Journal of Applied Horticulture, 24(1): 105-109, 2022
DOI: https://doi.org/10.37855/jah.2022.v24i01.20
Journal of Applied Horticulture
ISSN: 0972-1045

Genetic divergence analysis in muskmelon (*Cucumis melo* L.) genotypes using morphological and biochemical traits

Kumar Harsh[1]*, Akhilesh Kumar Pal[2] and Madhuri Choudhury[2]

Department of Horticulture, Institute of Agriculture Sciences, Banaras Hindu University, Varanasi- 221005 (U.P), India.
**E-mail: kumarharsh12312@gmail.com*

Abstract

An investigation was carried out at Vegetables Research Farm of Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, during Zaid season (Feb-May) of 2019 to evaluate 26 genotypes of muskmelon (*Cucumis melo* L.) for genetic diversity based on 32 morphological and 4 biochemical traits. Since any breeding program's success depends broadly on the available genetic diversity and the rational selection of parents, the wider genetic diversity of the genotypes offers plentiful room for further improvement in available cultivars. Therefore, Mahalanobis's D^2 statistic was adopted for quantitative assessment of genetic divergence and based on the relative magnitude of D^2 values, twelve clusters were formed. Of the twelve clusters, cluster I was largest with the nine genotypes, followed by cluster III with seven genotypes. Among the traits studied, maximum genetic divergence was contributed by the character index seed weight (15.38%). The maximum inter-cluster distance was recorded between cluster VIII and XI (106.09) while, the intra-cluster distance was highest in cluster III (46.03) which marked the presence of wide genetic diversity among the genotypes GP-150, Pusa Madhuras, MHY-3, GP-20, MM-1, Durgapur Selection, and GP-73. The inter-cluster distance was more than the intra-cluster distance indicating the presence of wide genetic diversity, among the genotypes under study.

Key words: Cluster, Genetic divergence, Germplasm, Mahalanobis D^2 statistic, Tocher's method

Introduction

Melons exhibit a wide range of biochemical, morphological and physiological diversity (Eduardo *et al*., 2007) and hence referred to be as a polymorphic taxon. Muskmelon (*Cucumis melo* L.) is a annual fruit vegetable climbing, creeping or trailing. Although the species is generally known as melon, it is also called cantaloupe, muskmelon casab and sweet melon (Nayar and Singh, 1998). The wild species of *Cucumis* is found in Africa. However, it is of Asian origin, likely originated from India to Persia (Sebastian *et al.*, 2010). It was domesticated for the first time in Egypt and Iran during the second and third millennia BC (Pangalo, 1929). Being a drought tolerant crop from family Cucurbitaceae, muskmelon is found in warm temperate, sub-tropical and tropical areas of the world. The largest muskmelon producing countries in the world are China, Iran, Spain and USA. In India, it is produced on an area of about 54.10 thousand ha with a production of 1230.66 thousand tonnes (Horticultural Statistics at a Glance, 2018). Muskmelons are extensively cultivated in hot and dry areas of Bihar, Madhya Pradesh, Karnataka, Punjab, Rajasthan, and Uttar Pradesh. While in Uttar Pradesh, muskmelons are cultivated prominently in the Ganga and its tributaries riverbeds. The fruits are popular during summer and extensively used as dessert fruit.

Muskmelon has a lot of dietary fibre, vitamins, and minerals; hence, both ripe fruits and immature ones are very useful in curing human diseases like kidney problems, eczema, tan freckles and dyspepsia. Hence, in the world's fresh fruit market, it is the fourth most important fruit with several varieties (Mabaleha *et al.*, 2007). Due to its medium duration, high production potential, and high nutritional, medicinal, and industrial value, it is gaining a stronger foothold. When compared to other fruit vegetables, it commands a higher price in the market. Despite its many benefits, its productivity is low when compared to other Indian fruit vegetables. Lack of advanced varieties has contributed to the low productivity and quality of muskmelon in India and other production constraints. Improving cultural practices and developing genetically superior cultivars can leads to higher yield. As muskmelon production is gaining importance at every horizon, be it domestic or international, identifying new germplasm lines and their systematic studies is a pre-requisite to develop cutting edge varieties that can withhold the challenges of both quantity and quality aspects on commercial lines.

