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Study of genetic diversity in muskmelon (*Cucumis melo*) from different horticultural groups

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ABSTRACT

An experiment was carried out to analyze genetic divergence through multivariate analysis based on D^2 and principal component analysis (PCA) for 24 yield contributing traits among 67 muskmelon (*Cucumis melo* L.) genotypes from 3 horticultural groups. The 67 genotypes were grouped into 15 distinct clusters. Cluster I consisted of 27 exotic lines from *inodorous* and *cantalupensis* group followed by cluster XIVwith 14 genotypes. Majority of genotypes of cluster XIV were developed in India except 4 exotic lines. The remaining13 clusters comprised of only 2 genotypes each and thus clustering pattern indicated enough genetic divergence in the germplasm under study. The highest value of intra cluster distance (43. 68) was found for cluster XV with 2 genotypes followed by XIV (38. 35) possessing 14 genotypes and cluster I (31. 07) having 27 genotypes. The highest inter cluster distance was observed between cluster XV and XIV (42. 24), followed by the cluster XV and XI (40. 70) and cluster XV and VI (40. 48). The first 3 principal components accounted for majority (53. 77%) of the total variation. The traits which contributed positively to PC1 were days to first male flower opening, average fruit weight, fruit length, cavity length and yield per plant. The high yielding muskmelon genotypes with better fruit quality traits like DM-31, DM-145, DM-159 and DM-162 from *inodorous* group of Cluster I and Pusa Madhuras (Cluster VII), Kashi Madhu, Punjab Sunheri, Hara Madhu (Cluster XIV) from *cantalupensis* group should be utilized for hybrid development between two horticultural groups to incorporate theyield and desirable fruit quality traits from both groups.

Key words: Genetic divergence, Muskmelon, Multivariate analysis, Principal component analysis

Muskmelon (*Cucumis melo* L., 2n = 24) is one of the important Cucurbitaceous vegetable grown throughout the world. African continent especially eastern region of south Sahara desert is generally regarded as the centre of origin of *Cucumis melo* while India has been considered as an important secondary centre of diversity. However, recent studies showed that cucumber and muskmelon are both of Asian origin and wide diversity of this species exists in India and China (Sebastian *et al.* 2010). Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization programme. Multivariate analysis has been found useful for characterization, evaluation and classification of plant genetic resources when a large number of accessions are to be assessed for several characters of agronomic and physiological importance. Different types of analysis such as cluster analysis and principal component analysis (PCA) can be used to obtain idea about how to identify groups of accessions that have desirable traits for breeding, and enlighten the patterns of variation in the germplasm collection, to identify relationships among accessions and possible gaps. The information usually needed for developing high yielding varieties with better fruit quality in melon pertains to the genetic variability for these specific traits in the available germplasm for breeding programmes. Multivariate analysis of elite germplasm collections of cucurbits including melons for choosing promising genetically diverse lines for desirable traits have been successful in the past (Choudhary *et al.* 2003, Mladenovic *et al.* 2012). But majority of these studies have been limited to a particular horticultural group of melons in India, although there is enough possibility of utilizing germplasm from different horticultural groups for improvement of Indian muskmelon for yield, quality or resistance to biotic stresses. Keeping in view the above facts, the present study was carried out to investigate the extent of genetic diversity in 67 muskmelon genotypes belonging to 3 horticultural groups.

MATERIALS AND METHODS

The experiment was carried out at the Research Farm

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of Indian Agricultural Research Institute, New Delhi during the summer 2014, situated at 228.61m (750 feet) altitude over mean sea level, with 28°08'N latitude and 77°12'E longitudes. The climate is sub-temperate and semi-arid type with alluvial soil, experiences very hot summers (above 40°C) and relatively dry and cool winters (below 5°C). The experiment was laid out in a randomized block design with 67 genotypes and three replications. The seeds were sown at a spacing of 2m from row to row and 0.6 m from plant to plant with in a row. Recommended agronomic and cultural practices were adopted to obtain good phenotypic expression of the characters. Data were recorded for yield and 23 yield contributing traits, viz. days to first staminate flower opening, node number of first staminate flower, days to first pistillate flower opening, node number of first pistillate flower, node number of first fruit set, number of fruits per plant, average fruit weight (kg), number of primary branches per plant, vine length, days from pollination to fruit harvest,days to first fruit harvest, total crop duration, fruit length (cm), fruit width (cm), fruit shape index, flesh thickness (cm), cavity width (cm), cavity length (cm), rind thickness (cm), seed length (cm), seed width (cm), seed shape index, yield per plant (kg) and TSS (ºBrix). Data of five plants from each genotype was averaged for each replication and mean data was used for statistical analysis. Genetic diversity was analysed by Mahalanobis's (Mahalanobis 1936) generalized distance (D^2) and clustering of genotypes was done according to Tocher's method (Rao 1952). Average intra and inter cluster distance was calculated as per the standard procedures. Trait variability analysis was performed by the PCA method, with the number of principal components being chosen based on the screen test.

