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

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Abstract
Twenty five genotypes of muskmelon (*Cucumis melo* L.) were evaluated in a randomized block design with three replications at the vegetable farm, College of Horticulture, Anantharajupeta, Andhra Pradesh, India during late *kharif* (August 2017 to December 2017) for assessment of genetic diversity based on 29 morphological traits. Cluster analysis revealed distinct clustering pattern and grouping of genotypes in to six clusters. Cluster II was the largest (7 genotypes) followed by cluster I and III (5 genotypes) followed by cluster IV (3 genotypes), while cluster VI consisted of only one genotype. Intra cluster D^2 values ranged from 0.00 (cluster VI) to 1980.14 (cluster II) while, intercluster D^2 values ranged from 2286.05 (cluster I and II) to 17401 (cluster VI and V). Cluster V and VI were extremely diverse from the rest of the clusters. Hence the genotypes falling in these clusters being genetically more divergent, can be used in hybridization programme.

Keywords: Genetic divergence, *Cucumis melo,* Mahalanobis D^2 statistic, Ward's minimum variance method

Introduction

Muskmelon (*Cucumis melo* L., 2n=24) is one of the most admired cucurbitaceous fruit crop grown throughout the world, particularly in tropical and sub-tropical countries. It is a good cash crop in Asia and South American countries and is an unavoidable item of Western dietary. It is considered to be originated in Africa however, India is considered as secondary center of diversity. In India, muskmelon occupies an area of 52 thousand hectares with an annual production of about of 1135 thousand metric tonnes during the year 2017-2018 (Anon, 2017) [1] and is mostly grown in the states of Punjab, Tamil Nadu, Uttar Pradesh, Maharashtra and Andhra Pradesh. In Andhra Pradesh, it is mostly grown in the river beds and along canals in Kadapa, Chittoor and Ananthapur districts (Singh, 1998) [11]. Being a hot and dry season crop, which is sensitive to cold temperature was widely grown as a summer crop in Rayalaseema region of Andhra Pradesh.

Muskmelon, gets its name from the musky aroma it produces when ripe. The fruits are sweet and musky in flavor and relished by millions as it is packed with a bevy of minerals and antioxidants. Melons are a store house of health benefits and are also used as a salad. Nutritionally, muskmelon is a rich source of vitamin A, C, β- carotene, carbohydrates, sugars, proteins and traces of vitamin K, B1, B2, B6 and niacin which makes muskmelon a nutrient dense food, meaning its nutritional benefits outweigh its calorie content. Besides its multiple uses, lack of advanced varieties had contributed to very low productivity and quality of muskmelon in India. Higher yield can be obtained by developing genetically superior cultivars and improving cultural practices.

For the breeding of muskmelon, diverse germplasm is available ranging from the accessions collected on small farms to hybrids developed by seed companies, representing a source of numerous possible crosses to generate lines. For an effective choice of parents for hybridization plant breeder has to know the information on genetic divergence among the available germplasm. However, only limited information is available on intraspecific genetic diversity and relationships within muskmelon germplasm collections. The germplasm of muskmelon also has not been well characterized from the point of view of its exploitation for the improvement of yield in general, and fruit quality in particular. Further, there is an increased interest for a meaningful understanding of the germplasm of the muskmelon and the extent of their genetic diversity.

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Multivariate analysis by means of Mahalanobis D^2 statistics is a convenient tool in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence both at inter and intra-cluster levels (Murthy and Arunachalam, 1966; Das and Gupta, 1984) [1 8]. D^2 statistics can help in selection of desirable parents for cross combinations that are likely to generate the highest possible variability for the economic characters. Grouping of accessions of muskmelon on the basis of divergence using cluster analysis was reported by Stepansky et al. (1999) [12]. Cluster analysis helps to form groups of closely related individuals which help in determining genetic distance between them. Though information on genetic divergence is available in most of the crops, such information in muskmelon is very rare (Kalloo et al., 1982) [4].

