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ASSESSMENT OF GENETIC DIVERGENCE IN TOMATO (*SOLANUM LYCOPERSICUM* L.)

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ABSTRACT
The present investigation evaluated 25 tomato genotypes during the *Rabi* 2025 season under a randomized block design with three replications. Eighteen quantitative traits related to flowering, fruit development, yield, quality, and plant growth were recorded to estimate genetic diversity using Mahalanobis D^2 statistics and Tocher's clustering method. The analysis grouped the genotypes into seven distinct clusters, indicating substantial genetic variability. The highest inter-cluster divergence was observed between Clusters II and VII, suggesting that hybridization between these groups may generate superior recombinants with greater heterotic potential. Cluster V exhibited superior vegetative growth, while Cluster III was characterized by desirable fruit quality attributes, including thicker pericarp. Cluster VI recorded the highest fruit yield per plant and per hectare, whereas Cluster VII produced the largest fruits. Genotypes such as Pusa Sheetal, Kashi Amrit, Rosemary, Oaklyan, Punjab Chhuhara, Black Cherry, Pusa Uphar, Money Maker, NF-54, Kashi Hemant, Kashi Anupam, Kashi Sharad, Pusa Rohini, Pusa Sadabahar, Kashi Adarsh, EC 620444, CO-3 and ZS21 were identified as genetically diverse and promising parental lines for hybridization. The findings demonstrate considerable scope for exploiting genetic divergence in tomato breeding programmes aimed at improving fruit yield, quality and overall productivity through heterosis and selection.

KEYWORDS: Tomato, genetic divergence, Mahalanobis D^2 analysis, Tocher clustering, heterosis breeding

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the most important vegetable crops cultivated worldwide and belongs to the family Solanaceae. It is a diploid species with a chromosome number of 2n = 24 (Saini et al., 2026). The crop is believed to have originated in the Andean region of South America, where its wild relatives are naturally distributed across Peru, Ecuador, Bolivia, Chile and Colombia. Tomato has evolved from being an ornamental plant once considered poisonous to becoming one of the most extensively cultivated and consumed vegetable crops across the globe (Dorais et al., 2008). Owing to its exceptional nutritional value, it is often described as a "protective food" (Sepat et al., 2013). The fruits are consumed in fresh as well as processed forms, including juice, puree, ketchup, sauces, canned products and several value-added food preparations such as pizza and soups (Maurya et al., 2022). It is an excellent source of vitamin C, provitamin A, potassium, dietary fibre, carotenoids, phenolic compounds and other natural antioxidants that contribute significantly to human nutrition (Perveen et al., 2015). Regular dietary intake of tomato has been associated with reduced risks of cardiovascular disorders, type 2 diabetes, certain cancers and neurodegenerative diseases owing to its antioxidant and health-promoting bioactive compounds (Ganesan et al., 2012; Ali et al., 2020). In India, tomato is cultivated throughout the year under diverse agro-climatic conditions and plays a vital role in nutritional security as well as the horticultural economy. In Haryana, the crop occupies an important position among vegetable crops. According to the Third Advance Estimates (2024 - 25), tomato was cultivated over 22.27 thousand hectares, producing 484.37 thousand tonnes with an average productivity of 21.74 t ha^{-1} (Department of Agriculture & Farmers Welfare, 2025). Although the state is not among the leading tomato-producing regions of the country, its productivity remains competitive under the agro-climatic conditions of the northern Indo-Gangetic Plains. Adoption of improved cultivars, efficient irrigation management and integrated crop protection practices is expected to further enhance productivity and strengthen horticultural development within the state. Wild tomato species exhibit remarkable adaptation to diverse ecological environments ranging from coastal areas to elevations of nearly 3,600 m in western South America and the Galápagos Islands. Such broad geographical distribution has resulted in substantial genetic and phenotypic diversity among wild taxa, providing valuable genetic resources for crop improvement (Peralta et al., 2008; Tieman et al., 2017). In contrast, cultivated tomato possesses a relatively narrow genetic base because domestication and continuous selection have retained only a limited proportion of the diversity available in wild relatives (Bai et al., 2007; Aflitos et al., 2014; Caramante et al., 2021). Nevertheless, sustained breeding efforts have

