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Morphological Diversity of Tomato Germplasm (*Lycopersicum esculentum* L.) for Yield Traits

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ABSTRACT: The goal of this study was to determine the genetic diversity of 60 tomato genotypes for fruit yield and related traits using a field experiment in an RBD with three replications. The Mahalanobis distance (D2) was used to calculate the genetic distance between clusters. Cluster analysis revealed that the genotypes were divided into 11 distinct clusters, with cluster I having the most genotypes (43), and clusters II through XI being monogenetic. The inter-cluster distances ranged from 9698.09 (between clusters II and IX) to 47564.45 (between clusters IX and X). Intra-cluster distances ranged between 0.00 (in monogenotypic clusters) and 10787.58 (in cluster I). The number of fruits per plant contributed the most to genetic divergence (17.40%), followed by average fruit weight. Seven lines (VRSL 8, VRSL 18, VRSL 24, VRSL 44, VRSL 66, VRSL 87, and VRSL 104) were chosen as potential parents for hybridization to produce F1 hybrids and study heterosis and combining ability in tomato based on genetic distance and resistance to ToLCV.

Keywords: Genetic distance, divergence, hybridization.

INTRODUCTION

Tomato (*Solanum lycopersicum*L) is a member of the Solanaceae family with chromosomal number 2n=2x=24. Solanum *lycopersicum* var. cerasiforme Bailey is the most likely progenitor of tomato. It was discovered in the wild in the Peru Equador area of the Andes (South America), and it is now grown in practically every country on the planet (Robertson and Labate 2007). It is a day neutral plant that is mostly self-pollinated, but some cross pollination does occur (Depra *et al.*, 2014). Tomatoes are often regarded as a "Protective food" (Thamburaj and Singh 2013). It is an excellent source of revenue for small and marginal farmers, as well as having a high nutritional value. It is a rich source of antioxidants such as ascorbic acid, vitamin C, carotenoids, flavonoids, and phenolic acids. Tomatoes contain 31 mg of ascorbic acid per 100 g. The red colour of tomatoes is caused by the presence of the pigment "lycopene," which has a concentration of 20- 50 mg/100 g in edible portions. After potatoes and sweet potatoes, tomatoes are the world's greatest vegetable crop. These states account for approximately 91% of total national output. Tomatoes have an area of around 0.81 million hectares and a yield of approximately 20.51 million metric tonnes (NHB, 2021-22).

The knowledge of genetic diversity among genotypes is crucial for selecting parents with maximum genetic divergence for hybridization, as they are likely to produce desirable recombination and segregation in their progenies. Therefore, research on genetic diversity is essential to identify such potential parents. These lines have been evaluated at different research centers for their fruit yield, quality, disease and insect resistance. As a result, a no of varieties have been released for different agro ecologies. Several authors from different countries, such as Sekhar *et al.* (2008); Kumar *et al*. (2020); Kathimba *et al.* (2022), have studied genetic diversity in tomato genotypes.

MATERIAL AND METHODS

This study comprised three experiments that were conducted from August 2021 to January 2023 at College of Horticulture, Venkataramannagudem, West Godavari District, Andhra Pradesh. The location belongs to Agro-climatic Zone-10, humid, East Coast

Plain and Hills (Krishna-Godavari zone) with an average rainfall of 900 mm and is geographically situated at 16° 63′ 120″ N latitude and 81° 27′ 568″ E longitude at an altitude of 34 m (112 feet) above mean sea level. The site has short humid summers and mild winters. The soil of the experimental site is red sandy loam with good drainage and moderate water holding capacity. The weather conditions were favourable for the growth and development of tomato throughout the crop stages. Sixty different tomato genotypes were examined for yield and yield-related characteristics. The experiment was set up in a RBD with three replications and 60 genotypes spaced 60 cm 60 cm apart. To guarantee a healthy crop, the experimental field was carefully prepared and conventional cultural, manual, and plant protection practises were followed. Observations were made on twenty-two different characteristics. For these features, several statistical and biometrical data were examined. To assess the degree of divergence, Mahalanobis (1936) generalised distance (D2) was employed, and the genotypes were classified into clusters using Tocher's approach (Rao, 1952).

