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

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Abstract
The field experiment on evaluating muskmelon genotypes collected from different geographic locations of Tamil Nadu was conducted from 2012-13 at Rice Research Station, Tirur, Tamil Nadu. A total of 24 accessions were evaluated under randomized block design, replicated twice. Biometrical observations for 24 accessions were recorded for seven traits and were subjected to statistical analysis using D^2 statistic and Euclidean distance. On clustering of the accessions by D square statistic, it was revealed that cluster I was found to be the largest containing 6 genotypes followed by cluster VIII with 3 genotypes. The cluster analysis using Euclidean distance clustered the genotypes into 11 clusters of which cluster II as largest with five genotypes followed by cluster III and VII with three genotypes. The fruit weight and yield are the parameters to be used as selection criteria to make single plant selection.

Keywords: Muskmelon, Mahalanobis D^2 statistic, Euclidean clustering analysis, germplasm

Introduction
Muskmelon also widely known as cantaloupe is the most polymorphic species of the cucurbitaceae family. It is likely to have originated in Asia from India to Persia with centre of development in present day Iran. It is grown as a fruit vegetable almost worldwide from tropical to subtropical regions. It is of good quality when grown under warm and sunny situation. Muskmelon is a highly relished cucurbit because of its attractive flavour, sweet taste and refreshing effect. The fruits are sweet and musky in flavour and relished by millions with good export potential. It is used for both salad and table purpose. Immature melons may be used fresh in salads, cooked or pickled. Mature fruits may be eaten fresh as a dessert fruit, canned or used for syrup or jam. Melon seeds are dietary source of unsaturated vegetable oil and protein and may be eaten lightly roasted like nuts or even used in sweets. It is a good source of dietary fibre, vitamins and minerals. It is gaining momentum because of its medium duration, high production potential, high nutritive value medicinal and industrial value. However its productivity is low as compared to other fruit vegetables. High yield can be achieved by developing superior cultivars. Hence mining into new germplasm collections and their systematic study is a pre-requisite to develop new varieties / hybrids with superior quality. Information on the genetic divergence among the available germplasm is vital to a plant breeder for selection of best performing lines for further breeding programs.

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. Plant breeding program aims at improving the existing types and creating a new type which will be better than the existing commercial cultivars. For developing a suitable and efficient breeding program, information regarding the nature and magnitude of genetic variation that exists in the breeding population is necessary (Sudhakar *et al.,* 2010).

Melons are cross pollinated and much genetic diversity may exist within a population. India being a secondary centre of origin of muskmelon, numerous diversified forms are available. Local market preferences in muskmelon made several land races/local cultivars have established themselves in different geographical pockets/river beds of India. These cultivars exhibit enormous variability with respect to fruit traits but are basically poor yielder as they are traditionally being grown and selected under low input agricultural systems by traditional growers who have developed their own skill and management practices to raise this crop. It was therefore considered worthwhile to collect such materials from various places and local markets for breeding towards an effective improvement in fruit traits and yield especially for North Eastern zone of Tamil Nadu.

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Multivariate analysis following Mahalanobis D^2 statistics revealed rich genetic diversity for various growth, earliness and yield associated traits in the germplasm offering a great scope for improvement of muskmelon (Singh and Lal, 2000 [1]; More and Seshadri, 2002 [3]; Choudhary and Ram, 2003 [2]; Krishnaprasad et al., 2004 [4]; Yadav et al., 2005 [5]; Singh and Dhillon, 2006 [6]. The aim of our study was to evaluate the nature and extent of genetic diversity among the genotypes of muskmelon using Mahalanobis D^2 statistics and Euclidean clustering analysis to identify promising genotypes, which can be used in different genetic improvement programs of this crop.

