

Studies on Genetic Diversity in Muskmelon (*Cucumis Melol.*) Under Tropical Condition of Tamil Nadu, India

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ABSTRACT

Muskmelon (*Cucumis melo* L.) is one of the most well-known dessert vegetables, belong to the Cucurbitaceae family. At Puthur village, Thalaivasal taluk, Salem district, from February to May 2022, a group of 33 germplasm lines were tested using a Randomised Block Design with three replications. The findings indicate that the clustering of genotypes revealed that Cluster I comprises highest number of genotypes (19) followed by cluster III comprising of 6 genotypes. Cluster IV had the greatest intra-cluster distance, which was followed by clusters II, III, I and V. The genotypes found in clusters IV and III had satisfactory values for the intercluster distance and the cluster mean. As a result, that genotype belongs to cluster IV, and cluster III may be utilised as parents in a hybridization programme to produce hybrids that are ideal for tropical climates.

Key words: Cluster, Genetic Divergence, Muskmelon

Introduction

Muskmelon (*Cucumis melo* L.) is one of the most popular dessert vegetable crops grown worldwide. It is also referred to as wholesome food or kharbooz. It is a member of the Cucurbitaceae family and is believed to have originated in tropical Africa. Its chromosome number is $2n=2X=24$. Because and romonoecious sex occurs, muskmelon is frequently cross-pollinated. In botanical terminology, the fruit is referred to as pepo. One of the most treasured summer fruits is the muskmelon. It is known as the most widely consumed vegetable because of its musky smell, sweet flavour, and cooling effect. It has plenty of dietary fibre, vitamins, and minerals. Muskmelons contain 94% water, 5% carbohydrates,

1% protein, 3420 IU of vitamin A, and 33 mg of vitamin C (Premnath and Swamy, 2016). According to Nandpuri (1989), muskmelon production takes up 80% of the entire area used for cucurbitaceous crops in riverbeds. 1.3 million tonnes of muskmelons are produced annually on 59,000 hectares of land in our country (Depart. Agri. Co & Farmers Welfare, 2019-2020). Prior to starting any breeding programme, gathering data on the kind of nature and degree of genetic divergence before starting any breeding programme will aid in selecting compatible parents for hybridization. The D^2 statistics that Mahalanobis introduced in 1936 have proven to be effective tools for estimating genetic diversity. Hence, the goal of the current study is to determine the degree of divergence at the genetic level among 33 genotypes.

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Materials and Methods

The current investigation utilised 33 different muskmelon genotypes. The plants were grown in three replications with spacing of 3 m x 60 cm over the months of February through May 2022 using a Randomised Block Design (RBD) at Puthur village, Thalaivasal taluk, Salem district. A successful crop was raised by adhering to advised cultural customs. Five plants were randomly selected from each entry in each replication to record observations on days to first female flower opening, first female flowering node, number of vines per plant, vine length (cm), sex ratio, days to first fruit harvest, average fruit weight per plant (g), fruit length (cm), fruit girth (cm), number of fruits per plant, rind thickness (cm), flesh thickness (cm), seed cavity length (cm), seed cavity width (cm), total soluble solids (%), titerable acidity (%), ascorbic acid content (mg/100g), seed yield per fruit (g), 100 seed weight (g), seed yield index and fruit yield per plant (kg). On a mean basis across the genotypes, statistical analysis was conducted. Genetic diversity was analyzed by evaluating Mahalanobis D2 statistics (Mahalanobis 1936). Grouping of genotypes into various clusters was done by Tocher's method (Rao 1952). The average inters and intra cluster distances and character contribution towards genetic divergence were calcu-

lated using formula given by Singh and Caudhary (1977).

Results and Discussion

Based on the result of divergence, the thirty three muskmelon genotypes were grouped into five clusters (Table 1). Cluster I had highest number of genotypes which had 19 genotypes followed by cluster III comprising of 6 genotypes, cluster II with 5 genotypes, cluster IV had 2 genotypes and cluster V had 1 genotype. Therefore, genotypes that originated in the same location can have had different architectural development. Likewise, genotypes at different places may possess similar characteristics. Thus, a number of variables, including geographic diversity, led to genetic diversity. Consequently, the choice of genotypes for hybridization programme is solely based on genetic diversity. Similar trends of observations were reported by Reetu *et al.* (2012) and Vijayalatha (2022) in muskmelon.

The intra cluster distance (Table 2) varied from 0.00 to 261.79. The cluster IV had highest intra cluster distance of 261.79, indicates the genotypes included in the cluster were extremely diverse, followed by cluster II (259.05), cluster III (254.20). The minimum intra cluster distance was recorded in cluster I (228.43). The cluster V had a single geno-

Table 1. Cluster composition of thirty-three genotypes of muskmelon

Cluster	Number of genotypes	Name of the Genotypes
I	19	CM 1, CM24, CM27, CM3, CM7, CM33, CM29, CM4, CM14, CM18, CM17, CM8, CM13, CM19, CM11, CM23, CM5, CM32, CM10
II	5	CM12, CM28, CM31, CM22, CM2
III	6	CM15, CM25, CM30, CM9, CM21, CM20
IV	2	CM6, CM16
V	1	CM26

Table 2. Intra and inter cluster distance between thirty-three genotypes of muskmelon

