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RESEARCH ARTICLE

GENETIC DIVERSITY ANALYSIS IN TOMATO (*SOLANUM LYCOPERSICUM L.*) UNDER PROTECTED CULTIVATION

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ABSTRACT

In this study, the genetic diversity of 20 tomato genotypes was assessed under protected cultivation, focusing on 22 different characteristics. Through the application of D^2 statistics, the genotypes were classified into seven distinct clusters. Cluster II consisted of the highest number of genotypes (six), followed by cluster III (four), cluster IV (three), cluster V (three), cluster I (two), cluster VI (one), and cluster VII (one). Cluster II exhibited the greatest intra-cluster distance, indicating a higher level of variation within the genotypes of this cluster. The inter-cluster distance between cluster I and cluster VI were the most significant. Among the clusters, cluster VI demonstrated the highest average values for several characteristics including fruit yield (1172.8 g), total number of fruits per plant (74.1), number of fruits per plant (5.2), number of clusters per plant (16.1), TSS (7.8 ^{0}Brix), plant height (181.3 cm), and primary branches (3.5).

INTRODUCTION

Tomato (*Solanum lycopersicum L.*) is a self-pollinated crop belonging to the Solanaceae family, with a chromosome number of 2n=2x=24. It is native to Central and South America and is recognized as a nutritious crop due to its content of vitamins A and C, minerals, sugars, organic acids, and lycopene (Rana *et al*., 2014). Protected cultivation offers several advantages to producers, including early harvesting, improved quality, higher productivity, and the production of pesticide residue-free crops, resulting in increased profits for growers (Singh and Kumar, 2017) and it plays a crucial role in modifying the natural environment to create optimal conditions for plant growth and development. This method provides a controlled and favorable environment that maximizes the yield potential and ensures the production of high-quality crops (Sinha *et al*. 2022). The genetic diversity of the initial plant material plays a critical role in determining the potential for crop improvement. Mahalanobis D^2 statistics is one of the current methods used to assess genetic diversity. The revised generalized D^2 statistic, introduced by Mahalanobis (1936), is a robust technique for identifying distinct groups within a given plant material. Additionally, grouping the accessions using Tocher's method can be particularly valuable when selecting appropriate parents for heterosis breeding, as it aids in identifying suitable combinations for hybridization (Lekshmi andCeline 2016, Prashanth *et al*. 2008).

Based on these considerations, the current study was conducted to investigate the genetic diversity analysis in tomato germplasm under the protected cultivation using D^2 statistics and various clustering procedures, based on yield and yield attributing characters.

MATERIALS AND METHODS

The study was conducted in a polyhouse located at the North Instructional Farm of Karunya Institute of Technology, Coimbatore. Twenty tomato genotypes from various regions were collected and utilized in the research. To initiate the experiment, the seeds were planted in polybags measuring 40*40 cm. The potting mixture consisted of equal parts of soil, sand, and cow dung in a 1:1:1 ratio. The crops were cultivated using a Completely Randomized Design (CRD), with each of the twenty genotypes replicated three times. To assess the genetic diversity in yield and related characteristics among the 20 genotypes, Mahalanobis D^2 statistics were employed. Various traits such as plant height, number of primary branches, number of secondary branches, fruit length, fruit width, Fruit Shape Index (FSI), number of locules, pericarp thickness, days to 50% flowering, days to first flowering, days to first harvest, days to maturity, number of seeds per fruit, 100-seed weight, fruit weight, number of clusters per plant, number of fruits per cluster, the total number of fruits per plant, ascorbic acid content, lycopene content, total soluble solids, and fruit yield were recorded.

Based on the methodology proposed by Rao in 1952, the genotypes were grouped to determine their genetic dissimilarity or similarity to the studied traits related to yield. Total soluble solids (TSS) were measured using a hand refracto meter following the guidelines outlined by AOAC (Association of Official Agricultural Chemists) in 1975. This method provides information about the sugar content present in the sample. The ascorbic acid content was determined using the procedure developed by Sadasivam, S. in 1996. This method allows for the quantification of ascorbic acid, which is an essential component of vitamin C and is crucial for evaluating the nutritional quality of the sample. Lycopene content was assessed using the method established by Alda in 2009. This procedure enables the measurement of lycopene, a pigment responsible for the red color observed in numerous fruits and vegetables. Lycopene is well-known for its antioxidant properties and is commonly associated with the health benefits associated with consuming tomatoes and tomato-based products.

RESULTS AND DISCUSSION

The method proposed by Rao (1952) was employed to evaluate the genetic divergence by utilizing Mahalanobis D^2 statistics. According to the D^2 analysis, a total of twenty genotypes were divided into seven clusters (Table 2).