Genetic divergence in muskmelon has been utilized in various breeding programmes for the development and release of good number of varieties. However, the released varieties cannot be continued longer due to genetic drift and susceptibility to various pest and diseases. This demands the replacement of current varieties by new varieties. The aim of this study was to evaluate the nature and extent of genetic diversity among the genotypes of muskmelon using Euclidean clustering analysis to identify promising genotypes, which can be used in different genetic improvement programmes of this crop.

Material and Methods
The experimental material comprised of a set of 25 genotypes. Out of these, fifteen genotypes were obtained from NBPGR, Regional Station, Jodhpur and nine local genotypes were procured from farmers of Vontimitta mandal, Kadapa district and one genotype from IIHR, Bangalore. Genotypes were evaluated in randomized block design with three replications at experimental vegetable farm, College of Horticulture, Anantharajupeta, Andhra Pradesh, India. This study was done during late kharif season (August 2017 to December 2017). Each genotype in each replication was grown in a single row of 8 m length with a spacing of 100 X 70 cm accommodating eight plants in each replication. Genetic divergence between genotypes was worked out by using Mahalanobis D^2 statistics (Mahalanobis, 1936) [5]. The clustering of genotypes was done following Ward's Minimum Variance method.

Results and Discussion
Grouping of genotypes into different clusters
Based on D^2 values, the 25 genotypes were grouped in to six clusters. Among the six clusters, cluster II was the largest comprising of seven genotypes followed by cluster I and III each comprising of five genotypes, cluster IV comprising of three genotypes and cluster VI consisted of only one genotype (Table 1, Fig 1).

Average intra and inter cluster distances
The intra and inter cluster D^2 values among six clusters were presented in (Table 2). Intra-cluster average D^2 values ranged from 0.00 to 1980.139. Among the clusters, cluster II had the maximum intra cluster distance (1980.139) followed by cluster IV (1713.243) and cluster III (1544.492). While the intra cluster distance of cluster VI recorded zero value. The intra cluster values are lower than the inter cluster values in present study indicates that the homogenous and heterogenous nature of the genotypes within and between the clusters.

Maximum inter cluster D^2 value was recorded between the clusters VI and V (17401) indicating wide genetic distance between these clusters. The genotypes belonging to the clusters with maximum inter cluster distance show high genetic diversity and hybridization between genotypes of divergent clusters is likely to produce wide variability with desirable segregants (Arunachalam, 1981) [2]. The minimum inter cluster D^2 value was recorded between cluster I and II (2286.05) indicating close genetic makeup of the genotypes included in these clusters which suggests the lower degree of divergence in the genotypes. These results are in accordance with the findings of More and Seshadri (2002) [7], Yadav et al. (2005) [14], Singh and Lal (2005) [6], Tomar et al. (2008) [13], Mehta et al. (2012) [6] and Rahman et al. (2016) in muskmelon.

The nearest and distant clusters from each of the cluster based on D^2 values are presented in (Table 3). Cluster I was nearest to cluster II (228.05) and distant from cluster VI (13467.52). Cluster II exhibited close proximity with cluster I (2286.05) and maximum divergence with cluster VI (9344.94). Cluster III was nearest to cluster I (2440.33), while it was farthest from cluster VI (17071.54). Cluster IV was nearest to cluster V (2538.89) and distant from cluster VI (12149.04). Cluster V exhibited intimate relation with cluster IV (2538.89) and wide diversity with cluster VI (17401.9113). Nearest and farthest clusters for cluster VI are II (9344.94) and V (17401.93) clusters, respectively.

Performance of characters in a cluster
The comparison of cluster means revealed considerable difference exist among the clusters of different characters (Table 4). Results of analysis revealed that wide range of variation was registered in the cluster means for most of the characters studied. Cluster VI ranked first with respect to the desirable characters viz., vine length, number of nodes, fruit firmness, TSS, total sugars, beta carotene. It also ranked first for characters like days to appearance of first staminate flower, node at which first staminate flower appeared, days to appearance of first pistillate flower, node at which first pistillate flower appeared, days to 50% flowering and node number of first fruit set. Cluster V ranked first for fruit volume, fruit length, fruit weight, yield per plant, number of seeds per fruit and flesh thickness.

