ASSESMENT OF GENETIC DIVERSITY IN MUSKMELON (*CUCUMIS MELO* L.) GENOTYPES THROUGH D^2 STATASTICS

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ABSRACT

One hundred and twenty-four diverse genotypes of muskmelon (*Cucumis melo* L.) were used for assessment of genetic diversity in muskmelongenotypes through Mahalanobis D^2 technique in Randomized Complete Block Design with two replications during summer 2019. D^2 analysis indicated wider genetic diversity among 124 genotypes of muskmelon, which were grouped into 14 clusters. In general, intra-cluster distances were lower than inter-cluster distances, indicating that genotypes included within a cluster tended to diverse less from each other. The maximum inter-cluster distance (D = 1086.24) was found between cluster III and XIV. The minimum inter-cluster distance was observed between cluster I and II (D = 169.03). The intra-cluster distance (D) ranged from 0.0 (cluster- XIII and XIV) to 337.38 (cluster- XI). The cluster XI showed the highest mean values for most of the morphologicalparametersdesirable for yield. The most productive hybrids and diverse segregating materials may come from high yielding parents with high genetic diversity. Therefore, based upon high yielding genotypes and large inter-cluster distances, crossing of the genotypes belonging to cluster XI and V may be used in hybridization programme to produce derived transgressive segregants for traits of interest to improve muskmelon.

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Keywords: Muskmelon, genetic diversity, MahalanobisD^2statistic, Tocher's method, transgressive segregants.

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INTRODUCTION

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[4]. The fruits of muskmelon are sweet with musky flavour which is mainly grown as a dessert crop and has good export potential. This crop is very popular in developed countries where the per capita calorie consumption is high. It is grown worldwide mainly for fresh market consumption. The fruits are used for both salad and table purpose. It is gaining importance due to its short duration, high nutritive, medicinal and industrial values. It is highly relished because of its sweet and

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musky flavour. In India muskmelon is cultivated in around 54000 ha area with 1.14 MT production[1].

Though muskmelon is most nutritious, its productivity is very low as compared to other vegetable fruits in India. This certainly indicates that there is a great scope for improving the productivity by using suitable varieties and hybrids. 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.

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A new variety as per farmer's demand can be developed from an assembled diverse genetic stock of any crop. So, success of any breeding program depends much on the genetic diversity available and the judicious selection of parents. The importance of genetically diverse genotypes as a source of obtaining transgressive segregants with desirable combinations has been reported by several workers [3], [19]. The importance of genetic diversity in any crop improvement programme has been stressed both in self andcross pollinated crops[6]. Genetic resources are, in the sense, the building blocks and also fundamental not only to a crop improvement program, but also for the very survival of the species in time and space[20.] Moreover, evaluation of genetic diversity is important to know the source of genes for particular trait within the available germplasm[21]. Multivariate analysis by means of Mahalanobis' D^2 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 [12,5]. From the plant breeding point of view the degree of genetic diversity between two parents is an index for determining the hybridity over parents or nature of the segregants in the follow-up generation. D2 statistics can help in selecting desirable parents for achieving desired goal by the breeder. Though information on genetic divergence is available in most of the crops, such information in muskmelon is very rare[8]. Considering the above facts, the present investigation was undertaken to assess the genetic diversity among the collected germplasm and to identify the diverse parents for use in further genetic study.

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Material and Methods

The present study carried out at main vegetable research station, AAU, Anand,Gujarat during summer 2019. The 124 genotypes were assessed in a field experiment under a

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randomized complete block design with two replications. Tenplants maintained in each treatment with spacing of 2.0 × 1.0 m between rows and plants, respectively. The data were recorded on three randomly selected plants from each genotype for eighteen growth and yield characters. Observations recorded for days to 50% male flowering, days to 50% female flowering, primary branches per plant, fruit length, fruit girth, fruit weight, fruits per plant, fruit yield per plant, flesh thickness, total soluble solid, phenol, total soluble sugar, β-carotene, flavonoid.

Genetic divergence between genotypes was worked out using MahalanobisD^2 statistics[11]. The clustering of genotypes was done following Tocher's method as described by [14]. The average intra and inter cluster distances were calculated by the formula given by[18]. The character contribution towards genetic divergence was computed using method given by [18].