Table 1 List of the genotypes

Sl .NO	Name of the genotypes	Source
1	Kashi Amman	IIVR, Uttar Pradesh
2	Thenganikotai	Thenganikottai, Karnataka
3	Thingalur – 2	Thanjavur, Tamilnadu
4	Thingalur – 1	Thanjavur, Tamilnadu
5	Kashi	Udupi, Karnataka
6	Thirupur -1	Kangeyam, Tamilnadu
7	Muthur local	Coimbatore, Tamilnadu
8	Thirupur - 2	Dharmapuri, Tamilnadu
9	Kashi Adarsh	IIVR, Uttar Pradesh
10	Kumkuma kesari	Mysore, Karnataka
11	Junnar	Pune, Maharashtra
12	CTRm - 2	Kozhikode, Kerala
13	CTY	Mysore, Karnataka
14	CTR m	Kozhikode, Kerala
15	Vetiyarpalayam	Krishnarayapurum, Tamilnadu
16	FRPT	Mysore, Karnataka
17	Balaramapuram - 1	Balaramapuram, Trivandrum
18	Sujitha Kashi	Madurai, Tamilnadu
19	PKM 1	TNAU
20	Pusa Rubi	Ricca seeds and garden, Pune

Table 2. Clustering pattern of 20 genotypes of tomato using Mahalanolobis D^2 statistics

Clusters	No. of Genotypes	Name of the Genotypes
I	2	Kashi Amman, Thenganikotai
II	6	Thingalur -2, Thirupur -1, Thirupur - 2, Junnar, Balaramapuram -1, Sujitha Kashi
III	4	Thingalur -1, Kashi, Kashi Adarsh, PKM -1
IV	3	Muthur local, CTY, Vetiyarpalayam
V	3	Kumkuma Kesari, CTRm, Pusa Rubi
VI	1	CTRm -2
VII	1	FRPT

The largest cluster was cluster II, which contained six genotypes, followed by cluster III with four genotypes. Clusters IV and V consisted of three genotypes each, while cluster I had two genotypes. Cluster VI and VII each consisted of only one genotype. The inter and intra-cluster D^2 values are given in Table 3. Among the seven clusters, cluster II with six genotypes showed the maximum intra-cluster distance (29.46) followed by cluster III (28.98), cluster I (25.29), cluster IV (24.42), cluster V (24.17), cluster VI and VII (0.00). Based on the distance between clusters, i.e., inter-cluster distances, the maximum divergence was observed between cluster I and cluster VI (35.94) followed by cluster I and cluster II (35.50), cluster VI and cluster VII (34.83), cluster I and IV (34.35), cluster III and cluster VI (34.35), cluster IV and cluster VII (34.30), cluster II and IV (34.07), cluster II and cluster III (33.92), cluster IV and cluster VI (33.90), cluster II and cluster V (33.80), cluster I and cluster VII (31.83), cluster II and cluster VI(33.73), cluster IV and cluster V (33.29), cluster I and cluster III (33.18), cluster II and cluster VII (33.12), cluster III and cluster V (33.11), cluster III and cluster IV (32.62), cluster I and cluster V (32.71), cluster V and VII (32.44) and cluster V and cluster VI (32.20). The smallest distance was found between cluster I and cluster VII (31.83). Similar to the findings of Ganapathi and Aksha (2020), Debnath *et al*. (2020), and Prajapati *et al*. (2015), it was reported that the highest inter-cluster D^2 values could be employed to obtain superior recombinants or transgressive segregants.

Table 3. Average inter and intra cluster D^2 values among seven clusters

	I	II	III	IV	V	VI	VII
I	25.29	35.50	33.18	34.35	32.71	35.94	31.83
II		29.46	33.92	34.07	33.80	33.73	33.12
III			28.98	32.62	33.11	34.35	31.95
IV				24.42	33.29	33.90	34.30
V					24.17	32.20	32.44
VI						0.00	34.83
VII							0.00

Note: Bold figures indicate intra cluster distance

This was because these genotypes represented a highly diverse group, as indicated by their D^2 values. The scatter diagram (Fig 1) visually depicted the same relationships among the genotypes as mentioned above.