Materials and Methods
The field experiment on muskmelon was conducted during 2014-2015 at Rice Research Station, Tirur, Tamil Nadu, India to evaluate different genotypes collected from different geographic locations of Tamil Nadu. A total of 24 genotypes were collected and seeds were sown directly in main field at a spacing of 2m x 45 cm under randomized block design, replicated twice. Biometrical observations for 24 genotypes were recorded for seven traits viz., vine length (cm), fruit length (cm), fruit girth (cm), number of fruits/vine, fruit weight (kg), TSS (%) and yield (kg/vine). The description of the muskmelon genotypes based on their fruit characteristics is presented in Table 1.
Multivariate analysis following Mahalanobis D^2 statistics (Mahalanobis, 1936) has been used to quantify the genetic divergence between the genotypes and to identify diverse parents for hybridization. The genetic divergence between the genotypes was worked out using Mahalanobis D^2 statistics (Mahalanobis, 1936) and also by Euclidean distance. (Table 2 and 3 respectively).

Results and Discussion
The D^2 statistic clustered 24 genotypes into 10 clusters. Among the ten clusters, cluster I was found to be the largest containing six genotypes followed by cluster VIII with three genotypes. The other clusters comprised two genotypes each. The clustering pattern revealed that genotypes from Coimbatore and Salem got clustered together. However, Salem 140 was found to be distinct and genotypes from same geographical location viz., Aranvoyalkuppam1 and Thiruvallur local 1 were clustered together (Table 2).
Several authors also reported profound diversity in the germplasm of muskmelon by assessing genetic divergence on the basis of quantitative traits following Mahalanobis D 2 statistics (Singh and Lal, 2000 [1]; More and Seshadri, 2002 [3]; Choudhary and Ram, 2003 [2]; Krishnaprasad et al., 2004 [4]; Yadav et al., 2005 [5]; Singh and Dhillon, 2006 [6]; Musmade et al., 2008 [7]; Tomar et al., 2008 [8]; Rao et al., 2010) [9]. Murthy and Arunachalam (1960) pointed that Mahalanobis D^2 statistics is an important breeding tool to evaluate the clustering pattern.
The cluster analysis using Euclidean distance clustered the genotypes into 11 clusters of which cluster II as largest with five genotypes followed by cluster III and VII with three genotypes. Among them, Madhur, Sun, Oddanchatram local 1 and Dharmapuri local were distinct from others and other clusters comprised two genotypes each. However, genotypes

from Salem, Thiruvallur were clustered together while genotypes from Kancheepuram local clustered separately as revealed by D^2 statistic also (Table 3 & Fig. 1).
The intra cluster distance by D^2 statistic values ranged from 0.00 (cluster X) to 4.15 (cluster VIII) which indicted that genotypes of cluster VI are highly divergent among them. The inter cluster distance was minimum between cluster II and VII (2.05) which indicated that close association among the genotypes. The inter cluster distance was maximum between cluster VIII and IX (6.07) which indicated maximum divergence among the genotypes (Table 4).
The average inter and intra cluster distances revealed that inter cluster distances were much higher than those of intra cluster distances suggesting homogenous and heterogenous nature of germplasm lines within and between the clusters respectively. These results are in accordance with the earlier researchers (Musmade et al., 2008 [7], Tomar et al., 2008 [8] and Rao et al., 2010) [9] in muskmelon. In general, the genotypes grouped together in one cluster are less divergent than those which are placed in a different cluster. Also, higher intra cluster distance indicates high degree of divergence within that cluster. Selectionof parents from these diverse clusters for hybridization program would help in achieving novel recombinants. This was opined by Krishnaprasad (2004) [4] and Singh and Dhillon (2006) [6].
Multivariate analysis by means of Mahalanobis D2 statistics is a useful 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. The D2 statistics helps in selecting desirable parents for achieving desired goal by the breeder.
The cluster mean values for various traits revealed that cluster IX recorded highest fruit length (12.72 cm), fruit weight (820 g), TSS (9.25%) and yield (2.63 kg/vine) while cluster VIII recorded highest vine length (61.51 cm), cluster III recorded highest fruit girth (11.69 cm) and cluster 7 recorded maximum no. of fruits vine (3.22). Contribution of each character to total divergence revealed that single plant yield (38.4%) contributed maximum divergence followed by fruit weight (28.2%) which is the parameters to be used in selection. (Table 5)
The percent contribution of each character towards divergence is also presented in Table 5. It was observed that yield (38.4%) followed by number of fruits (28.2%), TSS (14.49%) contributed maximum towards divergence. In contrast the fruit length (2.53%) contributed the least. From the results, it is evident that there was greater diversity in the material under study for yield, number of fruits and TSS offering ample scope for selection of desirable parents for breeding programme. The results of the study provide a positive contribution of genetic divergence and this can be of considerable help in selection of genotypes for high yield and other economic traits.
Traditional muskmelon landraces still extant in different ecosystems may provide the genetic diversity needed to diversify the depauperate gene pool of improved muskmelon varieties. Owing to their adaptation to a wide range of agro-ecological conditions, traditional land races represent tremendous genetic diversity not found in modern cultivars.