Table 1 Clustering pattern of muskmelon genotypes based on fruit yield attributes using D^2 analysis

Cluster	No. of genotypes	Genotypes
I	27	DM-31, DM -35, DM -38, DM-54, DM-55, DM-56, DM-145, DM-143, DM-144, DM-146, DM-150, DM-152,DM-147, DM-153, DM-156, DM-159, DM -160, DM-162, DM-163, DM -169, DM-2, DM-3, DM-4, DM-5, DM-6, DM-16, DM-20
II	2	MS-1, DM-17
III	2	DM-15, DM-154
IV	2	DM-13, M-2
V	2	DM-8, DM-171
VI	2	DM-19, DM-176
VII	2	DM-151,Pusa Madhuras
VIII	2	DM-18, DM-177
IX	2	DM-14, DM-180
X	2	DMDR-1, Ananas
XI	2	DM-175, DM-166
XII	2	DM-172, DM-174
XIII	2	DM-46, DM-36
XIV	14	DM-7, DM-10, DM-11, DM-12, DM-148, Kashi Madhu, DSM-11, Hara Madhu, Arka Jeet, Punjab Sunheri, Durgapura Madhu, IC274026, DM-149,DM-170
XV	2	DM-155, DM-173

RESULTS AND DISCUSSION

Analysis of variance showed that mean squares were significant for yield and 23 yield contributing characters which reflected presence of high magnitude of variability among the muskmelon germplasm utilized for this study. Based on D^2 values for 24 yield contributing traits, these 67 genotypes could be grouped into 15 distinct clusters (Table 1). Twenty seven exotic lines from *inodorous* and *cantalupensis* group were grouped together into a big cluster I while another cluster (XIV) consisted of 14 genotypes and most of them (DM-148, Kashi Madhu, DSM-11, Hara Madhu, ArkaJeet, Punjab Sunheri, Durgapura Madhu, IC274026, DM-149, DM-170) were indigenous lines which have been developed in India except 4 exotic lines DM-7, DM-10, DM-11, DM-12 which were introduced from other countries. This group consisted of genotypes from all 3 horticultural groups (*inodorous, cantaloupensis* and *momordica*) of melon. All other 13 clusters consisted of only two genotypes in each cluster. Genetic diversity observed among the genotypes may be due to factors like history of selection, heterogeneity, selection under diverse environments and genetic drift. The important traits which could contribute largely for genetic diversity in the melon germplasm were TSS (24.60%), yield per plant (23.24%), seed length (14.60%), rind thickness (10. 49%) and days to first fruit harvest (6.06%). Most of these traits are directly related to yield, fruit quality and earliness and grouping based on these traits will be more effective for germplasm utilization in future breeding programme. The result was in agreement to earlier study by Reddy *et al.* (2012) wherein it was reported that total soluble solids, seed yield, days to appearance of first staminate flower, average fruit weight contributed maximum towards divergence and 35 genotypes was classified into 6 groups. Singh and Lal (2000) classified 51 diverse genotypes of muskmelon for yield and yield-related traits and grouped them into 13 clusters. Choudhary *et al.* (2003) grouped 70 germplasm lines of muskmelon into 11 clusters. Prasad *et al.* (2004) classified 34 genotypes of muskmelon into eight clusters. Rukam *et al.* (2008) and Tomar *et al.* (2008) also reported that total soluble sugars and fruit yield per plant contributed maximum towards genetic divergence.