generated numerous cultivars and hybrids exhibiting considerable variation in fruit size, shape, colour and agronomic performance (Bai et al., 2007; Schouten et al., 2019). The success of any crop improvement programme largely depends on the availability of sufficient genetic variability and the identification of genetically diverse parents possessing desirable traits. The systematic evaluation of germplasm enables plant breeders to understand the genetic potential of available material and to select suitable parents for hybridization, thereby facilitating the development of superior cultivars (Singh et al., 2002). In the context of increasing population pressure and changing climatic conditions, broadening the genetic base of cultivated tomato has become essential for enhancing yield potential, resilience and long-term productivity (Agele et al., 2008; Arena et al., 2020; Francesca et al., 2022; Asare-Addo et al., 2022). Assessment of genetic diversity through multivariate statistical techniques provides an effective approach for identifying divergent genotypes. Among these, the Mahalanobis D^2 statistic (Mahalanobis, 1936) has been extensively used to estimate genetic divergence by considering multiple quantitative traits simultaneously. The approach was introduced into biological research by Rao (1952) and subsequently applied to plant populations by Nair and Mukharji (1960), followed by its wider application in crop classification and breeding studies (Murthy and Pavate, 1962). Cluster analysis using Tocher's method further facilitates the grouping of genetically similar genotypes, thereby enabling the selection of diverse parents for hybridization programmes. Previous studies have shown that crosses involving genetically divergent parents generally produce higher heterosis and greater breeding gains than those involving closely related genotypes (Ram and Panwar, 1970; Moll and Stuber, 1974). Moreover, characterization of genetic diversity provides a strong foundation for developing improved breeding populations and achieving sustained genetic improvement (Van Ginkel and Ortiz, 2018). Keeping these considerations in view, the present investigation was undertaken to evaluate the genetic divergence among twenty-five tomato genotypes using seventeen important growth, yield and quality traits. The study also aimed to identify genetically diverse and agronomically superior parental lines and to examine the relationships among important traits, thereby providing valuable information for future hybridization programmes and the development of high-yielding, adaptable tomato cultivars.

MATERIAL AND METHODS

The experiment was performed at the Research Farm, GD Goenka University, Sohna, Gurugram, Haryana (28°15′ N, 77°04′ E; 210-230 m above MSL). A total of twenty-five tomato genotypes were collected from different sources, were evaluated using a Randomized Block Design (RBD) during the *Rabi* season of 2024-2025, as presented in Table 1. The soil of the experimental field was characterized as sandy loam that has a pH range of 6.5-7. Seeds were first sown in seedbeds and subsequently treated with Bavistin for five minutes to protect seedlings from fungal and soil-borne diseases, ensuring better germination and seedling vigor. After 30 days, seedlings were transplanted into plots measuring 2.5 m × 2.5 m, maintaining a spacing of 50 × 50 cm between rows and plants. All recommended agronomic practices were followed to achieve optimum crop performance. Observations were recorded from five randomly selected plants from each genotype in each replication. Data were collected on twelve different characters, namely: number of primary branches, plant height (cm), number of fruits per cluster, number of clusters per plant, number of fruits per plant, number of locules per fruit, harvest duration (days), average fruit weight (g), fruit yield per plant (g), fruit yield per hectare (q).

Statistical Analysis

Genetic divergence among the 25 genotypes was assessed using Mahalanobis D^2 statistics as described by Rao (1952). The collected data were analyzed using both univariate and multivariate statistical methods with software packages including the Agri Analyze tool [Online tool]. www.agrianalyze.com (Popat et al., 2024) and JMP® Version 19 (https://www.jmp.com/getstarted)

RESULTS AND DISCUSSION

Cluster analysis of genotypes based on genetic divergence

Genetic divergence among the twenty-five tomato genotypes was evaluated using Mahalanobis D^2 analysis, which classified the genotypes into seven distinct clusters, as presented in Table 2 and illustrated by the dendrogram in Fig. 1. The clustering pattern indicated the presence of substantial genetic variability, providing a strong foundation for selecting genetically diverse parents in tomato improvement programmes. Similar observations that genotype within the same cluster are genetically more similar than those belonging to different clusters have been reported by Khapte and Jansirani (2014) and Lekshmi and Celine (2016). Among the seven clusters, Cluster III was the largest, comprising six genotypes (Pusa Uphar, Money Maker, NF-54, Kashi Hemant, Kashi Anupam and Kashi Sharad), followed by Cluster VI with five genotypes (Kashi Aman, EC-620424, Kashi Vishesh, ND-04 and Rishi). Clusters I (Pusa Sheetal, Kashi Amrit, Rosemarry and Oaklyan) and IV (Pusa Rohini, Pusa Sadabahar, Kashi Adarsh and EC-620444) each contained four genotypes, whereas Clusters II (Punjab Chhuhara and Black Cherry), V (ND-02 and ND-

08) and VII (CO-3 and ZS21) consisted of two genotypes each. The distribution of genotypes across clusters demonstrated that genetic divergence was independent of geographical origin, indicating that geographical distance alone is not a reliable measure of genetic diversity. The presence of both large and small clusters further reflects the broad genetic variability available within the experimental material. Therefore, the selection of parents for hybridization should be based primarily on genetic divergence rather than geographical distribution to maximize heterosis and broaden the genetic base of breeding populations. Similar findings have been reported by Mulge et al. (2012), Reddy et al. (2013), Kiran et al. (2017), Maurya et al. (2019), Anuradha et al. (2020) and Kumar et al. (2021).