Table 1: Description Muskmelon genotypes based on their fruit characters

Treatment	Genotypes	Fruit shape	Fruit colour	Flesh colour	Source
T1	Madhurima	Round	Yellow	Dark orange	M/s.Nunhems Pvt. Ltd.,
T2	682	Round	Yellow	Yellowish	M/s.Sungro Seeds Pvt. Ltd.,
T3	Madhur	Round	Yellow	Orange	M/s. Syngenta Pvt. Ltd.,
T4	Sun*	Round	Yellow	White	M/s. Known you seeds Pvt. Ltd.,
T5	Sun no.2*	Oval	Yellow	Light yellow	M/s. Known you seeds Pvt. Ltd.,
T6	NS 7455	Oval	Yellow	Deep salmon	M/s. Namdhari Pvt. Ltd.,
T7	NS 910	Oval	Yellow	Deep salmon	M/s. Namdhari Pvt. Ltd.,
T8	TVL 1	Oval	Yellow	Yellow	Local collection from Tiruvallur
T9	AVK1	Round	Orange	Orange	Local collection from Aranvoyalkuppam
T10	KPL1	Round	Yellow	Yellow	Local collection from Kancheepuram
T11	KPL2	Oval	Yellow	Yellow	Local collection from Kancheepuram
T12	TIRL1	Round	Yellow	Yellow	Local collection from Tirchirapalli
T13	ODL1	Oval	Yellow	Yellow	Local collection from Oddanchatram
T14	DPIL1	Oval	Yellow	Yellow	Local collection from Dharmapuri
T15	CBE1	Round	Yellow	Yellow	Local collection from Coimbatore
T16	CBE2	Round	Yellow	Light orange	Local collection from Coimbatore
T17	Sweet orange	Round	Orange	Orange	M/s. Known you seeds Pvt. Ltd.,
T18	KY035	Round	Orange	Orange	Local collection from Salem
T19	S151	Oval	Yellow	Yellow	Local collection from Salem
T20	S 126	Round	Yellow	Yellow	Local collection from Salem
T21	S 128	Round	Orange	Orange	Local collection from Salem
T22	S 140	Oval	Yellow	Yellow	Local collection from Salem
T23	S137	Oval	Yellow	Yellow	Local collection from Salem
T24	S 112	Round	Orange	Orange	Local collection from Salem

* Lines from Taiwan, collected from M/s. Known you seeds Pvt. Ltd.,

Table 2: Cluster composition of muskmelon genotypes based on Mahalanobis D^2 statistic

Cluster No.	No. of genotypes	Cluster members based on D^2 statistic
I	6	Madhurima, No.682, Madhur, Sun, Kancheepuram local 1, Salem 151
II	2	Aranvoyalkuppam 1, Salem 151
III	2	Coimbatore 1, Coimbatore 2
IV	2	Tiruchirapalli 1, Oddanchattram local 1
V	2	Salem 128, Salem 112
VI	2	KY035, Salem 137
VII	2	NS 910, Tiruvallur local 1
VIII	3	Sun no. 2, NS 7455, Kancheepuram local
IX	2	Dharmapuri local 1, Sweet orange
X	2	Salem 140