Information on intraspecific genetic diversity and relationships within muskmelon germplasm is limited. Also, the available germplasm has not been well characterized from the point of view of its exploitation for crop improvement. And therefore, for efficient choice of parents, the available information on genetic divergence among the available germplasm is very important for hybridization. Since it reduces the hectic load of selecting the desired parents for crossing, as the improvement process is long and the lines are numerous in the form of farmer's line and seed companies' hybrids representing a huge possible crosses to generate lines, wrongly picked parents would, in this manner, bring about no benefit but a waste of time and resources. So, there is an expanded interest for a significant comprehension of the germplasm of muskmelon and the extent of genetic diversity in it.

It is well known that the use of diverse parents results in superior hybrids and desirable recombinants. So, analysis of multivariate using Mahalanobis D^2 statistic (Mahalanobis, 1936) has been

done to quantify the degree of divergence between the genotypes at the genetic level. Although, the genetic diversity has been utilized earlier in various breeding programmes, which resulted in some good and promising variety release in muskmelon. However, the released ones can't be continued longer due to susceptibility to various stresses (biotic and abiotic) and genetic drift. This demands replacement of these existing ones. Keeping in view all the above facts, the present study was formulated to determine the degree of divergence at the genetic level among the available muskmelon genotypes.

Materials and methods

The investigation was carried out at Vegetables Research Farm of Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, during Zaid season (Feb-May), of 2019. The experimental material comprised of 26 genotypes of muskmelon (*Cucumis melo* L.) collected from different sources in India (Table 1). The experimental site is situated at an elevation of 129.23 meter above the mean sea level, lying between 25°15" North latitude and 83°03" East longitude in the north Gangetic plains.

Table 1. List of sources of muskmelon genotypes

Source	Genotypes
RARI, Durgapura	GP-73, GP-150, RM-102, RM-43, Kazri, RM-101, GP-128(+), GP-105, Durgapur Kranti, MHY-3, MHY-5(+), GP-20, Pusa Madhuras, GP-176, Durgapur Madhu, GP-168, Golden Yellow, Durgapur Selection, RM- 49, RM-50
IIVR, Varanasi	VRMM-46, MMIIHR-653, Punjab Sunehri, MM-1, Kashi Madhu, VRM-4

The genotypes were grown in randomized block design (RBD) with three replications, in paired row system of layout with a row to row spacing of 1.5 m and plant to plant spacing of 0.5 m, having a channel width of 0.3 m between adjacent rows and seeds were directly shown in the basins made on the paired rows, allotted 4 for each genotype in every replication. Sowing was done on 25th of February, 2019. Observations were recorded on five randomly selected plants from each germplasm and every replication. The observations were recorded on the length of cotyledon (mm), width of cotyledon (mm), days to first male flower, days to first female flower, node to first male flower, node to first female flower, petiole length (cm), leaf blade length (cm), leaf blade width (cm), leaf area (cm^2), chlorophyll content (spad value), total number of male flowers, total number of female flowers, sex ratio (m/f), total no. of leaves, total no. of 1° branches, total no. of nodes, total no. of fruits, vine length (m), days to first fruit harvest, fruit weight (g), yield of fruit per plant (g), thickness of flesh (cm), cavity width (cm), cavity length (cm), fruit length (cm), fruit diameter (cm), pulp weight (g), seeds per fruit, seed weight (g), index seed weight (g), pulp to seed ratio , TSS (°B), ascorbic acid (mg/100 g), titratable acidity (%), and phenol content (mg/g). Abbe's Hand Refractometer measured TSS (0-32 %), titratable acidity and ascorbic acid were determined by visual titration method given by Ranganna (1976). Genetic divergence was estimated by evaluating Mahalanobis' D^2 statistics (Mahalanobis, 1936) among the genotypes. Grouping of genotypes into various clusters by Tocher's method as given by Rao (1952). The average inter and intra cluster distances were calculated by formula given by Singh and Chaudhary (1977). The character contribution towards genetic divergence was calculated using method given by Singh and Chaudhary (1977). All the statistical analysis was carried out using version 9.1 of Windo Stat software.