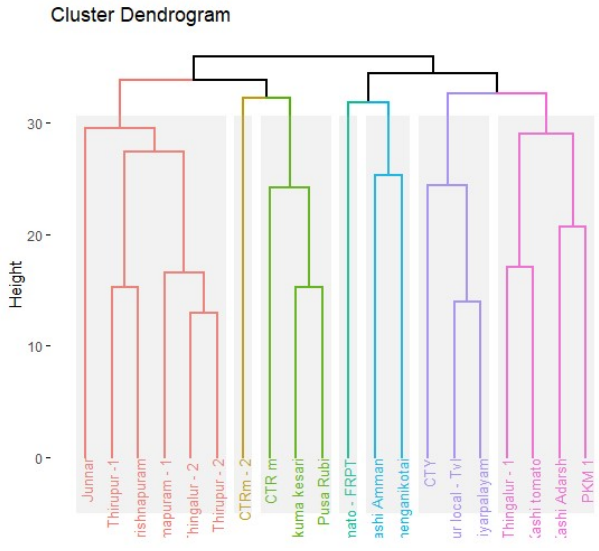

Fig 1. Cluster dendrogram

Table 4. Cluster mean values

	I	II	III	IV	V	VI	VII
PH	105.2	95.0	94.2	91.6	107.0	181.3	121.7
PB	3.1	3.2	3.3	3.3	3.1	3.5	3.4
SB	5.0	6.5	7.0	7.7	7.6	6.7	8.3
FL	37.7	30.7	28.4	29.5	31.4	29.2	28.6
FW	35.4	38.2	37.4	38.3	31.4	28.0	23.1
FSI	1.1	0.8	0.8	0.8	1.0	1.1	1.2
NL	3.0	4.4	4.2	4.6	2.9	2.6	2.4
PT	5.5	4.0	4.1	5.2	4.3	3.2	3.0
DFF	49.9	43.7	48.1	43.6	42.4	42.5	50.2
DTFF	33.8	33.3	35.8	32.6	32.6	32.1	39.5
FH	68.9	69.7	64.6	64.4	70.6	73.0	74.8
DM	33.4	29.6	27.1	32.6	26.6	26.0	30.5
SPF	104.8	145.6	127.7	166.3	92.7	88.7	105.3
SW	3.4	4.0	3.8	4.4	3.3	2.7	3.0
WF	19.9	32.1	29.6	27.3	23.7	13.9	7.9
NC	5.1	6.5	7.2	6.9	7.3	16.1	9.9
NFC	4.9	3.6	3.8	3.4	5.2	5.2	4.6
TNF	28.3	50.4	47.7	44.8	51.1	74.1	63.1
AA	14.3	15.5	12.3	15.7	17.6	13.4	11.3
LC	3.3	1.7	2.6	2.4	2.3	0.1	2.1
TSS	5.2	5.4	5.4	5.2	5.3	7.8	5.5
FY	602.6	871.1	914.3	792.3	882.9	1172.8	500.7

PH – Plant height, PB – Primary branches, SB – Secondary branches, FL – Fruit length, FW – Fruit width, FSI – Fruit shape index, NL – No. of locules, PT – Pericarp thickness, DFF – Days to 50% flowering, DTFF – Days to first flowering, FH – First harvest, DM – Days to maturity, SPF – Seeds per fruit, SW – Seed weight, WF – Fruit weight, NC – Number of clusters, NFC – Number of fruit per cluster, TNF – Total no. of fruits, AA – Ascorbic acid, LC – Lycopene content, TSS – Total soluble solids, FY – Fruit Yield

The cluster means (Table 4) indicated considerable differences in all the characteristics studied. Cluster I exhibited the highest values for fruit length (37.7), pericarp thickness (5.5), days to maturity (33.4), and lycopene content (3.3). Conversely, it had the lowest values for primary branches (3.1), secondary branches (5.0), number of clusters per plant (5.1), total number of fruits per plant (28.3), and TSS (5.2). Cluster II displayed the highest value for fruit weight (32.1) and the lowest value for Fruit Shape Index (FSI) (0.8). Cluster III did not demonstrate the highest value for any of the traits analyzed; instead, it had the lowest values for Cluster IV exhibited the highest values for fruit width (38.3), number of locules (4.6), seeds per fruit (166.3), and hundred seed weight (4.4). Conversely, it had the lowest values for plant height (91.6), FSI (0.8), first harvest (64.4), number of fruits per cluster (3.4), and TSS (5.2). Cluster V displayed the highest values for ascorbic acid (17.6) and number of fruits per cluster (5.2), while it had the lowest values for primary branches (3.1), days to 50% flowering (42.4), and days to maturity (26.6). Cluster VI showcased the maximum values for plant height (181.3), primary branches (3.5), TSS (7.8), number of clusters per plant (16.1), number of fruits per cluster (5.2), total number of fruits per plant (74.1), and fruit yield (1172.8). On the other hand, it demonstrated the minimum values for lycopene content (0.1), seed weight (2.7), seeds per fruit (88.7), days to maturity (26), and days to first flowering (32.1). Cluster VII exhibited the highest values for secondary branches (8.3), FSI (1.2), days to 50% flowering (50.2), days to first flowering (39.5), and first harvest (74.8). Conversely, it had the lowest values for ascorbic acid (11.3), fruit width (23.1), number of locules (2.4), pericarp thickness (3.0), fruit weight (7.9), and fruit yield (500.7).Similar findings to our study have been reported by Sinha *et al*. (2022), Pedapati *et al*. (2014), Ganapathi and Akshay (2020), Naveen *et al*. (2018), Narayan *et al*. (2018), Parthasarathy and Aswath (2002), and Sekhar *et al*. (2008).

CONCLUSION

The genotypes exhibited genetic diversity and were categorized into seven clusters. Cluster VI demonstrated superior performance in terms of fruit yield per plant. Cluster II had the highest intra-cluster distance, indicating greater variation within the genotypes of this cluster. The inter-cluster distance between cluster I and cluster VI were the highest, suggesting significant genetic diversity between these clusters. This information is valuable for selecting parents with the aim of obtaining more diverse offspring in subsequent generations, which can contribute to further improvements in tomato cultivation under protected conditions.

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