypes of same geographical region were grouped into different cluster and vice-versa. Therefore, selection of genotypes for hybridization should be based on genetic diversity rather than geographical diversity. Similar trends of observations were reported by Karadi *et al.* (2016) and Rai *et al.* (2018).

The intra and inter cluster distance are presented in Table 2 revealed that cluster VII showed maximum intra-cluster D^2 value (14868.85) followed by cluster XI (14525.61). This was an indicative of the fact that the genotypes included in the clusters VII were found to be very diverse. Whereas, minimum intra-cluster D^2 value (3517.72) was shown by cluster II. Maximum inter-cluster D^2 value was observed between the cluster VI and VIII (37544.53) followed by cluster VIII and XI (36950.25). Selection of parents from these diverse clusters for hybridization would help in achieving novel recombinants. Minimum inter-cluster D^2 value was observed between the cluster II and V (8480.68) which indicated the close relationship among the genotypes included in these clusters. Overall inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The information on intra and inter cluster distances were also available from the studies of Devi and Mariappan (2013), Singh *et al.* (2013) and Rahman *et al.* (2016).

The comparison of cluster means revealed considerable differences among the clusters of different characters in Table 3. The cluster mean values served as a parameter for selection of parents for recombination breeding. Cluster VIII exhibited highest number of fruits per vine (3.78), average fruit weight (812.39 g), fruit length (13.40 cm), pulp thickness (2.54 cm), total sugars (9.92 %), fruit yield per vine (3.08 kg) and lowest mean value for days to appearance of first staminate flower (33.73 days), days to appearance of first pistillate flower (39.07 days), node number of first staminate flower (2.93^{th} node), days to first fruit harvest (71.57 days) and sex ratio (7.25). The cluster V registered the highest value for TSS (9.43°brix), ascorbic acid (10.43 mg $100g^{-1}$) and beta carotene (2.27 mg $100g^{-1}$). Cluster II exhibited highest vine length (193.83 cm), number of primary branches per vine (4.89). Cluster IX was characterized by lowest fruit fly infestation (13.21 %) and rind thickness (1.76 mm). Cluster XI was found to have lowest values of node number of first pistillate flower (4.01^{th} node). Cluster VI had higher mean values for fruit diameter (9.85 cm) and cluster III exhibited lowest seed yield per fruit (3.40g). These observations of the present study were in conformity to the findings of Chaudhari *et al.* (2017) and Kasera *et al.* (2018).

The relative contribution of individual character towards genetic divergence was estimated based on ranking system indicated in Table 4. It was found that fruit yield per vine (24.54 %) contributed maximum towards expression of genetic divergence followed by beta carotene (23.53%) fruit fly infestation (18.49%), total sugars (6.72%), sex ratio (6.39%),

seed yield per fruit (5.21%), rind thickness (4.37%), ascorbic acid (4.03%), node to appearance of first pistillate flower (2.35%), days to appearance of first staminate flower (2.02%) and node to appearance of first staminate flower (1.51%). The traits *viz*., fruit yield per vine, beta carotene, fruit fly infestation, total sugars, sex ratio and seed yield per fruit contributed 85.88% towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population. Such observations were found similar to the findings of Hasan *et al.* (2015), Kumari *et al.* (2017) and Pradhan *et al*. (2018).

D^2 cluster analysis revealed wide genetic distance between the genotypes of cluster VI (VRMM 311, VRMM 313) and VIII (Mysore Local, Dharwad Local) indicating that crossing between the genotypes of these two clusters can be exploited to develop promising F1 hybrids (Kundu *et al.,* 2012 in bitter gourd and Reddy *et al.,* 2017 in muskmelon). The clusters VIII, V, II and IX were found superior for one or more characters. Therefore, a multiple crossing programme can be proposed involving genotypes from these clusters for the development of transgressive segregants in the future breeding programme (Rani *et al.,* 2017 in ridge gourd).

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Table 1. Clustering pattern of muskmelon genotypes based on D^2 analysis

Clusters	Number of genotypes	Name of the genotypes
I	7	VRMM 29, VRMM 60, VRMM 64 , VRMM 144, VRMM 260, VRMM 305, IC 524110
II	2	VRMM 270, VRMM 279
III	4	VRMM 266, VRMM 269, MM 4305, IC 524113
IV	3	VRMM 274, VRMM 301, VRMM 429
V	2	MM 4226, Yanakandla
VI	2	VRMM 311, VRMM 313
VII	5	VRMM 277, VRMM 315, VRMM 418, VRMM 419, VRMM 434
VIII	2	Mysore Local, Dharwad Local
IX	2	MM 502 , MM 3864
X	3	VRMM 441, VRMM 470, VRMM 498
XI	3	VRMM 442, MM 4216, MC 2013-2