Results

Analysis of dispersion: Mahalanobis's D^2 statistic was adopted for quantitative assessment of genetic divergence among twenty-six genotypes based on thirty-six characters for fruit yield and yield attributing characters. However, to test the significant differences between the groups, Wilk's 'V' (statistical) criterion was used which is based on the merged effects of all the characters. D^2 tested the significance of the (statistical) value of 'V' at 900 degrees of freedom by percent. The 'V' statistic value (data not presented) was turning out to be very significant for all the characters under study.

Clustering pattern: Based on D^2 values, 26 genotypes were divided into twelve very different clusters (Table 2). Of the twelve clusters, cluster I was the largest with the nine genotypes followed by cluster IIIwith seven while, the II, IV, V, VI, VII, VIII, IX, X, XI, and XII had one genotype each.

Table 2. Cluster composition of twenty-six genotypes of muskmelon (Tocher's method)

Cluster	No. of Genotypes	Name of the Genotypes
1	Nine	Durgapur Kranti, VRM-4, RM-102, RM-43, RM-101, RM-50, GP-105, GP-128, MMIIHR-653
2	One	RM-49
3	Seven	GP-150, Pusa Madhuras, MHY-3, GP-20, MM-1, Durgapur Selection, GP-73
4	One	VRMM-46
5	One	GP-176
6	One	Golden Yellow
7	One	MHY-5(+)
8	One	Kashi Madhu
9	One	GP-168
10	One	Kazri
11	One	Durgapur Madhu
12	One	Punjab Sunehri

Intra-cluster and inter-cluster distances: The average intra and inter-cluster D^2 values and statistical distance between 26 genotypes are presented in Table 3. Intra-cluster D^2 values ranged from 0.00 (clusterII, IV, V, VI, VII, VIII, IX, X, XI, and XII) having single genotype in each to 46.03 (cluster III) having seven genotypes. The maximum intra-cluster distance was observed in cluster III (46.03), followed by clusterI (39.73). The maximum inter-cluster distance was recorded between cluster VIII and XI (106.09) followed by cluster XI and XII (104.97) and cluster V and XI (90.56). While lower inter-cluster distance was recorded between clusters IV and VII (40.03) followed by clusters VI and VII (44.22).

Cluster means: The cluster means for each of 36 characters studied in muskmelon genotypes revealed considerable differences among all the clusters (Table 4). The data indicated that the high cluster means for days to first female flower in cluster X (48 days) and the lowest in cluster IV (43.53 days). Cluster IV exhibited the highest number of node at which first female flower appeared (6.13) whereas, cluster V had lowest

Table 3. Cluster distances

Cluster No.	1	2	3	4	5	6	7	8	9	10	11	12
1	39.73	48.3	53.47	50.6	51.6	50.05	52.14	51.8	57.24	58.97	70.81	56.59
2		0	52.17	48.39	66.33	66.91	62.2	67.56	75.49	75.98	72.3	52.22
3			46.03	53.87	65.11	72.48	54.09	76.45	56.45	63.57	61.95	64.86
4				0	72.17	50.62	40.03	73.09	63.49	68.07	56.81	70.2
5					0	63.07	65.02	49.82	54.47	67.15	90.56	66.18
6						0	44.22	61.05	66.17	75.89	70.36	82.38
7							0	76.22	54.95	68.26	45.41	83.54
8								0	80.46	68.02	106.09	48.15
9									0	49.55	56.98	87.21
10										0	77.59	75.8
11											0	104.97
12												0

Table 4. Cluster means for thirty-six characters in twenty-six genotypes of muskmelon (Tocher's method)