The intra cluster and inter cluster distance values ranged from 0.00 to 43.68 (Table 2). The highest value of intra cluster distance (43.68) was found for cluster XV followed by XIV (38.35) possessing 14 genotypes and cluster I (31.07) having 27 genotypes. Cluster XV comprised only two genotypes (DM-155 and DM-173) which indicated these two genotypes are highly diverse. The genotypes grouped in clusters XIV and I were highly divergent for yield attributes.

Table 2 Average intra-and inter-cluster distance (D^2) among 67 muskmelon genotypes

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	31.07	26.34	28.38	24.16	26.19	28.11	27.64	27.09	29.50	29.27	31.34	29.12	28.65	35.48	40.17
II		8.53	19.00	16.14	14.66	17.58	17.98	21.43	16.31	19.36	20.76	19.60	27.47	29.43	31.75
III			9.50	17.53	19.32	15.77	13.51	15.77	18.63	13.87	20.27	13.84	32.06	29.54	39.15
IV				11.35	16.10	18.44	16.10	13.96	18.95	19.57	19.67	18.09	22.18	28.78	33.88
V					11.65	17.50	16.40	20.25	20.74	17.39	18.15	18.53	27.86	28.84	31.89
VI						11.95	15.09	21.22	22.29	17.44	15.95	18.64	29.11	30.73	40.48
VII							12.21	16.06	19.44	15.70	16.00	13.36	30.12	29.82	38.23
VIII								12.40	17.59	21.88	22.43	16.88	25.78	30.91	36.32
IX									13.80	23.71	23.89	20.22	29.78	31.81	32.66
X										14.48	20.12	16.84	35.26	29.36	38.79
XI											14.68	19.63	32.18	32.46	40.70
XII												14.99	32.23	30.14	37.74
XIII													17.07	36.85	40.36
XIV														38.35	42.24
XV															43.68

The highest inter cluster distance was observed between cluster XV and XIV (42. 24), followed by the cluster XV and XI (40.70), cluster XV and VI (40.48), clusters XV and XIII (40.36) and clusters XV and I (40.17) while the lowest value of 13.36 was observed between cluster XII and VII. These results revealed that genotypes from cluster I and XIV should be selected for melon improvement programme based on the mean value for the specific trait. Data further revealed that there is good scope for selection for many traits of economic and horticultural importance within a cluster as indicated by the high magnitude of intra-cluster distance among clusters. Clusters with two genotypes each, indicated an independent identity and importance, due to various unique characters possessed by the genotypes. Similar observations were reported by Prasad *et al.* (2004) and Reddy *et al.* (2012) wherein intra cluster distance values was reported to be in the range of 0.00 to 85.51 in muskmelon. Tomar *et al.* (2008) also reported intra cluster distance values in the range of 0.00 to 41.24.

The highest yield per plant was observed in cluster XIII (2.99) and the lowest yield per plant was recorded in cluster III (1.35). Cluster XIII comprised of genotypes having higher TSS with an average of (13.65), while cluster III recorded minimum TSS (8.68). Thus genotypes with high yield and TSS from cluster XIII could be selected as parents for hybridization programme. Based on higher genetic distance, yield and TSS, DM-31, DM-145, DM-159 and DM-162 genotypes from *inodorous* group of Cluster I and Pusa Madhuras (Cluster VII), Kashi Madhu, Punjab Sunheri, Hara Madhu (Cluster XIV) from *cantaloupensis* group could be utilized for hybridization programme to facilitate better yield and fruit quality traits from both horticultural groups into a single variety or hybrid. The morphological data was standardised and pair wise genetic distance was calculated using Manhattan coefficient. The coefficient values were analysed using UPGMA based SAHN clustering. The coefficient values ranged from 0.35 to 1.71. At coefficient value of 1. 1 all the genotypes were grouped into two major clusters I and II (Fig 1). Cluster I comprised of only two accessions (DM-7, DM-155). Cluster II could be further sub-divided into two sub clusters sub cluster-IIB. Sub-cluster IIA comprised of 20 exotic germplasm accessions mainly from *inodorus* group. The group IIB comprised of 45 accessions mostly from *cantaloupensis* group including all Indian germplasm such as Punjab Sunheri, Kashi Madhu, Pusa Madhuras, Durgapura Madhu, Arka Jeet and Hara Madhu.