Intra and inter-cluster distances

The intra and inter-cluster distances estimated through Mahalanobis D^2 analysis provide an effective measure of genetic diversity among the tomato genotypes and assist in identifying suitable parents for hybridization (Table 3). Higher inter-cluster distances indicate greater genetic divergence, whereas lower intra-cluster distances reflect genetic similarity among genotypes within the same cluster. The average intra-cluster D^2 values ranged from 2.967 to 6.633 (Table 3). Cluster II exhibited the highest intra-cluster distance (6.633), followed by Cluster VI (5.816), Cluster V (5.516), Cluster III (5.416), Cluster IV (3.563) and Cluster I (3.390), while Cluster VII recorded the lowest value (2.967). The higher intra-cluster distance in Cluster II suggests the presence of relatively greater variability among its constituent genotypes. Among the inter-cluster distances, the minimum genetic divergence was observed between Clusters I and IV (3.320), indicating close genetic similarity. In contrast, the maximum inter-cluster distance was recorded between Clusters II and VII (10.829), followed by Clusters IV and VII (10.131), III and VII (9.590) and I and VII (8.849). These highly divergent clusters are expected to provide superior parental combinations for hybridization, as wider genetic divergence enhances the probability of obtaining transgressive segregants through increased recombination and crossing over (Thoday, 1969). Similar observations have been reported by Singh et al. (2008) and Sudeepthi et al. (2020). Therefore, the combined assessment of inter- and intra-cluster distances provides a reliable basis for selecting genetically diverse parents to improve breeding efficiency. Comparable findings have also been reported by Narolia and Reddy (2012), Reddy et al. (2013), Pedapati et al. (2014), Kiran et al. (2017), Maurya et al. (2019), Anuradha et al. (2020) and Kumar et al. (2021).

Cluster means of eighteen characters and characterization of different clusters of tomato genotypes

The cluster means for eighteen quantitative traits are presented in Table 4. The seven clusters exhibited substantial differences for growth, flowering, fruit, yield and quality attributes, confirming considerable genetic variability among the evaluated tomato genotypes. Cluster mean analysis was useful for identifying clusters with complementary traits that could serve as potential parents in future breeding programmes. Cluster I consisted mainly of early-flowering genotypes, showing the minimum days to first flowering (18.40 days), first fruit setting (13.02 days), and 50% flowering (16.79 days). However, these genotypes had comparatively low TSS, suggesting a possible association between earliness and reduced fruit quality. In contrast, Cluster II comprised late and relatively weak-growing genotypes, with maximum days to first flowering (69.76 days) and 50% flowering (48.87 days), along with poor performance for plant height, branching, locule number, clusters per plant, fruits per plant, and yield. Nevertheless, this cluster recorded the highest TSS, indicating its potential for improving fruit quality. Cluster III was notable for delayed fruit maturity, higher polar diameter (94.39 mm), and greater pericarp thickness (76.08 mm), making it useful for improving fruit firmness and processing attributes. Cluster IV recorded the maximum flowers per cluster (101.68) and generally intermediate performance for other traits, indicating a balanced combination of characteristics. Cluster V showed vigorous growth and prolific fruiting, but smaller fruits and thinner pericarp. Cluster VI recorded the highest fruit yield per plant (128.28 kg) and per hectare (128.28 t ha^{-1}), together with maximum equatorial diameter and locule number, highlighting its value for yield and fruit-size improvement. Cluster VII produced the highest average fruit weight (126.08 g), but fewer fruits per cluster. The contrasting cluster profiles provide opportunities for selecting complementary parents to combine earliness, productivity, fruit size, and quality. The effectiveness of Mahalanobis' D^2 analysis in identifying genetically divergent parents has also been reported by Kandhola and Panwar (1999), Kuchanur et al. (2009), Bhati et al. (2015), Vennela et al. (2017), Mounika et al. (2020), Roy et al. (2022) and Yeasmin et al. (2023).