Sr. No.	Characters	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6	Group 7	Group 8	Group 9	Group 10	Group 11	Group 12
1	Length of cotyledon (mm)	31.03	29.55	26.49	36.10	36.27	27.43	29.47	37.93	34.22	33.63	31.47	22.80
2	Width of cotyledon (mm)	16.18	17.15	14.36	20.93	18.96	16.05	15.78	19.80	16.13	18.90	15.28	11.33
3	Days to first male flower	41.99	42.27	41.73	38.93	43.13	40.80	42.80	41.60	42.87	41.07	41.73	39.67
4	Days to first female flower	46.81	47.53	46.74	43.53	47.07	45.67	46.27	45.73	47.93	48.00	46.67	44.47
5	Node to first male flower	3.79	2.47	3.61	3.60	3.40	2.20	3.27	4.40	4.13	4.00	2.93	2.80
6	Node to first female flower	5.73	4.67	5.75	6.13	3.27	4.73	5.20	5.47	4.93	5.73	3.93	5.00
7	Petiole length (cm)	13.30	12.73	11.98	13.00	12.26	10.65	11.03	12.13	16.85	16.93	17.52	12.03
8	Leaf blade length (cm)	9.19	9.34	9.11	7.67	8.92	8.64	9.17	8.80	8.05	10.05	9.62	10.47
9	Leaf blade width (cm)	12.76	11.91	11.93	10.98	11.61	11.16	11.25	12.19	10.49	13.19	10.66	12.05
10	Leaf area (cm^2)	55.42	68.50	43.98	42.83	64.57	60.08	42.57	53.03	62.57	63.67	63.23	43.22
11	Chlorophyll content (spad value)	51.68	41.25	52.42	54.57	47.63	46.50	46.48	51.43	54.97	52.55	46.63	60.37
12	Total number of male flowers	79.42	59.13	73.10	86.47	87.40	112.00	93.40	84.87	105.87	96.40	89.47	54.93
13	Total number of female flowers	2.81	2.40	3.01	1.87	3.40	7.13	3.40	2.13	7.47	4.53	4.27	1.87
14	Sex ratio (M/F)	29.98	25.76	27.44	46.83	26.12	15.73	27.92	40.08	14.22	21.43	21.29	30.65
15	Total no. of leaves	26.28	30.53	27.84	24.33	29.13	24.93	32.13	23.47	24.07	21.33	30.67	19.00
16	Total no. of branches	3.44	4.47	4.36	3.40	4.00	3.87	5.00	3.60	3.47	2.73	3.27	3.60
17	Total no. of nodes	20.16	24.33	21.81	17.13	22.53	17.40	24.13	18.00	17.67	15.87	25.20	10.80
18	Total no. of fruits	2.07	1.93	2.22	1.67	2.67	4.40	2.53	1.87	4.53	3.47	3.00	1.60
19	Vine length (m)	1.70	1.79	1.70	1.53	1.67	1.78	2.45	1.76	1.81	2.02	1.92	1.07
20	Days to first fruit harvest	83.14	80.87	83.19	73.93	91.47	85.93	88.00	90.47	78.53	81.07	82.67	81.33
21	Fruit weight (g)	390.51	190.35	449.09	421.83	257.01	214.17	205.75	397.31	687.10	406.12	337.28	225.33
22	Yield of fruit per plant (g)	803.76	367.96	1016.40	694.20	686.37	940.70	522.65	742.96	3109.50	1436.04	1019.71	360.30
23	Thickness of flesh (cm)	2.00	1.24	1.90	1.44	1.47	1.46	1.54	2.10	1.92	1.71	1.80	2.39
24	Cavity width (cm)	5.12	4.17	5.36	3.42	5.15	3.48	3.82	5.25	5.70	5.65	4.58	5.65
25	Cavity length (cm)	5.10	4.83	5.75	4.38	5.20	3.69	4.78	5.55	6.60	4.52	8.48	5.35
26	Fruit length (cm)	7.92	7.27	9.04	7.62	7.15	5.68	7.83	7.22	10.02	7.92	12.27	8.19
27	Fruit diameter (cm)	8.40	6.80	8.69	6.35	8.08	6.02	7.08	10.07	8.22	9.28	7.88	10.42
28	Pulp weight (g)	276.70	137.13	302.48	385.40	168.55	180.92	139.53	219.58	543.50	211.99	235.85	141.97
29	Seeds per fruit	302.48	263.33	305.24	307.33	371.67	218.00	275.00	303.67	355.67	285.00	254.67	221.00
30	Seed weight (g)	4.09	3.19	7.29	4.26	6.96	2.72	5.10	7.07	7.13	8.70	4.16	4.61
31	Index seed weight (g)	1.32	1.17	2.02	1.40	1.82	1.17	1.81	2.26	1.99	3.02	1.30	2.01
32	Pulp to seed ratio	56.97	43.55	38.18	55.56	24.21	66.39	27.76	31.03	57.60	24.61	56.54	30.74
33	TSS (°B)	8.36	6.27	11.56	10.50	7.00	9.07	11.13	11.30	8.07	7.90	10.80	8.77
34	Ascorbic acid content (mg/100 g)	20.23	17.33	19.36	22.50	16.67	14.33	29.67	28.67	19.67	30.33	22.67	23.23
35	Titratable acidity (%)	0.93	0.58	1.38	0.88	2.69	0.74	1.10	1.08	2.07	0.42	0.68	1.45
36	Phenol content (mg/g)	0.19	0.08	0.17	0.15	0.13	0.14	0.25	0.17	0.17	0.12	0.18	0.21