Table 1: Clustering pattern of 25 muskmelon genotypes based on D^2 analysis

S. No.	Cluster	No. of genotypes in a cluster	Genotypes
1.	I	5	IC 321370
			IC 321375
			IC 321380
			IC 321329-1
			IC 321374
2.	II	7	IC 315330-2
			IC 321343
			Papasa
			Sirangi
			Alpur orange
			KSP 1060
			Alpur green
3.	III	5	IC 321344
			Sharbathi
			IC 321375-1
			IC 321328
			Improved sharbathi
4.	IV	4	IC 321333
			IC 321366
			Suvarna
			ArkaJeet
5.	V	3	IC 321327
			IC 315323
			IC 315330
6.	I	1	Alpur-1

Table 2: Inter and intra-cluster distances of muskmelon genotypes for various morphological traits using Euclidean² Distance

Cluster	I	II	III	IV	V	VI
I	1237.89	2286.05	2440.33	2551.71	2667.47	13467.52
II		1980.13	4744.68	3138.08	4362.18	9344.94
III			1544.49	2685.15	3337.66	17071.54
IV				1713.24	2538.89	12149.04
V					1421.59	17401.93
VI						0.00

Table 3: The nearest and farthest clusters from each cluster based on D² values in muskmelon genotypes

Cluster	Nearest cluster with D² values	Farthest cluster with D² value
I	II (2286.05)	VI (13467.52)
II	I (2286.05)	VI (9344.94)
III	I (2440.33)	VI (17071.54)
IV	V (2538.89)	VI (12149.04)
V	IV (2538.89)	VI (17401.93)
VI	II (9344.94)	V (17401.93)

Table 4: Mean performance of six clusters for 29 morphological traits of muskmelon genotypes studied