Table 3: Cluster composition of muskmelon genotypes based on Euclidean distance

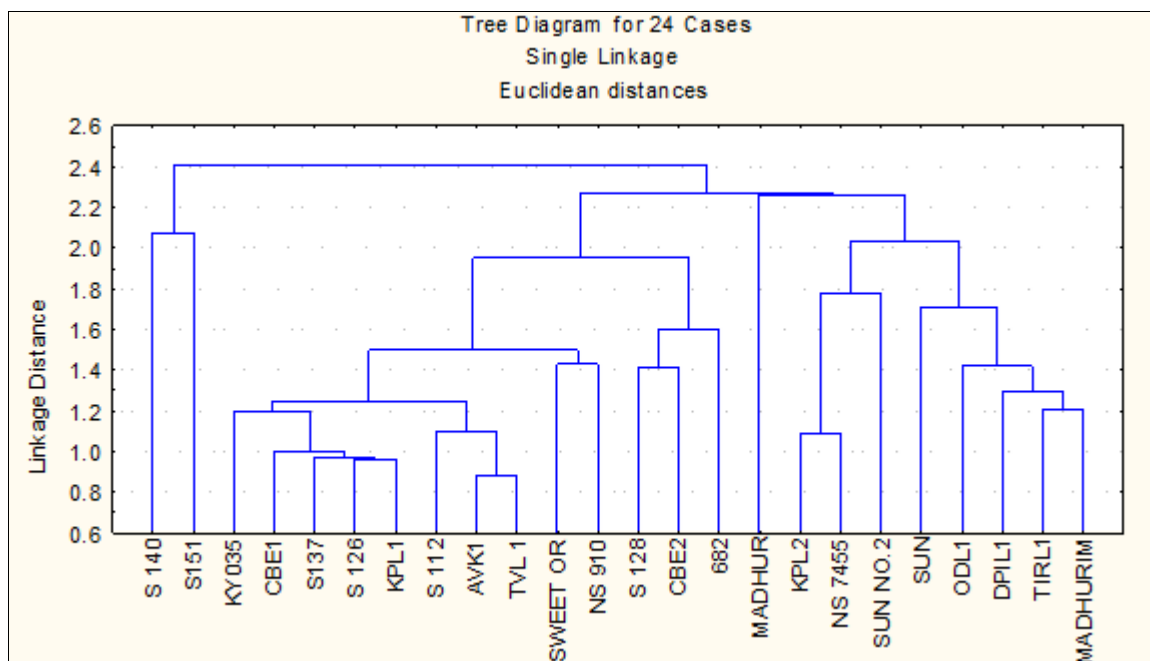| Cluster No.	No. of genotypes	Cluster members based on Euclidean distance
I	2	Salem 140, Salem 151 (2 nos.)
II	5	KY035, Coimbatore 1, Salem 137, Salem 126, Kancheepuram local 1
III	3	Salem 112, Aranvoyalkuppam 1, Tiruvallur local 1
IV	2	Sweet orange, NS 910
V	3	Salem 128, Coimbatore 2, 682
VI	1	Madhur
VII	3	Kancheepuram local 2, Sun no. 2, NS 7455
VIII	1	Sun
IX	1	Oddanchattram local 1
X	1	Dharmapuri local 1
XI	2	Tiruchirapalli 1, Madhurima