(3.27). The chlorophyll content was reported highest in cluster XII (60.37) whereas, the lowest was in cluster II (41.25). Total number of female flowers exhibited highest and lowest means in cluster VI (7.13) and cluster IV (1.87), respectively. Cluster VII exhibited highest mean for a number of primary branches per vine (5.00) while lowest was in cluster X (2.73). Vine length at harvest exhibited highest and lowest means in cluster VII (2.45 m) and cluster XII (1.07 m), respectively. Cluster IX exhibited highest mean for yield of fruit per plant (3109.5 g) while, the lowest was in cluster XII (360.3 g). Flesh thickness had highest

in cluster XII (2.39 cm) whereas, lowest in cluster II (1.24 cm). The maximum cavity length was recorded in cluster XI (8.48 cm) while minimum in cluster VI (3.69 cm). The minimum cavity width was recorded in cluster IV (3.42 cm) whereas, maximum in cluster IX (5.7 cm). The fruit length was highest in cluster XI (12.27 cm) and lowest in cluster VI (5.68 cm). Cluster XII showed highest fruit diameter (10.42 cm) while in cluster VI it was lowest (6.02 cm). TSS was recorded highest in cluster III (11.56 °B) while, minimum in cluster II (6.27).

Percentage contribution of individual characters to diversity: The percentage contribution of 36 characters towards genetic divergence is presented in Table 5. The character index seed weight (15.38 %) contributed the maximum to genetic divergence followed by titratable acidity and fruit diameter (14.46 %) each, phenol content (11.38 %), width of the cavity (11.08 %), ascorbic acid content (10.77 %), number of male flowers (7.08 %), seeds per fruit (6.77 %), and pulp to seed ratio (4.31 %). However, the rest of the characters did not contribute materially towards total diversity.

Table 5. Percentage contribution of individual characters to diversity

Sr. No.	Characters	Number of times ranked 1st	Contribution %
1	Leaf area (cm²)	4	0.0123
2	Total number of male flowers	23	0.0708
3	Thickness of flesh (cm)	5	0.0154
4	Cavity width (cm)	36	0.1108
5	Fruit diameter (cm)	47	0.1446
6	Seeds per fruit	22	0.0677
7	Seed weight (gm)	3	0.0092
8	Index seed weight (gm)	50	0.1538
9	Pulp to seed ratio	14	0.0431
10	TSS (°B)	2	0.0062
11	Ascorbic acid content (mg/100 g)	35	0.1077
12	Titratable acidity (%)	47	0.1446
13	Phenol content (mg/gm)	37	0.1138

The rest of the characters such as length of cotyledon (mm), width of cotyledon (mm), days to first male flower, days to first female flower, node to first male flower, node to first female flower, petiole length (cm), leaf blade length (cm), leaf blade width (cm), chlorophyll content (spad value), total number of female flowers, sex ratio (m/f), total no. of leaves, total no. of branches, total no. of nodes, total no. of fruits, vine length (m), days to first fruit harvest, fruit weight (gm), yield of fruit per plant (gm), cavity length (cm), fruit length (cm) and pulp weight (gm) did not contribute materially towards total diversity *i.e.* they ranked number of times 1st is zero.

Discussion

Due to Asian centre of diversity and related domestication history of muskmelon from the Mediterranean basin (Turkey) to Central Asia (Iran, Uzbekistan) to India to East Asia, muskmelon has several landraces over ages. Existing landraces of muskmelon in different ecosystems may provide the genetic diversity needed to diversify the distress gene pool of improved varieties, because of their adaptations to a wide range of agro-ecological conditions. Therefore, these landraces can be exploited significantly to enhance the productivity of muskmelon.