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Results and Discussion

Composition of Clusters

Grouping of the genotypes was carried-out by following the Tocher's method[14] with the assumption that the genotypes within cluster have smaller D^2-values among themselves than those from genotypes belonging to different clusters. In all, 14 clusters were formed from 124 genotypes. The composition of clusters is given in Table 1. The cluster I was the largest cluster having 41 genotypes. Cluster II was the second largest cluster with 29 genotypes. The cluster VI ranked third with 9 genotypes, while, cluster III and VII ranked fourth with 8 genotypes each. The cluster V ranked fifth with 7 genotypes, the cluster IV ranked sixth with 6 genotypes, the cluster VIII ranked seventh with 5 genotypes, cluster X ranked eighth with 3 genotype, cluster IX, XI and XII ranked ninth with 2 genotypes of each and the clusters XIII and XIV were a solitary cluster with single genotype. Therefore, genotypeGP-MM 122 and GP-MM 131 were mono-genotypic, which indicated wide diversity from the rest. Thus, this genotype had entirely different genetic make-up from the others.

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In a similar study, thirty-five diverse genotypes of muskmelon were grouped into six clusters by[12]. Thirty-three landraces of muskmelon were grouped in only three clusters by

[10,13] conducted a research using sixty-four genotypes of muskmelon and grouped them into six clusters. [15] studied twenty-five genotypes of muskmelon for genetic divergence and grouped them into six clusters. [7] studied twenty-five diverse genotypes of muskmelon were grouped into six clusters and [9] studied twenty-four diverse genotype and grouped them into eight clusters.

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The clustering pattern indicated that the genetic diversity was not fully associated with geographical diversity, hence there was no formal relationship between geographical diversity and genetic diversity. This could be because there were forces other than geographical separation such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation responsible for genetic diversity.

Inter and Intra-Cluster Distances

The inter-cluster and intra-cluster distance are shown in Table 2. The maximum inter-cluster distance was found between cluster III and XIV (D = 1086.24), followed by between XI and XIII (D = 971.74) and between III and XII (D = 940.99). The minimum inter-cluster distance was observed between cluster I and II (D = 169.03). The intra-cluster distance (D) ranged from 0.0 (cluster- XIII and XIV) to 337.38 (cluster- XI). The clusters XIII and XIV contained single genotype and therefore, intra-cluster distance was zero. Selection of parents based on large inter-cluster and intra-cluster distances for hybridization work gives a range of useful combination.

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Cluster Means of Various Characters

The mean performance of cluster values for all fourteen characters is presented in Table 3. A considerable amount of inter cluster variation was observed among the days to 50% male flowering, days to 50% female flowering, primary branches per plant, fruit length, fruit girth, fruit weight, fruits per plant, fruit yield per plant, flesh thickness, TSS, phenol, total soluble sugar, β-carotene and flavonoid.

Characters contribution towards Genetic Divergence

The analysis of variance for each character was carried out using mean of the 124 genotypes. Estimation of inter and intra cluster variances, along with ratio of inter cluster variance to the total variance (R^2) and inter cluster coefficient of variation (CV_b) for 14 characters were worked out and presented in Table 3. The maximum value of R^2 was observed for phenol content (0.95) followed by fruit yield per plant (0.94) and total soluble solid and total soluble sugar (0.91). While, the minimum value for R^2 was observed for fruits per plant (0.23).

From inter cluster coefficient of variation (CV_b), it was observed that the fruit yield per plant contributed the maximum (87.65%) towards the total divergence in yield. The next major contribution came from the total soluble sugar content (82.69%) followed by phenol (69.85%), fruit weight (45.40%), β-carotene (37.94%) and fruit length (32.65%). Apart from above mentioned traits, other characters *viz.*, flavonoid (29.01%), fruit girth (25.88%), flesh thickness (18.24%) and primary branches per plant (12.73%) contributed medium divergence towards the yield, while, days to 50% male flowering (7.89%), days to 50% female flowering (5.93%), phenol (10.79%) and fruits per plant (7.39%) contributed less divergence towards yield.

