Plant Archives Vol. 25, No. 1, 2025 pp. 1257-1261 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.1.186

GENETIC DIVERGENCE FOR YIELD AND YIELD ATTRIBUTES IN TOMATO (*SOLANUM LYCOPERSICUM* L.)

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(Date of Receiving-20-11-2024; Date of Acceptance-16-01-2025)

ABSTRACT

The present experiment, entitled Lucknow Condition of Uttar Pradesh, was carried out at the Horticulture Research Farm of the Department of Horticulture, Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh, during the rabi season of the year 2021-2022. The experimental materials comprised of Twenty genotypes of tomato collected from different sources. The research aimed to assess genetic variability based on nineteen characters contributing to yield and quality traits. Using Mahalanobis D^2 statistics and Tocher's clustering method, the genotypes were grouped into eighteen clusters. Key findings highlighted significant genetic diversity among genotypes, with some clusters displaying high intra-cluster distances and others wide inter-cluster diversity. Clusters II, IV, and V emerged as promising sources for traits such as plant height, fruit yield and number of fruits per plant. Hybridization between genetically distant clusters was suggested for enhanced breeding outcomes, emphasizing the role of divergent parental selection in heterosis breeding and we can used for crop improvement programme.

***Key word*:** Genetic divergence, Heritability, Tomato, Intra-cluster distances, Fruit yield.

Introduction

Tomato (*Solanum lycopersicum* L.) belongs to the family solanaceae and is native of Peru and Equador region (Rick 1969). Tomato is a typical day neutral plant that is primarily self-pollinated, but some cross pollination occurs. It is a warm-season crop that is somewhat resistant to heat and drought and can thrive in a variety of soil and climatic conditions. Globally, tomatoes are one of the most significant solanaceous vegetable crops. It is a very adaptable vegetable in terms of cooking. Ripe fresh tomato fruit is used to make a variety of processed foods, including puree, paste, powder, ketchup, sauce, soup, and canned whole fruits. It is also eaten raw in salads and cooked. Unripe green fruits are used to make chutney and pickles. Tomatoes are valued for their color and flavour and are a significant source of beta carotene, ascorbic acid and the antioxidant lycopene. Yield is a complicated character that is influenced by several contributing factors and how they interact. The relative strength of each character's link with yield should be taken into account for any successful selection procedure. In tomatoes, commercial F_1 hybrids are prevalent and the process of choosing new parents for greater heterosis is ongoing. Generally diverse plants are expected to give high hybrid vigour (Harrington 1940). Therefore, in order to identify parents for a subsequent breeding work, it is necessary to investigate genetic divergence among the germplasm collection. When organizing the breeding

program, the information on genetic divergence of different traits especially those that contribute to yield and quality would be most helpful. Mahalanobis (1936) discovered D^2 statistics, which give a measure of the degree of divergence between two genotypes being compared. It will be helpful to group genotypes according to D^2 analysis in order to select appropriate parental lines for heterosis breeding.

Such investigations are also useful in selecting parents for hybridization in order to retrieve superior transgressive segregants. Better open pollinated cultivars for commercial agriculture might also be released as a result of this procedure. Taking into consideration the above-mentioned facts, the study was developed to assess the level of genetic variability in the available germplasm based on fifteen characteristics, including both qualitative and quantitative properties.

Materials and Methods

Experimental Details

The present experiment, entitled Lucknow Condition of Uttar Pradesh, was carried out at the Horticulture Research Farm of the Department of Horticulture, Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh, during the rabi season of the year 2021-2022. The experimental materials comprised of Twenty genotypes of tomato collected from different sources. The experiment was laid out in a Randomized Block Design with three replications accommodating 16 plants in each genotype. Seeds were transplanted at a spacing of 60 × 60cm. Every suggested cultural practice was followed in order to successfully raise the crop. The following 19 characters were observed on five randomly chosen plants per replication for each genotype: plant height at 30, 60, and 90 days after transplanting (cm), days to first flowering (days), days to 50% flowering, days to maturity (days), number of flowers/cluster, number of clusters/plant, number of locules/fruit, pericarp thickness (mm), number of fruits/truss, number of fruits/plant, average single fruit weight (g), yield/plant (kg), fruit length (cm), fruit diameter (cm), total soluble solids (°Brix), and acidity (%).