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Table 2. Average intra (bold) and inter cluster D^2 values for five clusters in muskmelon genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**13441.34**	11873.05	15544.84	13968.70	13622.00	15027.46	14628.75	26541.42	15228.47	13234.37	17684.4
II		**3517.72**	12794.90	13507.82	8480.68	14059.89	14795.86	28247.48	13457.18	12780.43	17275.55
III			**12316.79**	22028.88	14268.65	18474.91	13718.74	33003.27	10909.63	14010.33	19502.84
IV				**9907.948**	15476.58	17941.52	18495.47	20463.31	21590.5	15942.71	19397.26
V					**5388.78**	16394.65	18698.48	25324.16	11548.1	17123.14	22335.45
VI						**6098.76**	18052.83	37544.53	18711.06	17070.42	15470.05
VII							**14868.85**	29910.6	14125.17	13923.1	15046.74
VIII								**6776.96**	28217.54	30363.61	36950.25
IX									**6809.20**	15926.82	17025.85
X										**13725.29**	17388.97
XI											**14525.61**

Intra cluster distance: diagonal values **Inter cluster distance: off-diagonal values**

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Table 3. Cluster mean analysis of muskmelon genotypes for growth, yield and quality

SI.NO	Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
1.	Vine length (cm)	142.46	193.83	168.01	147.12	162.17	127.87	127.66	172.84	126.65	179.39	114.09
2.	Number of primary branches per vine	3.64	4.89	3.60	3.94	4.18	4.04	4.09	3.65	3.99	4.32	3.83
3.	Days to appearance of first staminate flower	38.22	36.59	35.22	36.80	37.44	36.69	36.24	33.73	36.58	37.15	36.30
4.	Days to appearance of first pistillate flower	44.67	41.97	41.69	44.55	42.71	41.90	42.54	39.07	39.90	42.85	43.04
5.	Node number of first staminate flower	3.81	4.26	3.65	3.23	4.73	4.74	3.25	2.93	4.63	4.11	3.78
6.	Node number of first pistillate flower	5.54	7.00	5.09	5.59	5.74	5.14	5.20	4.91	5.96	5.66	4.01
7.	Days to first fruit harvest	74.39	75.46	75.81	74.71	76.31	75.72	75.60	71.57	75.72	74.05	74.68
8.	Number of fruits per vine	3.24	3.33	3.32	3.11	3.58	2.50	2.96	3.78	3.24	3.04	2.58
9.	Average fruit weight (g)	403.30	371.98	433.05	395.94	653.87	506.70	465.61	812.39	481.10	390.59	469.05
10.	Fruit length (cm)	9.48	10.21	9.85	9.11	11.66	10.81	9.94	13.40	8.96	9.91	8.78
11.	Fruit diameter (cm)	8.38	8.25	9.27	7.99	9.63	9.85	8.84	9.82	8.82	9.25	8.07
12.	Pulp thickness (cm)	1.63	1.79	1.70	1.49	1.61	2.08	1.63	2.54	2.18	1.49	1.52
13.	Rind thickness (mm)	3.94	6.89	3.25	3.80	3.80	6.55	4.15	2.51	1.76	4.41	5.72
14.	Seed yield per fruit (g)	4.15	4.33	3.40	5.34	4.23	3.83	3.54	5.84	4.20	5.61	4.08
15.	Sex ratio	10.51	13.02	11.99	11.69	13.47	13.53	10.99	7.25	12.23	10.50	13.57
16.	TSS (^{o}Brix)	7.22	4.90	8.05	7.18	9.43	6.88	8.56	7.95	7.65	8.47	7.62
17.	Ascorbic acid (mg $100g^{-1}$)	8.76	10.31	6.00	8.61	10.43	5.29	6.99	7.84	5.13	8.57	7.06
18.	Total sugars (%)	6.07	3.19	6.12	9.34	5.52	8.50	5.34	9.92	2.34	7.83	5.10
19.	Beta carotene (mg $100g^{-1}$)	1.88	1.05	0.69	2.27	2.27	1.92	1.05	2.24	0.70	0.58	0.94
20.	Fruit fly infestation (%)	30.00	15.39	30.31	23.56	21.68	38.54	28.75	19.80	13.21	31.60	18.23
21.	Fruit yield per vine (kg)	1.26	1.18	1.42	1.23	2.26	1.24	1.42	3.08	1.57	1.17	1.17

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Table 4. Per cent contribution of different characters towards genetic divergence in muskmelon genotypes

SI.NO.	Characters	No. of first rank	% contribution
1.	Vine length (cm)	0	0
2.	Number of primary branches per vine	0	0
3.	Days to appearance of first staminate flower	12	2.02
4.	Days to appearance of first pistillate flower	0	0
5.	Node number of first staminate flower	9	1.51
6.	Node number of first pistillate flower	14	2.35
7.	Days to first fruit harvest	0	0
8.	Number of fruits per vine	0	0
9.	Average fruit weight (g)	0	0
10.	Fruit length (cm)	0	0
11.	Fruit diameter (cm)	0	0
12.	Pulp thickness (cm)	5	0.84
13.	Rind thickness (mm)	26	4.37
14.	Seed yield per fruit (g)	31	5.21
15.	Sex ratio	38	6.39
16.	TSS (ºBrix)	0	0
17.	Ascorbic acid (mg $100g^{-1}$)	24	4.03
18.	Total sugars (%)	40	6.72
19.	Beta carotene (mg $100g^{-1}$)	140	23.53
20.	Fruit fly infestation (%)	110	18.49
21.	Fruit yield per vine (kg)	146	24.54
	TOTAL	595	100