Table 1. Grouping of 124 genotypes of muskmelon in various clusters on the basis of D^2 statistics

Sr. no.	Clusters	No. of genotypes	Name of the genotypes
1.	I	41	GP-MM 36, GP-MM 90, GP-MM 28, GP-MM 101, GP-MM 15, GP-MM 85, GP-MM 23, GP-MM 129, GP-MM 110, GP-MM 123, GP-MM 135, GP-MM 34, GP-MM 46, GP-MM 20, GP-MM 100, GP-MM 60, GP-MM 64, GP-MM 130, GP-MM 53, GP-MM 82, GP-MM 39, GP-MM 124, GP-MM 91, GP-MM 114, GP-MM 72, GP-MM 77, GP-MM 88, GP-MM 128, GP-MM 106, GP-MM 134, GP-MM 133, GP-MM 57, GP-MM 132, GP-MM 79, GP-MM 87, GP-MM 54, GP-MM 107, GP-MM 40, GP-MM 94, GP-MM 42, GP-MM 31
2.	II	29	GP-MM 102, GP-MM 103, GP-MM 7, GP-MM 7, GP-MM 63, GP-MM 5, GP-MM 125, GP-MM 9, GP-MM 61, GP-MM 14, GP-MM 62, GP-MM 119, GP-MM 49, GP-MM 78, GP-MM 21, GP-MM 75, GP-MM 29, GP-MM 121, GP-MM 67, GP-MM 37, GP-MM 8, GP-MM 32, GP-MM 113, GP-MM 108, GP-MM 109, GP-MM 99, GP-MM 24, GP-MM 59, GP-MM 74, GP-MM 58
3.	III	8	GP-MM 1, GP-MM 2, GP-MM 45, GP-MM 96, GP-MM 10, GP-MM 17, GP-MM 12, GP-MM 35
4.	IV	6	GP-MM 43, GP-MM 55, GP-MM 105, GP-MM 50, GP-MM 52, GP-MM 97
5.	V	7	GP-MM 111, GP-MM 116, GP-MM 117, GP-MM 118, GP-MM 4, GP-MM 115, GP-MM 40-1
6.	VI	9	GP-MM 126, GP-MM 127, GP-MM 89, GP-MM 95, GP-MM

			104, GP-MM 92, GP-MM 80, GP-MM 51, GP-MM 86
7.	VII	8	GP-MM 30, GP-MM 81, GP-MM 38, GP-MM 93, GP-MM 83, GP-MM 84, GP-MM 112, GP-MM 56
8.	VIII	5	GP-MM 3, GP-MM 27, GP-MM 22, GP-MM 76, GP-MM 13
9.	IX	2	GP-MM 33, GP-MM 98
10.	X	3	GP-MM 65, GP-MM 120, GP-MM 11
11.	XI	2	GP-MM 44, GMM-3
12.	XII	2	GP-MM 41, GP-MM 69
13	XIII	1	GP-MM 122
14	XIV	1	GP-MM 131

Table 2. Average intra and inter cluster D value of 124 genotypes of muskmelon

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Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	**126.43**	169.03	249.61	183.78	279.25	316.64	211.82	299.75	465.02	316.93	410.69	501.02	397.20	596.86
II		**152.70**	258.93	309.98	232.10	457.74	313.46	446.59	383.32	303.57	523.34	523.57	388.30	748.52
III			**174.72**	389.00	388.17	460.76	329.88	450.78	798.71	632.46	726.36	940.99	538.84	1086.24
IV				**118.08**	480.68	301.82	239.22	189.72	595.55	381.19	276.93	452.67	589.96	427.37
V					**222.10**	547.25	410.45	630.07	423.04	359.92	670.07	591.95	368.81	818.19
VI						**213.80**	191.35	463.00	849.48	552.06	669.00	800.46	356.81	506.91
VII							**162.68**	373.67	691.12	432.42	585.14	681.38	315.23	528.01
VII								**140.09**	917.72	614.31	293.75	610.68	911.17	635.86
IX									**160.14**	189.26	672.47	329.40	516.52	611.59
X										**132.50**	469.13	184.94	327.02	304.31
XI											**337.38**	330.07	971.74	487.57
XII												**101.63**	737.29	292.83
XIII													**00**	590.26
XIV														**00**