Analysis of Genetic Divergence

The means for each trait were computed over three replications, and an analysis of variance was conducted. The Mahalanobis D^2 statistic (Mahalanobis 1936) was used for multivariate analysis, and Tocher's approach was used to arrange the genotypes into various clusters. In order to determine the true divergence inside and between the clusters, the inter and intra-cluster distances were calculated using the methodology proposed by Murty and Arunachalam (1967). Mahalanobis's D^2 statistics (1936) were used to evaluate the genetic divergence between genotypes. The distance D from the sample was calculated using the formula.

$$D^2p = d1\ S\text{-}1d$$

where,

D^2 p, Square of distance considering 'p' variables

d = Vector observed differences of the mean values of all the characters (xi_1- xi_2);

S-1, inverse of variance and covariance matrix.

Tocher's approach was used to cluster all of the genotypes into separate groups. The intra and inter-distances were also calculated. The criterion used to determine clustering to the same cluster should, on average, produce lower D^2 values than those from other clusters. Tocher's (Rao 1952) device began with two closely related populations and then found a third population with the smallest average D^2 of the first two. Similarly, the fourth was picked to have the lower average D^2 value among the first three, and so on. The acceptable rise in D^2 value displayed by a population relative to the next population. If the average D^2 value increased above the average of previously included genotypes due to the addition of new genotypes, that genotype was eliminated. The genotypes previously included in that group were termed the first cluster. This technique was repeated until the D^2 values of the remaining genotypes were exhausted, excluding those previously included in the former cluster and grouping them into new clusters. D^2 data were used

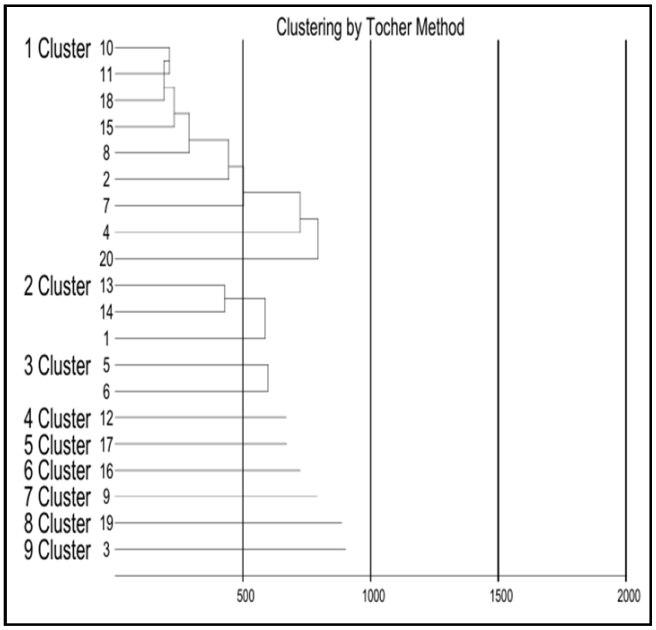

Fig. 1: Dendrogram showing clustering pattern for divergence of tomato genotypes.

Table 1: Cluster classification of 20 genotypes of tomato.

Cluster	No. of genotypes Genotypes	Genotypes
I	9	Kashi Sarad, Kashi Vishesh, Pusa Divya, Punjab Chhuhara, Pusa Gaurav, Kashi Amul, Pusa Rubey, Kashi Adarsh, Himsona
II	3	Pusa Sheetal, Pusa Sadabahar, Kashi Amrit
III	2	Kashi Anupum, Kashi Sarad
IV	1	Pusa Rohini
V	1	Kashi Hemant
VI	1	Many Makar
VII	1	Pusa Upkar
VIII	1	EC-538407
IX	1	Kashi Aman

to compute average intra and inter cluster distances using the Euclidean method.