Genetic resource reserves that have not received much attention in terms of conservation, evaluation, management, and utilization are proving to be crucial in crop improvement. Sometimes. by simple selection with desirable character combinations among existing genotypes in nature or by hybridization, the improvement desired in crop yield and quality is achieved. For a varietal development programme exhaustive information of the nature and magnitude of genetic divergence of the genotypes is the prerequisite, and has been stressed both in self and cross pollinated crops. The present need of muskmelon crop improvement industry is to assess diversity between existing landraces to identify and use them in breeding programmes. The biometrical procedures have made the quantification of genetic diversity possible to choose genetically diverse parents for a successful hybridization programme because selecting parents identified on the basis of divergence analysis would be more promising. Mahalanobis's D^2 statistic was adopted in the present study to quantitatively assess genetic divergence among twenty-six genotypes based on thirty-six characters for fruit yield and yield attributing characters. The 'V' statistic value was very significant for all the characters under study indicating that the genotypes differed significantly when taken simultaneously and it may be due to factors *viz*., heterogeneity, genetic drift, selection history and selection under diverse environments. The procedure (Tocher's method) suggested by Rao (1952) has been used for grouping. Based on D^2 values, 26 genotypes were divided into 12 very different clusters. This clustering approach suggested a high rate of heritability among genotypes. The above findings were quite similar to that of Tomar *et al.* (2008) for genetic divergence study, who evaluated 50 genotypes of muskmelon based on 12 characters and these genotypes were grouped into 7 clusters based on the relative magnitude of the D^2 values and Musmade *et al.* (2008) who evaluated 51 genotypes of muskmelon for 16 characters using Mahalanobis D^2 statistic and these genotypes were grouped into 7 clusters.

Average intra-cluster and inter-cluster distances revealed that the inter-cluster distance was more than the intra-cluster distance. Suggesting, the genotypes grouped in one cluster are less divergent than those placed in different clusters. Further, the huge intra-cluster distances marked the presence of wide genetic diversity among the genotypes of that cluster. The maximum inter-cluster distance was recorded between cluster VIII and XI followed by cluster XI and XII and cluster V and XI, indicating the presence of wide genetic diversity, among the genotypes included in these clusters. Also, the distance between two clusters is directly proportional to the wider genetic diversity. In the recombination breeding program, highly divergent genotypes would be of great use to make highly desirable recombinants. The findings of earlier workers (Tomar *et al.*, 2008; Musmade *et al.*, 2008; Reddy and Shanthi, 2013) also validate this findings in present study. In general, the maximum heterosis are expected from crosses involving parents belonging to most divergent clusters and thus, results in creation of huge variability in genetic make-up. Be that as it may, the divergent clusters need not be of attractively high or low mean values for all the growth, earliness

and fruit traits. Henceforth, aside from choosing genotypes from the clusters with high inter-cluster distance for hybridization, one can likewise consider choosing parents dependent on degree of genetic divergence regarding a specific character of interest.

The germplasm utilized for the present study consisted of ten solitary clusters (cluster II, IV, V, VI, VII, VIII, IX, X, XI, and XII) and these clusters showed zero intra-cluster distance could be attributed to restricted gene exchange or selection practices among the genotypes for different characters. The genotypes in these clusters namely RM-49, VRMM-46, GP-176, Golden Yellow, MHY-5(+), Kashi Madhu, GP-168, Kazri, Durgapur Madhu and Punjab Sunehri respectively, varies from others may serve as potential breeding parents. They demonstrate their autonomous identity and significance because of various one-of-a-kind characters possessed by them. The genotype VRM-46 with the lowest days to first female flower and minimum cavity width was found to be highly precocious and solid in terms of fruit weight. The genotype MHY-5 having highest mean for total number of primary branches per vine and highest vine length was found to be highly vigorous. The genotype Golden Yellow with the highest number of total female flowers and minimum cavity length was very prolific and high yielder. The genotype Punjab Sunehri with highest chlorophyll content, highest flesh thickness, highest fruit diameter and lowest vine length was found to have good yielding capacity and responsiveness towards reproductive yield. These unique genotypes can be used in crop improvement programmes as donor parents to improve particular traits. The results indicate that in the hybridization program, selection of the genotypes with higher cluster means for a particular character could be used to improve the particular character. The relative contribution of different characters to divergence was estimated with the help of Mahalanobis D^2 statistics and the character index seed weight, contributed the maximum to genetic divergence followed by titratable acidity and fruit diameter. Tomar *et al.* (2008), also reported the highest contribution of TSS towards diversity in fifty muskmelon genotypes. Hence, it can be concluded that these characters need more attention in crop improvement programmes of muskmelon.