S. No	Characters	I	II	III	IV	V	VI
1.	Vine length (cm)	278.40	245.09	236.0	312.33	266.33	354.66
2.	Internodal length (cm)	8.95	8.45	8.40	8.67	9.17	6.50
3.	Number of nodes	31.34	33.77	31.98	36.36	33.02	48.33
4.	Days to first staminate flower appeared	30.94	31.41	29.30	31.57	30.84	28.06
5.	Node at which first staminate flower appearance	3.04	3.14	2.85	3.11	2.97	2.46
6.	Days to first pistillate flower appearance	37.30	36.54	35.84	37.24	37.22	35.80
7.	Node at which first pistillate flower appeared	4.62	5.04	4.84	4.66	5.66	3.60
8.	Ratio of male to female flowers	17.33	13.36	11.08	12.75	11.61	16.91
9.	Days to 50% flowering	29.06	30.33	29.80	30.41	30.55	25.00
10.	Node number of first fruit set	7.82	6.48	5.85	4.70	6.84	6.40
11.	Days to first fruit harvest	76.97	69.52	72.92	73.23	77.20	68.66
12.	Fruit volume (cm3)	627.65	550.85	670.84	777.45	1216.08	523.66
13.	Fruit length (cm)	12.30	15.18	11.61	11.96	16.09	9.23
14.	Fruit diameter (cm)	10.27	10.29	11.97	10.47	10.94	8.42
15.	Cavity length (cm)	8.34	11.06	7.95	8.96	11.73	6.40
16.	Cavity diameter (cm)	6.71	6.66	6.85	6.26	5.58	5.45
17.	Number of fruits/ plant	2.21	3.53	4.20	4.20	3.11	2.86
18.	Fruit weight (kg)	0.85	0.87	0.83	0.90	1.15	0.65
19.	Yield /plant (kg)	1.88	2.93	3.56	3.64	3.64	1.88
20.	Number of seeds per fruit	316.88	385.87	324.33	554.26	642.06	416.60
21.	100 seed weight (g)	3.59	2.42	2.59	1.96	3.46	3.30
22.	Fruit firmness (kg/cm²)	2.08	2.46	2.48	2.39	2.26	7.53
23.	Peel thickness(mm)	0.36	0.50	0.66	0.75	0.61	0.70
24.	Flesh thickness(mm)	11.48	11.06	13.64	9.22	12.19	10.36
25.	TSS (⁰Brix)	6.17	7.21	6.14	8.10	5.69	12.09
26.	Titrable acidity (%)	0.11	0.08	0.12	0.07	0.10	0.02
27.	Total sugars (%)	7.51	8.93	7.77	9.55	7.54	12.87
28.	Ascorbic acid (mg/100 g)	17.77	16.28	17.74	15.55	17.81	13.22
29.	β- carotene (μg/g)	4.88	6.18	1.76	3.18	3.55	8.37
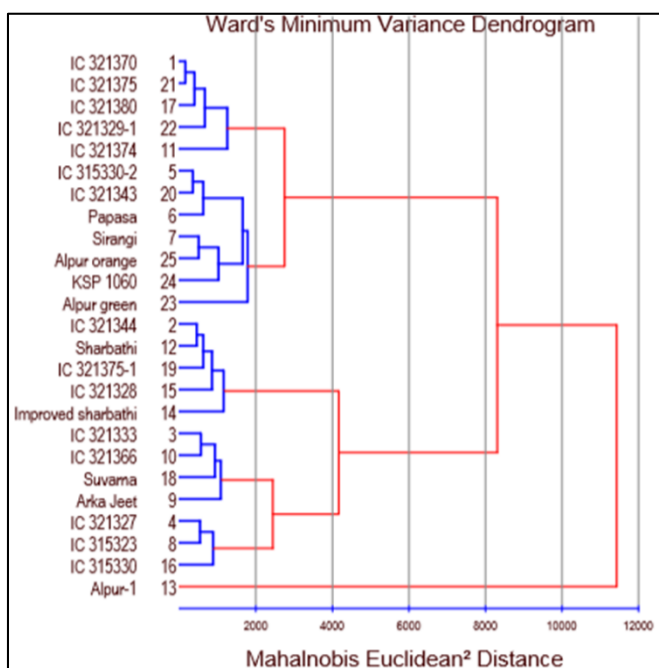
Fig 1: Ward's minimum variance dendrogram of 25 muskmelon genotype based on morphological characterization.

Cluster IV ranked first in node number of first fruit set, number of fruits per plant, yield per plant. cluster III recorded highest mean value for fruit diameter, cluster II recorded its highest mean for fruit length, Cluster I ranked first in 100-seed weight. Hence genotypes belonging to the clusters VI and V are amenable for exploitation in future crop improvement of muskmelon.

The results of Mahalanobis D² statistics confessed prominent and desirable genetic diversity among 25 genotypes of muskmelon included in the present study for all the 29 characters under examination collectively. Several authors also reported greater diversity in the genotypes of muskmelon by assessing genetic divergence on the basis of quantitative traits by following Mahalanobis D² statistics (Prasad *et al.*, 2004, Singh and Dhillon. 2006) [9, 10].

Conclusion
Multivariate analysis considering 29 morphological traits following Mahalanobis D² statistics revealed good variability among 25 muskmelon genotypes which were divided into six clusters. In the present study, the inter cluster D² values ranged with a minimum value of 2286.05 to a maximum value of 17071.54. Cluster V and VI were extremely diverse

from rest of the clusters, the divergence between these two clusters was high as evident from their high inter cluster D^2 value (17071.54). Intercrossing the genotypes from these two clusters may generate wider variability and is expected to throw high yielding transgressive segregants in a population improvement programme in muskmelon.

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