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## ASSESSMENTS OF THE GENETIC DIVERGENCE AMONG THE TOMATO GERMPLASMS

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The presence of diverse genotypes and their identification is a major requirement for any crop improvement program. Current study aims to estimate the genetic diversity present in 48 tomato genotypes using  $D^2$ analysis. Experiment was conducted during Rabi 2022-2023 and Rabi 2023-2024 using 48 diverse genotypes at the Horticulture Research Centre, located at Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, following Randomized Complete Block Design within three replications. Genetic diversity analysis revealed that in both seasons of 2022-2023 and 2023-2024, including pooled analysis of 48 genotypes, was categorized into six clusters. The distribution of genotypes of pooled data indicated that clusters V and VI (10 each) comprise the highest number of genotypes. The mean of clusters revealed that the fruit yield per plant was highest in cluster I in pooled analysis. The maximum inter-cluster distance in the ABSTRACT 2022-2023 season was observed between clusters I and III, while in 2023-2024, it was between clusters III and IV and, in pooled data, between clusters I and III. Pooled analysis revealed that selection of genotypes from clusters having the highest inter-cluster distance, like cluster I (Kashi Amul, Kashi Shardul, Punjab Chhuhara, Naveen, EC-620441, EC-617055, EC-620482 and EC-631404) and III (Pusa Ruby, Pusa Gavaru, Pusa Upakr, Pusa Sheetal, KashiAmrit, Moany Makar and EC-620440), can be further selected for generation of genetic variation to exploit heterosis in other breeding programs.

*Key words:* Tomato, Genetic diversity, D<sup>2</sup> analysis, Germplasm.

#### Introduction

Tomato (*Lycopersicum esculentum* Mill.) belongs to Solanaceae family along with other economically important crops such as pepper, eggplant and potato. It is a significant vegetable crop of special economic importance in the horticultural industry worldwide. Tomato is diploid (2n = 24) and self-pollinated annual crop (Ullah *et al.*, 2007). Tomato possesses unique properties due to its diploid, fairly compact and recently sequenced genome with the genome size of 950 mb (Mega base pair). The C.M. Rick Tomato Genetics Resource Center (TGRC) at the University of California, Davis maintains seed stocks of accessions of wild relatives, monogenic mutants, and miscellaneous genetic stocks of tomato. Tomato is one of the important vegetable crops grown throughout the world because of their wider adaptability, high yielding potential, and suitability for a variety of fresh and processed form. An increasing population with shrinkage of land per capita requires the development of high yielding varieties suitable for protected structures in the current era (Kumar *et al.*, 2021). Tomato is the warm season fruit vegetable grown throughout the world. Tomato as a fresh vegetable used in several dishes, sandwiches, salad, etc. and can be processed into several forms like paste, puree, syrup, juice, ketchup, sauce, whole peeled tomato etc. Tomato is universally treated as the important 'Protective Food' because of its special nutritive value viz., it is rich source of minerals, vitamins, organic acids and regular consumption of tomatoes and tomato based products has been associated with a reduced risk (Giovannucci et al., 1999). Tomatoes are an excellent source of vitamin C, which is important for immune function, collagen synthesis, and antioxidant protection. Vitamin C content in tomatoes can vary based on the variety and ripeness. Tomato fruit contain 93.1 g water, protein 19 g, fat 0.1 g, carbohydrate 3.6 g, mineral matter 0.6 g, calcium 20 mg, phosphorous 36 mg, iron 0.8 mg, carotene (as vitamin A) 320 I U, thiamine 2.27 mg, nicotinic acid 0.4 mg, riboflavin 0.01 mg and ascorbic acid 31 mg per 100 g of pulp of fruit. It also contains folic acid, vitamin K and inhibitors which are related to Vitamin-E (Van Deynze et al., 2007). The tomato growth characteristics range from indeterminate to highly determinate type; indeterminate plant keeps growing and produces fruits until frost kills the plant. However, welldrained, sandy or red loam soils rich in organic matter with a pH range of 6.0-7.0 are considered as ideal (Tam et al., 2005). The best fruit colour and quality is obtained at a temperature range of 21- 24°C. Tomato is one of the most important vegetables in India accounting for about 11.04 percent of the total vegetables production in the country. But, due to its high perishability it cannot be preserved in fresh form throughout the year. Leading producers of tomato in the World are China (67.63 million tonnes), accounting for 26% of the total production, followed by India (21.18 million tonnes), Turkey (13.09 million tonnes), USA (10.47 million tonnes), Italy (6.64 million tonnes), Egypt (6.24 million tonnes) and Spain (4.75 million tonnes). In the 2023-24 agricultural year, India reported a total tomato production of approximately (20.82 million tonnes) across an area of (8.50 lakh hectares). The major tomato-producing states and their respective production figures are as follows like Madhya Pradesh (3.50 million tonnes), Karnataka (2.44 million tonnes), Andhra Pradesh (2.19 million tonnes) and Gujarat (1.44 million tonnes) (NHB 2023 -2024).