CONCLUSION

According to present investigation demonstrated considerable genetic diversity among the twenty-five tomato genotypes, as shown by their distribution into seven distinct clusters using Mahalanobis D^2 analysis. The clustering pattern was independent of geographical origin, highlighting the importance of genetic divergence over geographical distance for selecting superior breeding materials. Wide inter-cluster distances indicated the availability of highly diverse parental combinations, while cluster mean analysis

identified complementary traits associated with earliness, fruit yield, fruit size, and quality. Cluster VI was distinguished by its superior yield potential, Cluster VII by high fruit weight, Cluster I by earliness and Cluster II by enhanced soluble solids content. These findings suggest that hybridization between genetically divergent clusters possessing desirable attributes would enhance the probability of obtaining superior recombinants with improved productivity and fruit quality. The identified diverse genotypes provide valuable genetic resources for developing high-yielding and quality tomato cultivars in future breeding programmes.

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Author contribution
SY and DM conceptualized and drafted the manuscript. JS, APM and SD assisted in preparing the manuscript. All authors read the final version of the manuscript, provided necessary suggestions and approved it for publication.

Conflict of interest:
On behalf of all authors, the corresponding author states that there is no conflict of interest. The corresponding author confirms that the submitted manuscript is original, unpublished and not under simultaneous consideration by another journal**.**

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Table 1: List of genotypes (Experimental Materials)

Sr. No.	Genotype	Sources
01	Pusa Sheetal	IIVR, Varanasi
02	Pusa Rohini	IIVR, Varanasi
03	Pusa Uphar	IIVR, Varanasi
04	Pusa Sadabahar	IIVR, Varanasi
05	Kashi Hemant	IIVR, Varanasi
06	Kashi Aman	IIVR, Varanasi
07	Kashi Anupam	IIVR, Varanasi
08	Kashi Amrit	IIVR, Varanasi
09	Kashi Adarsh	IIVR, Varanasi
10	Kashi Sharad	IIVR, Varanasi
11	Kashi Vishesh	IIVR, Varanasi
12	ND-02	ANDUAT, Ayodhya
13	ND-04	ANDUAT, Ayodhya
14	ND-08	ANDUAT, Ayodhya
15	EC-620424	IIVR, Varanasi
16	EC 620444	IIVR, Varanasi
17	Punjab Chhuhara	IIVR, Varanasi
18	Rishi	Local collection from MP
19	CO-3	IIVR, Varanasi
20	Money Maker	IIVR, Varanasi
21	NF-54	Local Collection from MP

22	ZS21	Local Collection from MP
23	Black cherry	Collected from All that Grow
24	Rosemarry	Collected from All that Grow Pvt.
25	Oaklyan	Collected from All that Grow Pvt.

Table 2: Clustering Pattern of 25 tomato genotypes

Cluster		I	II	III	IV	V	VI	VII
I		**3.390**	4.824	4.198	3.320	4.390	4.369	8.849
II			**6.633**	4.820	5.257	6.412	6.884	10.829
III				**5.416**	5.148	4.165	5.060	9.590
IV					**3.563**	4.434	6.051	10.131
V						**5.516**	5.243	8.808
VI							**5.816**	6.122
VII								**2.967**

Table 3: Intra and inter-cluster distances

No. of clusters	Number of genotypes included in the cluster	Name of the genotypes
I	4	Pusa Sheetal, Kashi Amrit, Rosemarry and Oaklyan
II	2	Punjab Chhuhara and Black cherry
III	6	Pusa Uphar, Money Maker, NF-54, Kashi Hemant, Kashi Anupam and Kashi Sharad
IV	4	Pusa Rohini, Pusa Sadabahar, Kashi Adarsh and EC 620444
V	2	ND-02 and ND-08
VI	5	Kashi Aman, EC-620424, Kashi Vishesh, ND-04 and Rishi
VII	2	CO-3 and ZS21

Table 4: Cluster means of eighteen characters and showing cluster characteristics of different clusters of tomato genotypes

