



## Genetic diversity analysis in muskmelon (*Cucumis melo*) for yield and quality traits

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Muskmelon (*Cucumis melo* L.), popularly known as kharbuja in India, is one of the important and economic species of fruit vegetables. It is believed to be originated in tropical Africa and India is regarded as its secondary centre of origin (Chadha and Lal 1993). The fruits of muskmelon are sweet with musky flavour which is mainly grown as a dessert crop and has good export potential. In India muskmelon is cultivated in around 54000 ha area with 1.14 MT production (Anonymous 2018-19). Despite its recognized potential as high-value dessert fruit vegetable, commercial muskmelon cultivation is less remunerative due to low yield potential and sub-optimal fruit quality of current open-pollinated cultivars. Hence, further genetic improvement in cultivars for yield and quality is needed. The wide genetic diversity within the available genotypes and cultivars offers ample scope for further improvement. Hence, the present study was carried out to assess the diversity within the available muskmelon genotypes to identify genetically diverse lines with a desirable combination of characteristics.

A total of 32 muskmelon genotypes were evaluated in a randomized block design (RBD) with three replications during summer (March–June) 2018. Each genotype was grown in a double-row plot of 7.0m length. Rows were spaced 2.0 m apart, while plants were spaced 0.6 m apart accommodating 10 plants in a row. All the recommended agronomical practices were followed during the experiment. The observations for growth and development characters like main vine length at harvest, number of primary branches/vine, length of internode, number of node at which first female flower appeared, fruit set (per cent), number of marketable fruits/plant, and days to first fruit harvest was recorded from five randomly selected plants from each plot. The fruit characters, viz. fruit diameter, fruit length, fruit weight, fruit yield, rind thickness, flesh thickness, cavity

width, and cavity length were measured from five fruits randomly selected from each plant. Among the quality characters, total soluble solids (TSS) were determined by Abbe's hand refractometer and shelf-life was determined based on 15% weight loss of fruits at room temperature. Statistical analysis was done on the mean basis across the genotypes. Mahalanobis D<sup>2</sup> statistics (Mahalanobis 1936) was used to analyze genetic divergence between genotypes. Genotypes were clustered using Tocher's method as described by Rao (1952). The average intra-cluster and inter-clusters distance and character contribution towards genetic divergence were calculated following Singh and Chaudhary (1985).

The analysis of variance revealed significant differences among 32 genotypes for each of 18 characters and suggested appreciable variability among the genotypes. The D<sup>2</sup> values

Table 1 Clustering pattern among 32 genotypes of muskmelon based on D<sup>2</sup> analysis for 18 characters

Cluster	Number of genotypes	Genotype (s)
I	13	GMM-3, MHY-5, MHY-3, RM-50, Pusa Madhuras, Pusa Sharabati, IC-0624304, VRMM-163, VRMM-313, VRMM-307, VRMM-423, VRMM-402, VRMM-106
II	8	Arka Jeet, Hara Madhu, VRMM-207, VRMM-201, VRMM-153, VRMM-196, VRMM-158, VRMM-11
III	4	Kashi Madhu, RM-43, IC-0599709, IC-0624305
IV	1	VRMM-315
V	3	Punjab Sunehri, VRMM-205, VRMM-194
VI	1	VRMM-127
VII	1	Durgapura Madhu
VIII	1	Jodhpur Local

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estimated for 32 genotypes in  $n(n-1)/2 = 496$  combinations varied from 0.21 to 220.25 indicating the presence of a substantial amount of genetic diversity in the population. Based on  $D^2$  values, the 32 genotypes were grouped into eight highly distinct clusters (Table 1) suggested the presence of a high degree of divergence in the material studied. Cluster I was largest and comprised of 13 genotypes followed by cluster II with eight genotypes. Cluster III consisted of four genotypes, cluster V comprised of three genotypes while cluster IV, cluster VI, cluster VII and cluster VIII comprised of one genotype each. The distribution pattern of genotypes of diverse origin in a single cluster indicated that the geographical origin in muskmelon was not related to genetic divergence. The tendency of genotypes occurring in clusters cutting across the geographical boundaries demonstrates that geographical isolation need not necessarily be related to genetic diversity and may not be the factor in determining genetic divergence. These findings are in close conformity with the report of Reddy *et al.* (2017).

Average intra-cluster and inter-cluster  $D^2$  values among 32 genotypes revealed that the values of intra-cluster distance were 0 (cluster IV and VI to VIII) to 39.82 (Cluster V), the lower intra-cluster values indicating that genotypes within this cluster were similar. These results are as per the Reddy and Shanthi (2013), however, higher intra-cluster values revealing the existence of diverse genotypes in these clusters. Maximum inter-cluster value (355.14) was found between cluster V (Punjab Sunehri, VRMM-205, VRMM-194) and

cluster VIII (Jodhpur Local) followed by cluster VII and cluster VIII (232.01) which indicates that genotypes included in these clusters had maximum divergence. Hence, inter mating between the genotypes included in these different clusters may give high heterotic and better segregates. The results of the present experiment were in accordance to those of Karadi *et al.* (2017) in wild melon.