### **Materials and Methods**

# Experimental site, design, soil properties and planting material

The experimental site was carried out at Horticulture Research Centre, located at Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut at 29.010 North latitude, 77.750 East longitudes and an altitude of 237 meter above mean sea level (MSL). Used in RBD method with three replications during the *Rabi* season of 2022-23 and 2023-24 by taking 48 diverse genotypes of Tomato (Table 1). The data or observations

Table 1:	List of 48 tomato varieties/genotypes included in
	the study.

Sr. No.	IIVR, varieties Varanasi	Sources								
1.	Pusa Ruby	IARI								
2.	Pusa Gavaru	IARI								
3.	Pusa Upakr	IARI								
4.	Pusa Sheetal	IARI								
5.	Pusa Sadabahar	IARI								
6.	Kashi Adarsh	IIVR								
7.	Kashi Aaman	IIVR								
8.	Kashi Amul	IIVR								
9.	Kashi Anupama	IIVR								
10.	Kashi Hemant	IIVR								
11.	Kashi Shardul	IIVR								
12.	Kashi Vishesh	IIVR								
13.	KashiAmrit (DVRT-1)	IIVR								
14.	Hisar Lalit	HAU								
15.	H-24	HAU								
16.	Punjab Chhuhara	PAU								
17.	Naveen	IIHR								
18.	CO-3	TNAU								
19.	Selecation-7	IARI								
20.	Moany Makar	IARI								
Sr. No.	NBPGR, germplasm New									
21.	EC-620440									
22.	EC-620441									
23.	EC-620444									
24.	EC-620424									
25.	EC-620545									
26.	EC-620645									
27.	EC-538407									
28.	EC-538408									
29.	EC-538411									
30.	EC-759290									
31.	EC-615039									
32.	EC-615040									
33.	EC-617055									
34.	EC-620388									
35.	EC-620404									
36.	EC-620425									
37.	EC-620482									
38.	EC-620488									
39.	EC-620489									
40.	EC-620498									
41.	EC-620505									
42.	EC-620531									
43.	EC-631401									
44.	EC-631404									
45.	EC-631411									
46.	EC-645167									
47.	EC-687422									
48.	EC-687423									
-10.	LC-007423									

SV	DF	DTG	DTF	DFFS	DFFM	DFFH	PH	NPB	FL	NFPP	AFFW	FY	FYP	FYt
Rep.	2	0.54	0.90	0.73	0.71	0.20	2.23	0.30	0.47	5.69	318.89	0.001	0.039	0.044
Treat	47	4.49**	31.13**	100.03**	45.84**	43.96**	333.22**	1.43**	1.06**	99.77**	786.45**	0.032**	0.355**	1.969**
Error	94	0.17	3.29	0.92	1.31	1.36	10.12	0.24	0.06	4.50	64.33	0.002	0.027	0.096
Total	143	1.59	12.40	33.49	15.93	15.35	116.20	0.63	0.39	35.83	305.23	0.012	0.135	0.711
SV: Source of variation; DTG: Day taken to germination; DTF: Days to 50% flowering; DFFS: Days to first fruit set;														
DFFM	DFFM: Days to first fruit maturity; DFFH: Days to first fruit harvesting; PH: Plant height (cm); NPB: Number of primary branches;													

Table 2: Analysis of variance in 48 tomato genotypes for both season 2022-2023 and 2023-2024 (Pooled).