Multivariate analysis considering 32 morphological and 4 biochemical traits following Mahalanobis D^2 statistic revealed that the character index seed weight contributed the maximum to genetic divergence followed by titratable acidity, fruit diameter, phenol content, width of the cavity, ascorbic acid content, number of male flowers, seeds per fruit, and pulp to seed ratio. Also, there were good diversity among 26 genotypes of muskmelon, which were grouped into twelve distinct clusters. The genotypes of diverse clusters VIII and XI, clusters XI and XII and clusters V and XI could be used in a hybridization programme either to produce highly heterotic F_1s or to generate wide range of transgressive segregants in the population to develop high-yielding varieties of muskmelon.

Acknowledgments

The authors are highly obliged to RARI, Durgapura and IIVR, Varanasi for providing the germplasm of muskmelon for the present study. Also, the authors are grateful to the Banaras Hindu University, from which they are related, for their provided facilities.

References

Eduardo, I., P. Arús, A.J. Monforte, J. Obando, J.P. Fernández-Trujillo, J.A. Martínez, A.L. Alarcón, J.M. Álvarez and E. van der Knaap, 2007. Estimating the genetic architecture of fruit quality traits in melon using a genomic library of near-isogenic lines. *Journal of the American Society for Horticultural Science*, 132(1): 80-89.

Mabaleha, M.B., Y.C. Mitei and S.O. Yeboah, 2007. A comparative study of the properties of selected melon seed oils as potential candidates for development into commercial edible vegetable oils. *Journal American Oil Chemists' Society*, 84(1): 31-36.

Mahalanobis, P.C. 1936. On the generalized distance in statistic. *Proc. Nat'l. Instt. Sci.,* (India), 2: 49-55.

Musmade, A.M., S.S. Torkadi, R.S. Patil and G.B. Asane, 2008. Genetic divergence in muskmelon (*Cucumis melo* L.). *Journal of Maharashtra Agricultural Universities*, 33(1): 133-135.

Nayar, N.M. and R. Singh, 1998. Taxonomy, distribution, ethno botanical uses in Cucurbits (N.M. Nayar, and T.A. More, eds.), *Science Publishers, Inc.,* U.S.A. p. 1-18.

Pangalo, K.J. 1929. Critical review of the main literature on the taxonomy, geography and origin of cultivated and partially wild melons. *Trudy Prikl. Bot.*, 23: 397-442.

Ranganna, S. 1976. *Analysis of Fruit and Vegetable Products*. McGraw-Hill Publishing Company Ltd., New Delhi, India.

Rao, C.R. 1952. *Advanced Statistical Methods in Biometrical Research*, John Wiley and Sons, Inc., New York. p. 236-278.

Reddy, S.A.K. and A. Shanthi, 2013. Variability and genetic diversity studies of muskmelon accession in the coastal region of Karaikal. *Green Farming*, 4(6): 764-766.

Sebastian, P., H. Schaefer, I.R. Telford and S.S. Renner, 2010. Cucumber (*Cucumis sativus*) and melon (*C. melo*) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. *Proceedings of the National Academy of Sciences*, 107(32): 14269-14273.

Singh, R.K. and B.D. Chaudhary, 1977. *Biometrical Methods in Quantitative Genetic Analysis.* Kalyani publishers, New Delhi. p. 54-68.

Tomar, R.S., G.U. Kulkarni, O.K. Kakade, A.D. Patel and R.R. Acharya, 2008. Genetic divergence in muskmelon (*Cucumis melo* L.). *Asian Journal Horticulture*, 3(1): 103-105.

Received: June, 2021; Revised: October, 2021; Accepted: October, 2021