Fig 1: Cluster members based on Euclidean distance

Table 4: Average intra (diagonal) and inter cluster distance in muskmelon genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	3.57	3.49	2.96	3.00	3.82	3.18	3.27	4.36	4.53	4.30
II		1.45	2.13	3.05	2.63	3.11	2.05	5.77	3.66	3.12
III			1.52	2.27	3.04	3.07	2.35	4.80	3.61	3.83
IV				1.56	2.97	2.88	2.96	3.93	4.44	3.92
V					1.71	2.78	3.08	5.77	4.74	2.24
VI						2.05	2.56	4.64	4.96	2.37
VII							2.27	5.14	3.68	3.26
VIII								4.15	6.07	6.30
IX									4.01	5.77
X										0.00

Table 5: Cluster mean values and percent contribution for seven attributes in muskmelon genotypes

Cluster / Character	I	II	III	IV	V	VI	VII	VIII	IX	X	% contribution
Vine length (cm)	46.97	33.42	42.52	49.17	39.25	40.25	35.52	61.51	43.75	30.30	2.89
Fruit length (cm)	12.15	12.26	12.35	11.7	12.05	11.3	11.59	11.59	12.72	11.35	2.53
Fruit girth (cm)	11.25	10.29	11.69	10.81	11.19	11.53	11.04	11.41	10.54	11.4	4.71
No. of fruits / vine	2.63	2.97	2.87	2.75	2.3	2.52	3.22	2.7	3.07	2.35	28.2
Fruit weight (g)	0.71	0.62	0.65	0.51	0.51	0.67	0.71	0.72	0.82	0.55	8.69
TSS (%)	7.01	7.37	7.87	6.87	7.37	6.87	7.62	6.25	9.25	6.75	14.49
Yield (kg/vine)	1.93	1.85	1.84	1.37	1.16	1.74	2.3	2.01	2.63	1.25	38.4

Conclusion

Multivariate analysis on seven quantitative and qualitative traits revealed that Mahalanobis D^2 statistic grouped the accession into 10 clusters and Euclidean clustering grouped the genotypes into 11 clusters. The genotypes of diverse clusters VIII and IX could be used in further breeding programme to produce wide range of segregants in a population to develop high yielding varieties of muskmelon. The cluster IX recorded highest fruit length, fruit weight, TSS and yield from which single plant selection can be done. The contribution of each character to total divergence revealed that single plant yield contributed maximum divergence followed by fruit weight, which are the parameters to be used in further selection. The results of the present study point out a positive contribution of genetic divergence and yield components; this can be of considerable help in selecting for yield and other economic traits. It can be concluded that there was more divergence for these characters offering greater scope while making selection of Horticulturally superior genotypes.

Reference
1. Singh S, Lal T. Assessment of genetic divergence in melon (*Cucumis melo* L.). J Res.: Punjab Agric. Univ. 2000;37(1-2):36-41.
2. Choudhary H, Ram HH. Genetic diversity studies in muskmelon. Ann. Agric. Res. 2003;24(2):345-349.
3. Seshadri P, Ganesamurthy K. Genetic divergence in soybean (*Glycine max* (L.) Merrill.). Madras Agricultural Journal. 2002;89(1/3):18-21.
4. Krishnaprasad VSR, Pitchaimuthu M, Dutta OP. Variation, diversity pattern and choice of parental selection in musk melon (*Cucumis melo* L.) improvement. Indian J Hort. 2004;61(4):319-322.

5. Yadav JR, Gaurav M, Shukla NS, Singh HC, Singh B, Srivastava JP, 2005.
6. Singh G, Dhillon NPS. Genetic divergence in muskmelon germplasm. Haryana J Hort. Sci. 2006;35(3/4):340-341.
7. Musmade AM, Torkadi SS, Patil RS, Asane GB. Genetic divergence in muskmelon (*Cucumis melo* L.). J Maharashtra Agric. Univ. 2008;33(1):133-135.
8. Tomar RS, Kulkarni GU, Kakade DK. Genetic analysis in muskmelon (*Cucumis melo* L.). J Hortic. Sci. 2008;3(2):112-118.
9. Rao CR. Advanced statistical methods in biometrical research. John Wiley and Sons, New York, 1952.