A. Genetic Divergence

The Mahalanobis D2 statistics were used to categorise diverse tomato genotypes into clusters. In the current study, 60 genotypes were classified into eleven clusters based on their D2 values, as shown in table-1. Cluster I was the biggest, with 43 genotypes, followed by cluster III with 8 genotypes, and clusters II, IV, V, VI, VII, VIII, IX, X, and XI with just one genotype (mono-genotypic clusters), indicating genetic heterogeneity. Kumar *et al.* (2016); Nalla *et al.* (2014); Lekshmi and Celine (2020) conducted similar studies using the D2 statistic.

B. Average intra and intercluster distances

D^2 analysis is the most effective method to measure the forces of differentiation at two levels namely, intra cluster and inter cluster levels. The inter-cluster distance was higher than intra cluster distance (Table 2) indicating the presence of average genetic diversity among the genotypes under study.

The intra-cluster D^2 values varied from 0.00to10787.58.Theintra-cluster distances in cluster II, IV, V, VI, VII, VIII, IX, X and XI were zero because only one genotype included in each. The maximum inter-cluster distance was found between cluster IX and X(47564.45) followed by clusters II and IX (44457.03). The minimum inter-cluster distance was recorded between cluster II and cluster IX(9698.09).

C. Percent contribution of the traits

The percent contribution towards genetic divergence by all the seventeen characters is furnished in the Table 3 and Fig 1. first with a contribution of 17.40 % followed by average fruit weight with 15.36 %. The characters *viz*, pericarp thickness, days to first fruit harvest, leaf curl virus incidence, no of primary branches per plant, no of flowers per cluster, fruit length, no. of locules/fruit, number of fruits/cluster, fruit yield/plant, days to 50% flowering, plant height, days to first flowering and per cent fruit set have contributed by 14.86, 12.15, 10.51, 5.37, 3.90, 3.90, 3.73, 3.70, 3.45, 1.92, 1.36, 0.06 and 0.03 per cent respectively. However, fruit firmness did not contribute anything to the diversity.

Table 1: Distribution of tomato genotypes into different clusters.

Cluster No.	Number of genotypes	Name of the genotypes
Cluster I	43	VRSL94, VRSL185, VRSL63, VRSL86, VRSL175, VRSL105, VRSL92, VRSL160, VRSL118, VRSL154, VRSL128, VRSL22, VRSL133, VRSL122, VRSL109, VRSL206, VRSL192, VRSL145, VRSL209, VRSL45, VRSL244, VRSL210, VRSL39, VRSL223, VRSL88, 187, VRSL44, VRSL174, VRSL183, VRSL178, VRSL176, VRSL82, VRSL81, VRSL113, VRSL43, VRSL26, VRSL177, VRSL40, VRSL41, VRSL56, VRSL104 and VRSL72.
Cluster-II	1	VRSL 42
Cluster III	8	VRSL8, VRSL18, VRSL24, VRSL87, VRSL106, VRSL134, VRSL180 and VRSL180
Cluster IV	1	VRSL78
Cluster V	1	VRSL30
Cluster VI	1	VRSL114
Cluster VII	1	VRSL66
Cluster VIII	1	VRSL90
Cluster IX	1	VRSL38
Cluster X	1	VRSL46
Cluster XI	1	VRSL107

Table 2: Average inter and intra–cluster (diagonal) distance D^2 values in tomato.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
Cluster I	**8201.76**	14562.21	14963.58	11802.02	12006.99	12733.33	13547.34	17153.22	17958.99	19220.49	15368.05
Cluster II		0.00	17579.72	16741.70	9988.90	23756.78	22160.48	26076.96	9698.09	44457.03	18540.37
Cluster III			**10787.58**	24113.15	22376.42	19942.89	14398.14	25378.66	20433.14	33502.43	18905.04
Cluster IV				0.00	15071.92	20766.04	23184.28	18323.59	23046.31	29817.57	23545.68
Cluster V					0.00	20336.26	17468.35	26448.73	18027.72	27612.95	21769.95
Cluster VI						0.00	21343.42	29314.37	18070.42	18986.48	16861.58
Cluster VII							0.00	25141.44	29535.00	18152.81	27633.32
Cluster VIII								0.00	32520.94	30498.49	24241.10
Cluster IX									0.00	47564.45	19130.05
Cluster X										0.00	30712.12
Cluster XI											0.00

Table 3: Relative contribution of traits.