The genetic divergence present in the material was also supported by the appreciable amount of variation among cluster means for different characters (Table 2). Cluster I exhibited the highest mean for flesh thickness and cavity width. Cluster III showed the highest values of the number of node at which the first female flower appeared and fruit yield. Highest mean for main vine length at harvest, internodal length, per cent fruit set, number of marketable fruits/plant, fruit diameter, fruit yield and shelf life was recorded in cluster V. Cluster VII exhibited the highest mean for the number of primary branches per vine, fruit length, fruit weight, length of cavity (cm) and TSS. Cluster VI exhibited the highest mean for rind thickness, while Cluster VIII showed the highest mean for days to first fruit harvest. These results suggest that the improvement of a particular character through hybridization, the selection of genotypes with high cluster mean values could be used. These findings further indicate that the genotypes included in the diverse cluster, viz. cluster V (Punjab Sunehri, VRMM-205, VRMM-194) and cluster II (Arka Jeet, Hara Madhu, VRMM-207, VRMM-201, VRMM-153, VRMM-

Table 2 Cluster means and contribution of different characters toward genetic divergence in muskmelon

Character	Cluster number								Contribution towards divergence (%)
	I	II	III	IV	V	VI	VII	VIII	
Main vine length at harvest (cm)	92.08	89.96	92.35	81.09	98.76**	96.64	91.95	73.16*	0.00 (0)
Number of primary branches/vine	5.17	5.34	4.95	4.68*	5.42	5.10	6.37**	4.72	0.20 (1)
Length of internode (cm)	5.53	5.91	5.32	5.75	6.04**	5.05	4.67*	4.91	0.00 (0)
Number of node at which first female flower appeared	5.28	5.21	5.52**	4.13	5.28	3.98	5.25	3.82*	0.00 (0)
Fruit set (%)	77.28	75.27	78.43	74.28	79.66**	76.09	78.19	65.81*	0.00 (0)
Number of marketable fruits/plant	3.06	3.00	3.45	2.37	3.67**	2.10	2.80	1.72*	0.00 (0)
Days to first fruit harvest	73.35	74.35	71.66	72.20	73.11	76.15	70.82*	78.3**	0.00 (0)
Fruit diameter (cm)	10.05	11.06	10.00	9.76	11.89**	7.77	7.90	6.22*	2.02 (10)
Fruit length (cm)	10.81	11.20	10.78	13.01	12.00	12.17	14.75**	9.65*	0.40 (2)
Fruit weight (kg)	0.50	0.43	0.64	0.36	0.57	0.28	0.82**	0.21*	7.26 (36)
Fruit yield (kg/plant)	1.48	1.23	1.66	1.04	2.03**	0.60	2.07	0.35*	0.40 (2)
Fruit yield (q/ha)	156.28	133.15	220.25**	98.54	204.95	64.30	210.08	38.80*	0.00 (0)
Rind thickness (cm)	0.91	0.94	0.87	0.65*	0.74	1.11**	0.72	1.07	0.60 (3)
Flesh thickness (cm)	2.12**	1.84	1.95	1.95	2.03	1.83	2.11	1.40*	0.20 (1)
Width of cavity (cm)	6.16**	5.72	5.55	4.38	5.28	3.96*	5.90	3.98	4.23 (21)
Length of cavity (cm)	8.14	8.32	9.16	9.96	8.63	9.00	11.95**	8.02*	2.62 (13)
TSS (%)	8.79	8.81	11.16	7.99	10.47	7.55	11.19**	7.07*	27.82 (138)
Shelf-life (days)	3.12	4.20	2.57	2.54	5.10**	3.39	3.77	2.05*	54.23 (269)

\*Lowest mean value; \*\* Highest mean value

196, VRMM-158, VRMM-11) hold good promise as parents for obtaining potential hybrids and thereby creating large variability for these characters in muskmelon.

The contributions of different characters of muskmelon genotypes toward genetic divergence were 54.23% for shelf life, 27.82% for TSS, 7.26% for fruit weight, 4.23% for cavity width, 2.62% for cavity length, 2.02% for fruit diameter and 0.6% for rind thickness (Table 2). These results point out a positive contribution of genetic divergence on yield and quality components and this can be of considerable aid in selection for yield and other economic characters. Thus, these characters need more attention in the genetic improvement of muskmelon. The more divergence observed for these characters offering greater scope while making the selection of superior genotypes of muskmelon. The results are in accordance with the earlier findings of Reddy and Shanthi (2013). Thus considering the inter-cluster divergence mating between the genotypes like Punjab Sunehri, VRMM-205, VRMM-194 with locally grown genotype Jodhpur Local can realize good recombinants which may serve as potential parents for future breeding programmes of muskmelon.

#### SUMMARY

In present study, 32 diverse genotypes of muskmelon (*Cucumis melo* L.) collected from different parts of the country were evaluated to study the correlation, path analysis and divergence for yield and quality characters using 18 morphological traits. In cluster analysis, genotypes were grouped into eight distinct clusters with a maximum of 13 genotypes in cluster I. The highest inter-cluster distance (355.14) was obtained between cluster V and VIII. Among the traits studied, shelf-life (54.23%), total soluble solids (27.82%) and fruit weight

(7.26%) contributed a major share in the divergence of the genotypes. Four genotypes, viz. VRMM-315, VRMM-12, Durgapura Madhu, and Jodhpur local accommodated into a single cluster, probably share a genetic similarity. The genotypes of cluster V (Punjab Sunehri, VRMM-205, VRMM-194) and cluster VIII (Jodhpur Local) being most divergent from others may serve as potential parents for breeding programmes.

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