Table 3. Cluster mean for 14 different characters in 124 genotypes of muskmelon

Clusters	1	2	3	4	5	6	7	8	9	10	11	12	13	14
I	53.9	59.2	3.1	18.5	35.8	432.6	4.9	2.05	6.28	0.09	0.71	1.703	0.034	2005
II	52.2	58.4	3.1	16.0	31.5	408.9	4.9	1.93	6.17	0.09	0.58	1.394	0.032	1288
III	47.9	53.8	3.1	15.2	30.7	527.4	4.8	2.18	7.60	0.03	0.67	1.258	0.027	1304
IV	53.0	58.2	3.1	22.3	43.3	634.5	4.8	2.28	7.26	0.10	0.67	2.074	0.029	3252
V	55.4	59.1	2.5	12.6	28.0	529.3	5.3	1.73	4.12	0.10	0.72	1.472	0.038	1072
VI	54.5	59.7	2.7	19.4	38.6	522.5	4.9	2.16	6.45	0.08	1.43	2.098	0.030	2509
VII	53.3	58.3	2.7	17.9	36.1	424.8	4.9	2.07	7.07	0.08	1.22	1.697	0.035	2275
VIII	49.8	55.8	2.8	23.7	41.9	758.4	5.3	2.41	6.87	0.06	0.52	1.330	0.039	4065
IX	56.5	61.5	3.0	15.8	30.1	432.9	4.5	1.61	6.88	0.21	0.44	1.848	0.030	884
X	51.5	57.7	3.2	17.6	34.9	439.5	4.6	1.97	6.27	0.18	0.77	1.112	0.025	1876
XI	53.8	58.0	3.5	21.6	34.7	863.5	5.8	2.29	5.20	0.12	0.33	1.805	0.028	4103
XII	49.0	54.5	3.2	20.0	39.9	601.0	5.8	2.22	5.41	0.21	0.43	1.080	0.018	3233
XIII	54.0	59.0	3.0	15.2	30.6	310.6	5.1	1.55	5.53	0.13	1.61	1.410	0.015	355
XIV	47.5	55.5	2.8	21.7	40.7	784.2	4.8	2.43	6.00	0.20	1.27	2.105	0.022	3820
Mean	52.18	57.76	2.99	18.39	35.49	547.86	5.03	2.06	6.22	0.12	0.81	1.60	0.029	2288.64
S.Em.	2.65	2.10	0.35	1.63	2.94	78.14	0.40	0.18	0.13	0.01	0.13	0.28	0.01	298.66
CD @ 5%	7.38	5.85	0.97	4.54	8.18	217.69	1.10	0.50	0.35	0.03	0.35	0.77	0.02	831.97
R^2*	0.45	0.48	0.29	0.82	0.77	0.78	0.23	0.60	0.91	0.95	0.91	0.62	0.36	0.94
CV_b %	7.89	5.93	12.73	32.65	25.88	45.40	7.39	18.24	10.79	69.85	82.69	37.94	29.01	87.65

*** R^2: Ratio of the inter cluster variance to the total variance**
$CV_{b\%}$: Inter cluster coefficient of variation

1. Days to 50% male flowering
2. Days to 50% female flowering
3. Primary branches per plant
4. Fruit length
5. Fruit girth
6. Fruit weight
7. fruitsper plant
8. Flesh thickness
9. TSS
10. Phenol
11. Total soluble sugar
12. β-carotene
13. flavonoid
14. Fruit yield per plant