Results and Discussion

Clustering of genotypes under study is presented in Fig. 1. Based on D^2 values, the 20 genotypes were grouped into nine highly divergent clusters (Table 1). Some of genotypes were so divergent in all the characters; hence each single genotype formed a separate cluster. Thus, six clusters *viz*. IV (Pusa Rashmi), V (Kashi Hemant), VI (Many Maker), VII (Pusa Upkar), VIII (EC-538407) and IX (Kashi Aman) were solitary with one genotype in each cluster.

The remaining two clusters were having maximum number of genotypes. Cluster I was biggest with 9 genotypes viz. (Kashi Sarad, Kashi Vishesh, Pusa Divya, Punjab Chhuhara, Pusa Gaurav, Kashi Amul, Pusa Rubey, Kashi Adarsh and Himsona followed by cluster II with 3 genotypes *viz*. (Pusa Sheetal, Pusa Sadabahar, Kashi Amrit. There was no correlation between genetic divergence and genotype regional distribution in the clustering pattern. Therefore, in the material under investigation, genetic diversity could not be linked to geographical variety. This was consistent with the findings of Reddy *et al*., (2013) and Mahesha *et al*., (2006). According to Meena *et al*., (2015), breeding progenies typically include genes from several sources, which causes them to lose the genotype's fundamental geographic identity.

The intra-cluster distances indicate the divergence among the genotypes within the clusters and inter-cluster indicates diversity between clusters (Table -2). The intra cluster D^2 values ranged from 0.00 (Cluster IV, V, VI, VII, VIII and XI) to 27.03 (Cluster II). The cluster II had the maximum D^2 value (27.03) followed by Cluster I (24.89) and Cluster III (24.46). The inter cluster distance was minimum between cluster III and III (24.46) indicating close relationship and similarity for most of the characters of the genotypes included in these clusters.

Wider genetic variety among the genotypes represented in these groups was indicated by the largest inter-cluster distance between clusters VII and III (82.75), which was followed by clusters VIII and VII (67.54).

Cluster III showed the lowest intra-cluster distance, indicating genotype commonality. Cluster VII (82.75) had the largest intra-cluster distance, which may be the result of restricted gene exchange or selection among the genotypes for a variety of traits. In order to obtain good segregants, a hybridization procedure between the genotypes of clusters III and VII may be implemented. Characters that contribute the highest D2 values should be prioritized while selecting the cluster in order to identify additional parents for hybridization. Therefore, tomato heterosis breeding will benefit from character-based selection for divergent parents. Similar results were reported in tomato by Rai *et al*., (1998), Parthasarathy and Aswath (2002), Karasava *et al*., (2005), Mahesha *et al*., (2006), Chopra *et al*., (2008), Nandan Mehta and Asati (2008), Meena and Bahadur (2015) and Sunil Prajapati *et al*., (2015).

Table 2: Inter and intra cluster distance.

	I	II	III	IV	V	VI	VII	VIII	IX
I	**24.890**	34.440	39.600	32.880	44.100	38.400	54.290	39.800	37.320
II		**27.030**	48.900	45.740	54.230	38.970	54.610	50.460	39.270
III			**24.460**	55.770	64.250	61.770	82.750	40.830	39.190
IV				**0.000**	25.910	40.060	46.950	38.790	60.080
V					**0.000**	37.840	39.550	39.620	65.550
VI						**0.000**	28.110	56.650	47.160
VII							**0.000**	67.540	66.480
VIII								**0.000**	56.710
IX									**0.000**

Table 3: Cluster Means.