Eigen value of principal component axes of total variation obtained from principal component analysis (Table 3). The first three principal components accounted (53.77%) of the total variation among 24 characters describing 67 genotypes and 7 components accounting for 79.59 cumulative percent of total variation present in the population. The traits which contributed more positively to PC1 were days to first staminate flower opening, days to first pistillate opening, average fruit weight (kg), days from pollination to fruit harvest. The genotypes in the PC1 were more likely to be associated with higher days to first pistillate opening, average fruit weight (kg) and yield per plant (kg), whereas the genotypes with higher node number of first male flower, fruit length (cm), fruit width (cm), fruit shape index, flesh thickness (cm), were contributed by second PC. Principal component analysis has been also widely used in studying genetic variability in germplasm collections of many species. The selected genotypes on the basis of different groups could be identified for yield potential. Yildiz *et al.* (2014) reported that cumulative proportion of variation reached 44% by first three PCA axes. In this study, TSS, days to first fruit harvest, total growth duration, days to first pistillate flower opening, days to first

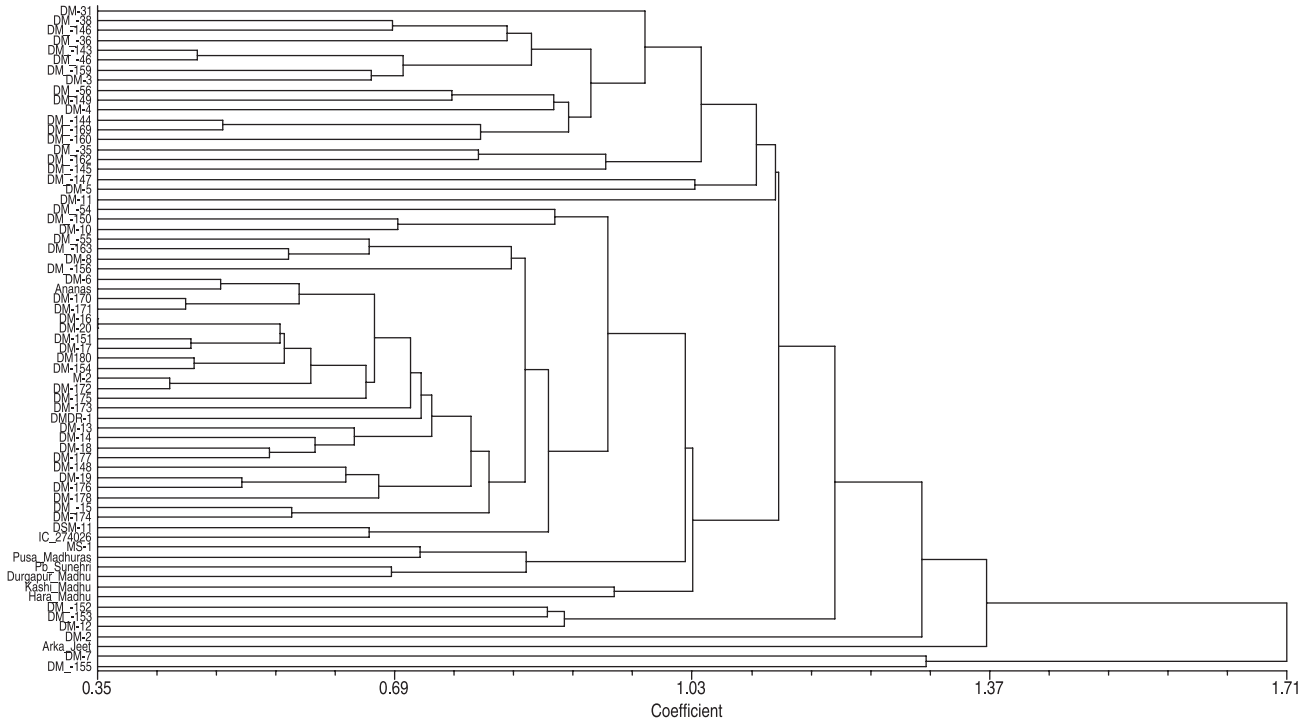

Fig 1 Clustering based Manhattan distance coefficient value of 24 quantitative traits in 67 genotypes of muskmelon.