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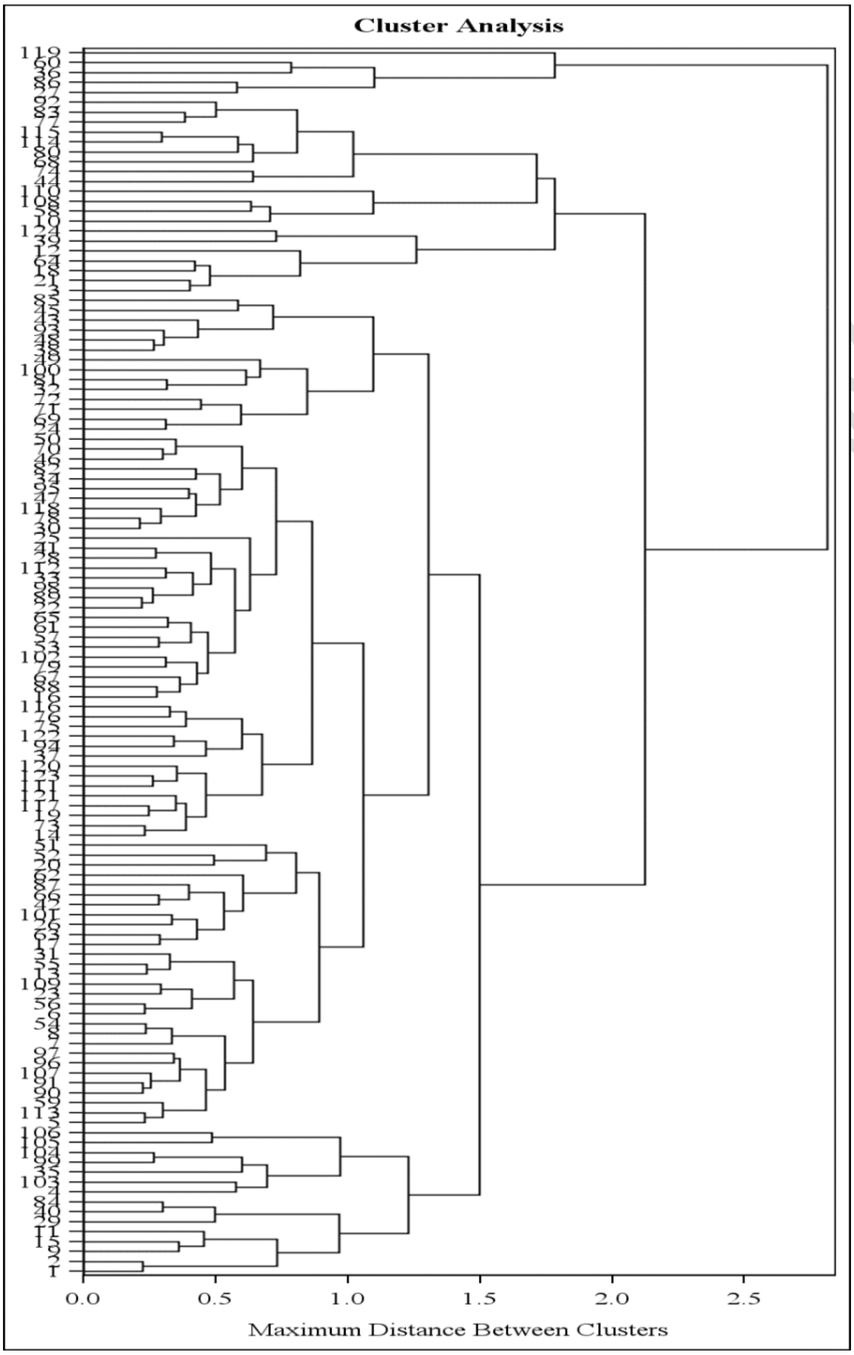

Fig.1 Cluster diagram of 124 muskmelon genotype developed through Tocher'smethod using D^2 statistics.

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Table 4. Contribution of various traits towards total genetic divergence

Sr. No	Characters	Time ranked first	Contribution (%)
1.	Days to 50% male flowering	3	0.04
2.	Days to 50% female flowering	1	0.01
3.	Primary branches per plant	684	8.97
4.	Fruit length	121	1.59
5.	Fruit girth	65	0.85
6.	Fruit weight	102	1.34
7.	Fruits per plant	152	1.99
8.	Flesh thickness	36	0.47
9.	Total soluble solid	352	4.62
10.	Phenol	1684	22.08
11.	Total soluble sugar	1623	21.28
12.	β – carotene	715	9.38
13.	Flavonoid	168	2.20
14	Fruit yield per plant	1920	25.18

Contribution percentage of various traits towards total genetic divergence presented in Table 4which showed that fruit yield per plant contributed the maximum percentage (25.18%) with 1920 time ranked first towards total genetic divergence followed by phenol (22.08%) and total soluble sugar (21.28%). While, other characters like days to 50% female flowering (0.01%), days to 50% male flowering (0.04%), flesh thickness (0.47%) and fruit girth (0.85%) contributed the minimum towards total genetic divergence.

In general, intra-cluster distances were lower than the inter-cluster distances. Thus, the genotypes included within a cluster tended to diverse less from each other. The intra-

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cluster distance (D) ranged from 0.0 (cluster-XIII and XIV) to 337.38 (cluster- XI). High intra-cluster distance indicated about the wider genetic diversity among the genotypes which could be used in yield improvement of muskmelon. The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants.

These findings are in consonance with those results reported by [16], [13], [15], [7], [9] and [17].

The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used either for direct adoption or for hybridization, followed by selection.

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It has been well established fact that more the genetically diverse parents used in hybridization programme, the greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations [2]. It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. Therefore, based upon high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes belonging to cluster XI and V may be used in hybridization programme to produce derived transgressive segregants for traits of interest to improve muskmelon.

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