SV: Source of variation; DTG: Day taken to germination; DTF: Days to 50% flowering; DFFS: Days to first fruit set; DFFM: Days to first fruit maturity; DFFH: Days to first fruit harvesting; PH: Plant height (cm); NPB: Number of primary branches FL: Fruit length (cm); NFPP: Number of fruits per plant; AFFW: Average five fruit weight (g); FY: Fruit yield (kg/plant); FYP: Fruit yield (kg / plot); FYt: Fruit yield (t/ ha) (\*, \*\* significant at 5% and 1% level, respectively)

were taken based on 5 randomly selected plants from each replication for 13 traits *viz*; day taken to germination, plant height (cm), number of primary branches, fruit length(cm), days to 50% flowering, days to first fruit set, days to first fruit maturity, days to first fruit harvesting, number of fruits per plant, average five fruit weight(g), fruit yield (kg/ plant), fruit yield per plot (kg/plot) and fruit yield per ha (tonne/ha).

#### Statistical analysis

The Mahalanobis  $D^2$  statical method was used to quantify genetic diversity among the genotypes. The  $D^2$ values were used to classify the entire germplasm into distinct clusters, following to Tocher's method Rao.

## **Results and Discussion**

The analysis of variance for 48 genotypes disclosed significant differences for all the 13 characters, representing a broad spectrum of variability among the **Table 3:** Clustering pattern of 48 genotypes of pea based on Mahalanobis D<sup>2</sup> statistics.

Clus- ters	No. of genotypes	Genotypes
		Kashi Amul, Kashi Shardul, Punjab
Ι	8	Chhuhara, Naveen, EC-620441,
		EC-617055, EC-620482 and EC-631404
Π	6	EC-620545, EC-538408, EC-615040,
ш	0	EC-620404, EC-620498 and EC-620531
		Pusa Ruby, Pusa Gavaru, Pusa
Ш	7	Upakr, Pusa Sheetal, KashiAmrit,
		Moany Makar and EC-620440
		Kashi Aaman, CO-3, EC-538407,
IV	7	Selecation-7, EC-538411,
		EC-620489, EC-620505
		Pusa Sadabahar, Kashi Adarsh,
v	10	Kashi Anupama, Kashi Vishesh,
v	10	Hisar Lalit, EC-620444, EC-615039,
		EC-620488, EC-631401, EC-687422
		Kashi Hemant, H-24, EC-620424,
И	10	EC-620645, EC-759290, EC-620388,
VI	10	EC-620425, EC-631411, EC-645167,
		EC-687423

genotypes represented in (Table 2).

#### Number of Genotypes in Each Cluster

Based on Mahalanobis  $D^2$  values, all the 48 genotypes of tomato under study were grouped in to six cluster, shown in Table 3. The Clustering pattern of tomato genotypes was grouped into six clusters.

Rabi Season (2022-2023) the genetic differentiation among the 48 genotypes was assessed using cluster analysis, and the genotypes were distributed into six clusters based on Mahalanobis' distances. Cluster VI had the highest number of genotypes (18), followed by cluster V (8), cluster IV (6), cluster II (6), cluster III (5), and cluster I (5). Rabi Season (2023-2024) in the second season, the same 48 genotypes were distributed into six clusters. Cluster V contained the maximum number of genotypes (15), followed by cluster VI (11), cluster II (10), cluster IV (5), cluster I (4), and cluster III (3). Pooled Rabi Seasons (2022-2023 and 2023-2024) for the pooled data from both seasons, the distribution of genotypes into clusters remained similar. Cluster VI and cluster V each contained (10) genotypes, followed by cluster I (8), cluster IV (7), cluster III (7), and cluster II (6).

#### Average of Inter and Intra Cluster Distance

The average intra and inter-cluster  $D^2$  value and average Intra and inter-cluster distance value are presented in Table 4.

Inter-cluster distances the maximum inter-cluster distance for the Rabi 2022-2023 season was observed between clusters I and III (8.691), followed by I-III (6.392), II-III (6.110), and others in a decreasing order. For the 2023-2024 season, the highest inter-cluster **Table 4:** Average of inter and intra cluster distances for both season 2022-2023 and 2023-2024 (Pooled).