Sr. No.	Source	Contribution (%)	Number of times Ranked first
1.	Plant height (cm)	1.36	24
2.	No. of primary branches/ plant	5.37	95
3.	Days to first flowering	0.06	1
4.	Days to 50% flowering	1.92	34
5.	No. of flowers per cluster	3.90	69
6.	No. of fruits per cluster	3.70	66
7.	Per cent fruit set	0.03	1
8.	Days to first fruit harvest	12.15	215
9.	Fruit length (cm)	3.90	69
10.	Fruit diameter (cm)	2.32	41
11.	Average fruit weight (g)	15.36	272
12.	Number of locules per fruit	3.73	66
13.	Pericarp thickness (mm)	14.85	263
14.	Fruit firmness (kg/cm^2)	0.00	0
15.	Number of fruits per plant	17.40	308
16.	Leaf curl virus incidence	10.51	186
17.	Fruit yield per plant (kg)	3.45	61

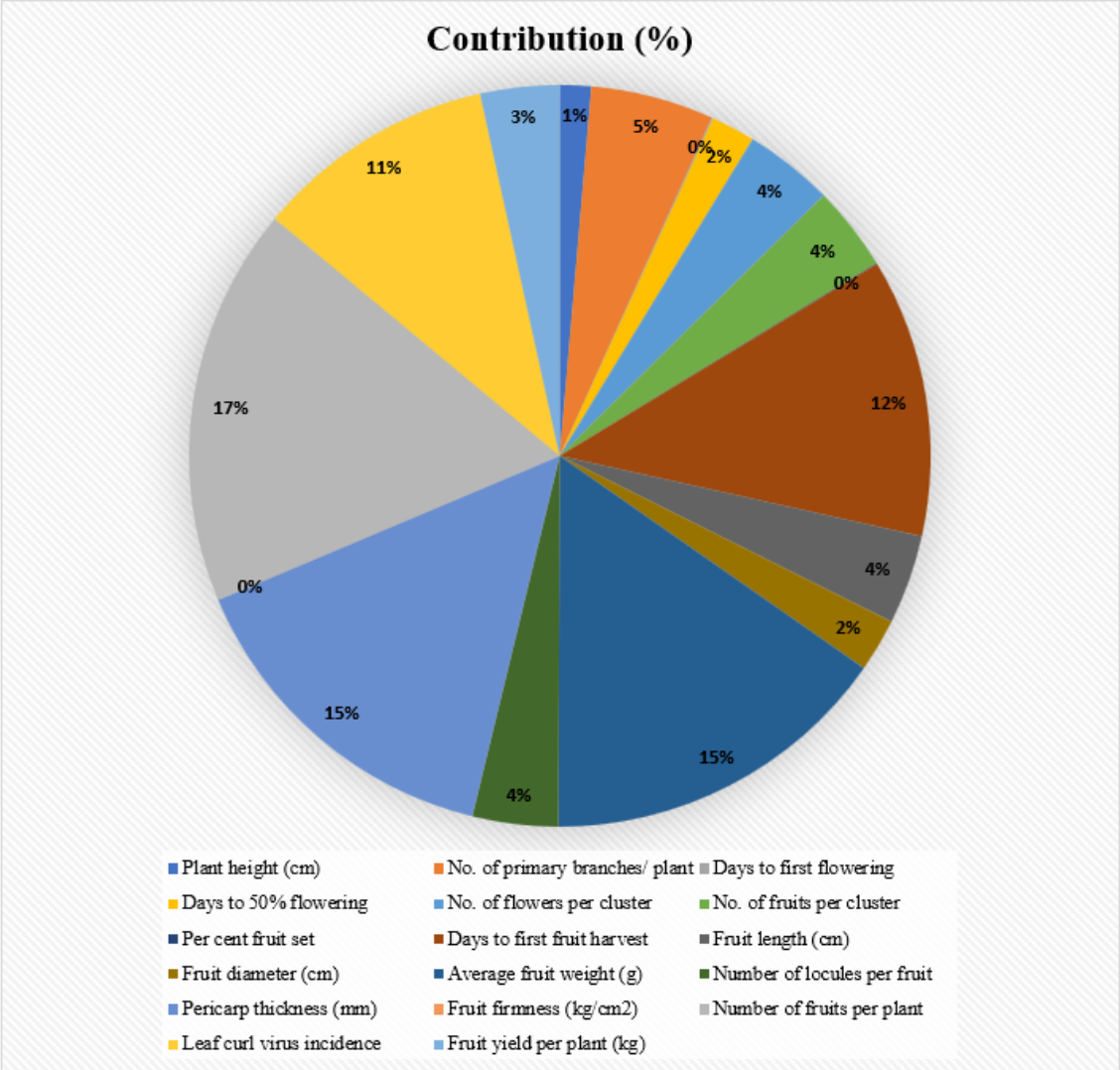

Fig. 1. Contribution of traits towards divergence in tomato.

CONCLUSIONS

The genetic diversity was measured using Mahalanobis D2 statistics for characters, and the clustering of genotypes resulted in the development of eleven groups. Clusters IX and X had the greatest inter-cluster distance (47564.45), followed by clusters II and X (44457.03). Cluster II and Cluster V had the shortest inter-cluster distance (9988.90). Among the features,

the number of fruits per plant (17.40%) and average fruit weight (15.37%) contributed the most to divergence. As a result, the breeder selects genotypes of clusters as parents that have a large inter-cluster distance between them in order to create recombinants and desirable segregates in the crop improvement plan. Maximum percent contribution was observed for no of fruit/plant followed by average fruit weight, pericarp thickness,) days to first fruit harvest, leaf curl virus incidence, no of primary branches/plant and no of flowers/cluster.

FUTURE SCOPE

The identified superior general combiners can be used in future breeding programmes. Selected parents with desirable *per se* performance and combining ability effects in respect of different component traits can be involved in multiple crossing scheme to recombine different productivity components.

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Conflict of Interest. None.