Cluster	I	II	III	IV	V
I	52179.04 (228.43)	151558.33 (389.31)	137927.70 (371.39)	125685.24 (354.52)	156383.64 (395.45)
II		67105.38 (259.05)	252358.00 (502.35)	213121.97 (461.65)	441748.60 (664.64)
III			64615.47 (254.20)	371512.56 (609.52)	255554.01 (505.52)
IV				68532.40 (261.79)	204248.89 (451.94)
V					(0.00)

type, therefore the intra cluster distance was absent. The inter cluster distance ranged between 354.52 to 664.64. the maximum inter cluster difference was noticed in between cluster II and V (664.64) followed by cluster III and IV (609.52), cluster III and V (505.52) and cluster II and III (502.35). It reveals the genotypes present in this cluster had greatest diversity. The minimum inter cluster distance was reported in between cluster I and IV (354.52). It indicates the presence of close relationship between the genotypes in these clusters. In turn, recombination between these genotypes may have resulted in superior hybrids with desired traits. Wider genetic diversity among the genotypes is shown by the fact that overall inter cluster distance was larger than the intra cluster distance. These results concur with Reddy *et al.* (2013) and Rahman *et al.* (2016) in muskmelon.

The cluster means values play a crucial role in choosing the parents for recombination breeding. Cluster IV showed high cluster mean values (Table 3) for 9 characters viz, number of vines per plant (4.25), average fruit weight (1.46 kg), fruit length (11.75 cm), fruit girth (14.25 cm), rind thickness (0.70 cm), flesh thickness (3.10 cm), TSS (9.66 °Brix), ascorbic acid content (20.33 mg/100g) and fruit yield per

plant (4.30 kg) and low cluster mean values for 5 characters viz., days to first female flower opening (45.65 days), first female flowering node (5.80), sex ratio (13.03), days to first fruit harvest (84.10 days) and titrable acidity (0.19 %) respectively. Similarly, cluster V showed maximum cluster mean for seed yield per fruit (6.99 g) and seed yield index (11.81) and minimum cluster mean values for seed cavity length (6.0 cm) and seed cavity width (6.70 cm). The cluster II reported maximum mean values for vine length (2.79 m) and 100 seed weight (3.17 g), cluster III exhibited highest cluster mean for number of fruits per plant (2.63). These findings are agreement with Senthilvadivu *et al.* (2018) and Priyanka *et al.* (2021) in muskmelon.

The percentage contribution of each character towards diversity was estimated based on ranking system was presented in Table 3. Seed cavity length (37.31%) and 100 seed weight (37.31%) contributed maximum towards genetic diversity followed by fruit yield per plant (5.30%), Seed cavity width (2.46%), vitamin-C (2.46%), days to first fruit harvest (1.89%), flesh thickness (1.89%), seed yield per fruit (1.71%), total soluble solids (1.52%), seed yield index (1.52%), average fruit weight (1.33%) and fruit girth

Table 3. Cluster mean values and Percentage contribution of each character towards diversity of muskmelon genotypes

S. No.	Characters	Cluster					Number of first rank	Percentage of contribution
		I	II	III	IV	V		
1	Days to first female flower opening	50.17	46.90	49.35	45.65	47.60	0	0
2	First female flowering node	7.75	7.14	9.35	5.80	10.60	5	0.95
3	Number of vines per plant	3.87	3.90	3.59	4.25	3.00	3	0.57
4	Vine length (m)	2.65	2.79	2.20	2.47	2.10	3	0.57
5	Sex ratio	18.66	18.34	18.47	13.03	17.71	5	0.95
6	Days to first fruit harvest	89.35	84.82	88.45	84.10	88.30	10	1.89
7	Average fruit weight per plant (kg)	1.09	1.27	0.95	1.46	0.59	7	1.33
8	Fruit length (cm)	9.92	10.98	9.83	11.75	10.20	1	0.19
9	Fruit girth (cm)	12.22	12.72	11.90	14.25	12.10	6	1.14
10	Number of fruits per plant	2.42	2.32	2.63	2.50	2.20	2	0.38
11	Rind thickness (cm)	0.54	0.56	0.42	0.70	0.50	3	0.57
12	Flesh thickness (cm)	2.28	2.40	2.15	3.10	2.60	10	1.89
13	Seed cavity length (cm)	7.30	6.90	6.62	7.85	6.00	197	37.31
14	Seed cavity width (cm)	7.89	7.90	7.57	7.75	6.70	13	2.46
15	Total soluble solids (%)	7.34	6.53	6.53	9.66	4.21	8	1.52
16	Titrable acidity (%)	0.20	0.22	0.23	0.19	0.28	0	0
17	Ascorbic acid content (mg/100g)	16.34	14.64	16.44	20.33	9.07	13	2.46
18	Seed yield per fruit (g)	5.52	6.53	5.24	4.76	6.99	9	1.71
19	100 seed weight (g)	2.49	3.17	2.63	2.32	2.22	197	37.31
20	Seed yield index	5.27	5.82	5.82	3.81	11.81	8	1.52
21	Fruit yield per plant (kg)	2.73	3.15	2.57	4.30	1.24	28	5.30
	Total						528	100

(1.14%). The remaining characters values were meager. Thus, during the hybridization programme, these traits should be given greater consideration. The above outcomes have consent of the findings of Tomar *et al.* (2008) and Harsh *et al.* (2022) in muskmelon.

Conclusion

Mahalanobis D2 statistics showed that 33 different muskmelon genotypes could be divided into five clusters. The genotypes from clusters IV and III displayed favourable intra and intercluster distances as well as cluster mean values for earliness, yield, and quality attributes. In order to develop elite hybrids under tropical conditions, the genotypes chosen from these clusters IV and III may be employed as ideal parents in a hybridization programme.

Conflict of interest: None

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