Clusters	Ι	I	Ш	IV	V	VI
Ι	2.395					
II	4.041	2.343				
III	6.800	5.302	2.113			
IV	4.631	2.529	3.616	2.202		
V	3.978	4.135	3.402	3.251	2.543	
VI	5.058	4.795	3.807	3.900	2.497	2.362

Cluster	DTG	DTF	DFFS	DFFM	DFFH	PH	NPB	FL	NFPP	AFFW	FY	FYP	FYt
I (Mean)	11.70	70.36	43.79	53.83	55.07	90.33	4.77	5.73	75.07	296.79	1.43	4.51	11.37
II (Mean)	12.42	68.34	38.82	48.09	49.40	88.00	4.81	4.67	68.52	288.64	1.31	4.03	10.11
III (Mean)	10.81	75.02	45.66	54.88	56.35	100.09	5.31	4.06	60.75	251.88	1.17	3.62	9.19
IV (Mean)	12.78	71.48	41.36	50.64	52.00	102.42	4.81	4.78	65.69	268.03	1.30	3.91	9.60
V (Mean)	11.16	74.61	48.95	55.74	57.14	92.15	4.53	4.81	67.69	277.68	1.25	3.97	10.34
VI (Mean)	12.80	71.09	52.74	58.51	59.65	87.06	5.00	4.67	63.78	279.01	1.23	3.89	9.73
DTG: Day	taken t	o germina	tion; DTF	Days to	50% flov	vering; DFI	FS: Days	to first i	fruit set; l	DFFM: Da	ys to firs	t fruit ma	turity;
DFF	H: Days	to first fi	uit harves	ing; PH:	Plant heig	ght (cm); N	PB: Num	nber of p	rimary bra	anches; FL	: Fruit lei	ngth (cm)	;
NFPP: N	NFPP: Number of fruits per plant; AFFW: Average five fruit weight (g); FY: Fruit yield (kg/plant); FYP: Fruit yield (kg / plot);												
FYt: Fruit yield (t/ ha)													
distance oc	istance occurred between clusters III and IV (9.896), II and VI (4.795), cluster I and IV (4.631), cluster II and												

Table 5: Cluster mean of 48 genotypes of tomato for 13 characters for both season 2022-2023 and 2023-2024 (Pooled).

distance occurred between clusters III and IV (9.896), followed by I-III (6.392) and II-III (6.110).For the pooled data, the maximum inter-cluster distance was between clusters I and III (6.800).Pooled Rabi Season (2022-2023 and 2023-2024) the maximum inter cluster distance was observed between cluster I and III (6.800) followed by cluster II and III (5.302), cluster I and IV (5.058), cluster II and VI (4.795), cluster I and IV (4.631), cluster II and V (4.135), cluster I and II (4.041), cluster I and V (3.978), cluster IV and VI (3.900), cluster III and VI (3.807), cluster III and IV (3.616), cluster III and IV (3.402), cluster IV and V (3.251), cluster V and VI (2.497) and cluster II and IV (2.529).

Intra-cluster distance for the 2022-2023 season, the

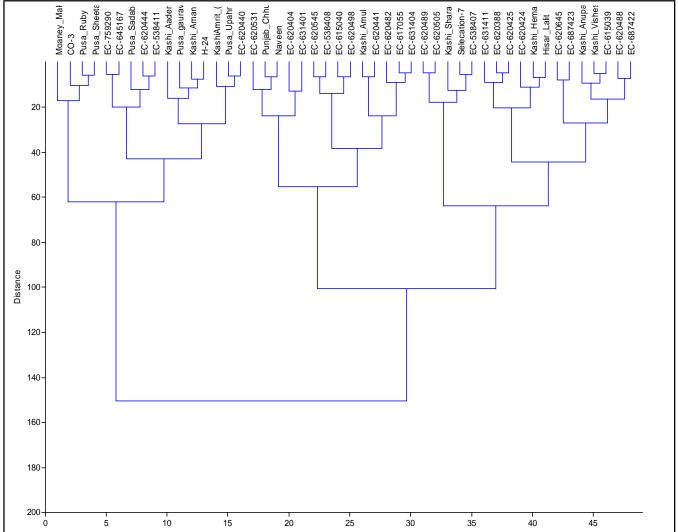


Fig. 1: Dendrogram Showing Diversity of Tomato Genotypes Generated Using Mahalanobis D<sup>2</sup> Cluster Analysis (Both *Rabi* Season 2022- 2023 and 2023-2024).