	H30D	H60D	H90D	NPB	FF	50% F	NFPC	NCPP	NFPC	DFM	AFW (g)	NFPP	FL (cm)	NLPF	PT (mm)	TSS	ACIDITY (%)	AYPP (Kg)
I	27.02	58.63	106.60	16.85	46.15	51.07	10.80	16.06	6.57	102.82	54.19	91.51	5.10	5.07	5.87	5.85	0.31	4.87
II	30.97	65.89	115.92	13.42	45.78	51.67	8.92	20.25	4.53	102.97	44.33	50.83	6.62	4.14	4.28	5.97	0.39	2.27
III	29.38	64.13	114.25	19.33	47.21	52.96	10.96	12.92	5.79	103.92	57.83	58.04	5.88	5.50	6.56	3.43	0.25	3.70
IV	26.25	59.58	103.08	15.33	45.17	51.00	16.83	24.17	9.00	104.58	29.67	105.67	4.78	2.50	5.80	5.69	0.44	4.78
V	28.25	62.25	107.00	14.75	42.92	50.25	14.17	23.50	9.25	102.08	41.17	149.50	4.46	3.92	4.50	5.28	0.86	6.13
VI	28.67	63.67	111.58	26.33	45.58	50.00	8.17	12.08	6.17	103.50	34.67	117.25	5.43	3.08	5.18	7.24	0.67	4.03
VII	28.00	62.50	112.92	15.58	46.83	53.42	10.92	15.67	7.17	103.17	50.67	112.42	4.08	4.83	3.25	8.42	0.84	5.68
VIII	25.00	56.33	102.33	16.17	41.42	48.00	11.25	22.42	6.50	102.75	54.67	87.17	7.00	5.25	3.42	3.54	0.55	4.78
IX	24.83	53.67	101.00	10.25	50.42	55.08	7.08	9.50	4.50	103.58	79.67	29.67	6.33	8.00	6.45	6.28	0.33	2.36

Where, H30D= Plant height at 30 DAT, H60D=Plant height at 60 DAT, H90D= Plant height at 90 DAT, NPB=umber of primary branches, FF=Days to first flowering (days), 50%F=Days to 50% flowering (days), NFPC=umber of flowers/cluster, NCPP=umber of cluster(truss) per plant, NFPC=Number of fruits per cluster, DFM=Day of maturity (Days), AFW=Average single fruit weight (g), NFPP=Number of Fruits per plant, FL=Fruit length (cm), NLPF=umber of locules per fruit, PT=Pericarp thickness (mm), TSS=Total soluble solids (°Brix), ACIDITY=Acidity(%), AYPP=Average yield per plant (kg).

Additionally, cluster II was determined to be superior for fruit diameter, plant height at 30 DAT, plant height at 60 DAT, and plant height at 90 DAT based on the cluster mean for the various features investigated. On the other hand, cluster V was found to be superior in terms of the number of fruits per cluster, the number of fruits per plant, the acidity (%), and the average yield of fruits per plant. Cluster IV was found to be superior in terms of the number of flowers per cluster, the number of days to maturity, and the number of clusters per plant. Fruit length, first flowering, and 50% flowering were found to be superior in cluster VIII.

Cluster IX was found superior for Average fruit weight and Number locules per fruit Cluster III was superior for Pericarp thickness, Cluster VI was superior for Number of primary branches, Cluster VII was superior for total soluble solids (^{0}Brix). So, hybridization between genotypes from cluster II, cluster V and cluster IV, VIII, IX for these characters can produce better sergeants in segregating populations. These findings are in line with the results. Mehta and Asati (2008).

It has been proposed that segregants for many economic characteristics would result from hybridization between the genotypes of the abovementioned clusters. In a hybridization program, the prospective lines are selected from several clusters and used as parents. Genetic distance and the breeding program's objective should be the basis for the selection.

Conclusion

Significant genetic diversity was observed, with the genotypes grouped into nine distinct clusters. Promising traits such as plant height, fruit yield, and the number of fruits per plant were identified in clusters II, IV, and V, while maximum inter-cluster diversity was found between clusters VII and III, indicating potential for hybridization. This research underscores the importance of utilizing genetically diverse parental lines to enhance breeding programs, particularly in heterosis breeding, to achieve better crop improvement outcomes. Hybridization among selected clusters could yield superior segregants for economic traits. The findings provide valuable insights for designing breeding strategies and identifying potential genotypes for future tomato improvement efforts.

Acknowledgments

The authors are highly thankful for the facilities provided by the Department of Horticulture, School of Agricultural Sciences and Technology, Babasaheb Bhimrao Ambedkar University (A Central University), Lucknow (U.P.)- 226025, India.

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