REFERENCES

Depra, M. S., Delaqua, G. C., Freitas, L. and Cristina, M. (2014). Pollination deficit in open field tomato crops (*Solanum lycopersicum* L.) in Riode Janeiro State, Southeast Brazil. *Journal of Pollination Ecology, 12*(1), 1-8.

Kathimba, F. K, Kimani, P. M, Narla, R. D. and Kiriika, L. M. (2022). Heterosis and combining ability for related traits in tomato. *African Crop Science Journal, 30,* 109-125.

Kumar, P. A., Reddy, K. R., Reddy, R. V. S. K., Pandravada, S. R., & Saidaiah, P. (2016). Genetic divergence studies in tomato genotypes. *The Bioscan, 7*, 2097-24.

Kumar, S. (2020). Estimation of genetic variability and divergence for fruit yield and quality traits in tomato (*Lycopersicon esculentum*). *Universal Journal of Plant Science, 1*(2), 27-36.7(3), 148.

Lekshmi, S. L. and Celine, V. A. (2020). Evaluation of tomato hybrids for fruit, yield and quality traits under polyhouse conditions. *International Journal of Applied and Pure Science and Agriculture, 1*(7), 58-64.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of National Institute of Sciences (India), 12*, 49-55.

Nalla, Manoj, Rana, Mahesh, Singh, Senjam, Sinha, Anjan, Reddy, P., Mohapatra and Priyadarshani (2014). Assessment of genetic diversity through D^2 analysis in tomato (*Solanum lycopersicon* L), *6*, 2028-9324.

National Horticulture Board (2020 – 2021). Ministry of Agriculture and Farmers welfare. Gurgoan. Annual reports.

Rao, C. R. (1952). Advanced Statistical Methods in Biometric Research. John Wiley Sons, New York, 390p

Robertson, Larry & Labate Joanne (2006). Genetic Resources of Tomato (*Lycopersicon esculentum* Mill.) and Wild Relatives. 10.1201/b10744-3.

Sekhar, L., Prakash, B. G., Salimath, P. M., Sridevi, O. and Patil, A. A. (2008). Genetic diversity among some productive hybrids of tomato (*Lycopersicon esculentum* Mill). *Karnataka J. Agric. Sci., 21*(2), 264-265.

Thamburaj, S. and Singh, N. (2013). Tomato. In: Vegetables, tuber crops and spices. ICAR publishers, New Delhi pp. 10-28.

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