Characters	Clusters									
	I	II	III	IV	V	VI	VII	Mean	Max.	Min
Days to first flowering	18.40	69.76	34.78	30.68	67.52	50.11	29.57	42.97	69.76	18.40
Days to first fruit setting	13.02	80.23	46.21	44.14	82.72	58.83	37.91	51.87	82.72	13.02
Days to 50% flowering	16.79	48.87	35.03	41.32	41.32	42.08	22.45	35.41	48.87	16.79
Days to first fruit harvest	93.98	92.40	96.60	64.00	29.29	59.58	70.31	72.31	96.60	29.29
Average fruit weight (g)	76.40	63.52	122.40	87.44	59.84	123.87	126.08	94.22	126.08	59.84
Fruit equatorial diameter (mm)	52.67	54.48	117.17	96.08	47.25	121.03	87.03	82.25	121.03	47.25
Polar diameter (mm)	66.10	77.31	94.39	77.31	29.26	74.10	67.70	69.45	94.39	29.26
Locule number	54.75	39.17	114.17	70.33	84.17	123.63	111.86	85.44	123.63	39.17
Pericarp thickness (mm)	41.35	54.19	76.08	62.76	19.94	62.19	48.48	52.14	76.08	19.94
Number of flowers/clusters	75.41	64.59	49.14	101.68	36.78	53.46	67.68	64.10	101.68	36.78
Number of clusters/plants	82.28	22.04	65.14	58.77	101.38	91.39	54.36	67.91	101.38	22.04
Number of fruits /clusters	46.05	39.55	30.88	41.72	54.72	34.78	20.04	38.25	54.72	20.04
Number of fruits/plants	126.08	48.80	85.60	94.80	155.52	119.45	52.48	97.53	155.52	48.80
Number of primary branches/plants	25.16	9.97	49.75	44.69	62.05	46.86	42.52	40.14	62.05	9.97
Plant height (cm)	105.12	40.02	89.45	70.76	134.05	113.80	61.72	87.84	134.05	40.02
Fruit yield/plant (kg)	96.64	48.80	113.81	92.96	89.28	128.28	74.56	92.05	128.28	48.80
Fruit yield/ha (t/ha)	96.64	48.80	113.81	92.96	89.28	128.28	74.56	92.05	128.28	48.80
TSS (Total Soluble Solids)	18.40	69.76	34.78	30.68	67.52	50.11	29.57	42.97	69.76	18.40

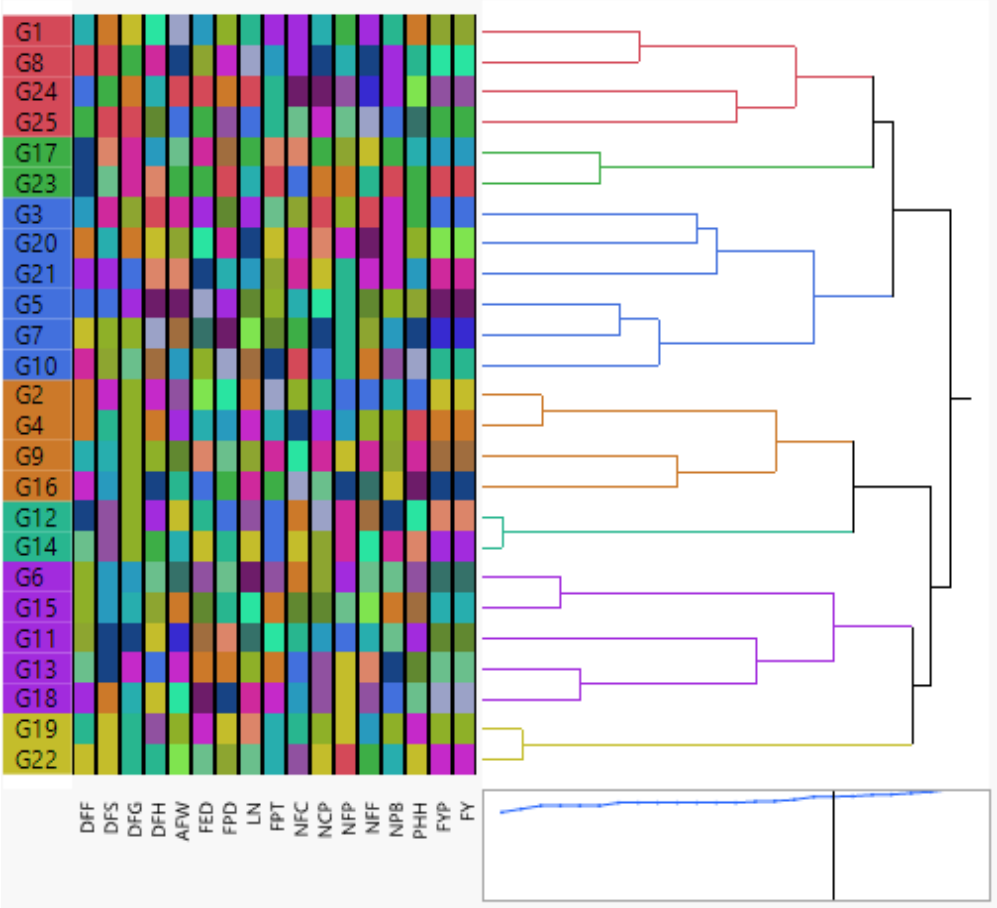

Fig. 1: Dendrogram representing the grouping of 25 genotypes of tomato generated using D^2 cluster analy