maximum intra-cluster distance was observed in cluster VI (2.530), while the lowest was in cluster IV (1.944). In the 2023-2024 season, cluster I exhibited the largest intra-cluster distance (2.869), while cluster III showed the smallest (1.814). For the pooled data, cluster V had the highest intra-cluster distance (2.543), while cluster III had the lowest (2.113).Pooled Rabi Season (2022-2023 and 2023-2024) the maximum intra cluster distance was observed between cluster V (2.543) followed by cluster I (2.395), cluster VI (2.262), cluster II (2.343), cluster IV (2.202) and cluster III (2.113)

#### **Cluster Mean Values**

Rabi Season (2022-2023) the mean values for 13 characters were recorded, revealing considerable variation between clusters for various traits. Cluster IV showed the highest mean for plant height (103.92), while cluster II had the lowest (84.34). For fruit yield per plant, cluster I had the highest mean (1.49), while cluster III had the lowest (1.07). Other traits such as fruit length, number of fruits per plant, and fruit yield per hectare also showed similar variation across clusters. Rabi Season (2023-2024) similar variations were observed for the 13 traits in this season. Cluster VI had the highest mean for days to germination (12.88), and cluster III had the lowest (11.32). Cluster IV had the maximum mean value for fruit yield per plant (1.53), while cluster III had the minimum (1.05). Pooled Rabi Seasons (2022-2023 and 2023-2024) for the pooled data, cluster VI again had the highest mean for days to germination (12.80), and cluster III showed the lowest (10.81). Cluster I exhibited the highest mean for fruit yield per plant (1.43), while cluster III had the lowest (1.17) Table 5.

All parameter similar findings were found to be consistent with the work of Reddy *et al.*, (2013), Chernet *et al.*, (2014), Figueiredo *et al.*, (2017), Herison *et al.*, (2017), Somraj *et al.*, (2017), Anuradha *et al.*, (2020), Kumar *et al.*, (2021), Rahimi *et al.*, (2022), Kerwin *et al.*, (2024).

#### Conclusion

Based on Mahalanobis D2 analysis, the tomato germplasm in the present study can be successfully used for planning future breeding programmes. Genetic diversity analysis revealed that in both seasons of 2022-2023 and 2023-2024, including pooled analysis of 48 genotypes, was categorized into six clusters. The distribution of genotypes indicated that in *Rabi* 2022-2023, cluster VI had the highest number of genotypes (18) and *Rabi* 2023-2024, cluster V contained 15, whereas in pooled data, clusters VI and V both contained 10 genotypes. The mean of clusters revealed that the fruit

vield per plant was highest in cluster I during 2022-2023, cluster IV in 2023-2024 and cluster I in pooled analysis. The maximum inter-cluster distance in the 2022-2023 season was between clusters I and III, while in 2023-2024, it was between clusters III and IV, and for the pooled data, it was between clusters I and III. In terms of intra-cluster distances, the highest intra-cluster distance in 2022-2023 was found in cluster VI, in 2023-2024, cluster I, and in pooled data, cluster V. The analysis revealed notable differences between the two Rabi seasons in terms of cluster composition, intra- and intercluster distances, and mean trait values. Pooled analysis revealed that selection of genotypes from clusters having the highest inter-cluster likeness, such as cluster I (8, 11, 16, 17, 22, 33, 37, 44 and the genotype name like Kashi Amul, Kashi Shardul, Punjab Chhuhara, Naveen, EC-620441, EC-617055, EC-620482 and EC-631404) and cluster III (1, 2, 3, 4, 13, 20, 21 and genotype name like Pusa Ruby, Pusa Gavaru, Pusa Upakr, Pusa Sheetal, KashiAmrit, Moany Makar and EC-620440), can be used further for the generation of genetic variation to exploit heterosis in other breeding programs.

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