Table 3 Eigen values and proportion of variance explained by 7 principal componentsfor 24 traits among 67 muskmelon genotypes

Parameter	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
Cumulative Eigen value	6. 65	4. 10	2. 16	1. 89	1. 78	1. 38	1. 14
Explained variation (%)	27. 71	17. 08	8. 98	7. 87	7. 42	5. 76	4. 76
Cumulative explained variation (%)	27. 71	44. 79	53. 77	61. 64	69. 07	74. 83	79. 59
Traits				*Eigen value*			
Days to first male flower opening	0. 78	-0. 41	0. 14	0. 08	-0. 10	-0. 08	0. 14
Node number of first male flower	-0. 20	0. 45	0. 39	0. 04	0. 28	-0. 37	0. 18
Days to first pistillate opening	0. 77	-0. 35	0. 18	0. 24	-0. 14	-0. 14	0. 23
Node number of first pistillate flower	-0. 03	0. 04	0. 70	0. 38	0. 28	0. 18	-0. 27
Node number of first fruit set	0. 00	-0. 01	0. 71	0. 34	0. 39	0. 26	-0. 14
Number of fruits per plant	-0. 28	0. 15	0. 38	-0. 03	0. 06	0. 29	0. 57
Average fruit weight(kg)	0. 70	0. 58	-0. 17	0. 08	0. 08	-0. 04	0. 08
Number of primary branches per plant	0. 36	-0. 08	0. 13	-0. 14	-0. 28	-0. 40	0. 15
Vine length (m)	0. 56	-0. 25	0. 28	-0. 27	-0. 37	0. 02	-0. 10
Days from pollination to fruit harvest	0. 70	-0. 53	-0. 12	0. 08	0. 16	-0. 02	0. 02
Days to first fruit harvest	0. 83	-0. 46	0. 09	0. 14	0. 02	-0. 06	0. 15
Total crop duration	0. 78	-0. 48	0. 10	0. 22	0. 08	-0. 07	0. 17
Fruit length (cm)	0. 71	0. 53	-0. 07	-0. 28	0. 33	0. 02	-0. 08
Fruit width(cm)	0. 32	0. 47	-0. 41	0. 61	0. 03	0. 05	-0. 07
Fruit shape index	0. 64	0. 38	0. 12	-0. 54	0. 32	-0. 01	-0. 04
Flesh thickness(cm)	0. 56	0. 37	-0. 18	0. 34	0. 01	0. 30	-0. 17
Cavity width (cm)	-0. 27	0. 36	-0. 27	0. 57	0. 06	-0. 41	0. 14
Cavity length(cm)	0. 64	0. 50	-0. 03	-0. 41	0. 36	-0. 07	-0. 05
Rind thickness(mm)	0. 17	0. 25	-0. 15	-0. 04	-0. 31	0. 49	0. 16
Seed length (mm)	-0. 07	0. 64	0. 31	0. 01	-0. 45	0. 12	0. 28
Seed width(mm)	0. 15	0. 64	0. 39	0. 02	-0. 60	-0. 06	-0. 09
Seed shape index	-0. 38	-0. 17	-0. 23	-0. 08	0. 39	0. 31	0. 55
Total soluble solids (°Brix)	0. 42	-0. 29	-0. 17	-0. 02	-0. 18	0. 50	-0. 14
Yield per plant (kg)	0. 65	0. 58	-0. 11	0. 17	-0. 01	0. 07	0. 17

male flower opening, flesh thickness, fruit shape index, yield per plant, average fruit weight and fruit length were the major characters for diversity of 67 genotypes. This was in agreement with earlier work of Koli *et al.* (2013) who reported that fruit length, fruit weight, fruit shape, were the principle characters to discriminate melon genotypes. The bi-plot between PC1 against PC2 depicts the combined results of correlation among the variable and diversity among the genotypes. This grouping pattern confirmed the results obtained by D^2 analysis and that the crosses involving parents belonging to the maximum divergent clusters are expected to manifest maximum heterosis in the progeny. The high intracluster distance between cluster I and cluster II confirms the presence of more divergent genotypes which may be directly used for hybridization programme. The results of present study are useful to breeders to organise specific breeding programme for higher yield and fruit quality improvement in muskmelon by utilizing genotypes from different horticultural groups.

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