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Genetic Diversity for Selection of Diverse Genotypes for Hybrid Breeding in Tomato (*Solanum lycopersicum* L.)

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ABSTRACT: An experiment was carried in tomato by using D^2 analysis, the 23 genotypes were grouped into ten clusters. Based on the intra cluster distance, the intra cluster III had the maximum D^2 value (102.28). Highest inter cluster generalized distance (597.76) was between cluster X and VIII indicating wider genetic diversity between these groups. The character number of fruits per plant contributed maximum (28.06 %) towards diversity by taking 71 times first ranking followed by ascorbic acid (16.60%) by 42 times. The remaining traits *viz*., days to first flowering, days to 50 % flowering, days to first harvest, days to last harvest and average fruit weight did not contribute to the total divergence. The genotypes performance and its characters with maximum contribution towards divergence should also be given due consideration, which appears as desirable in further crop improvement. Assessment of divergence in the germplasm is essential to know the spectrum of diversity so that improvement in fruit yield can be normally attained through involvement of the genetically diverse parents in breeding programmes.

Keywords: Cluster analysis, Inter cluster, Intra cluster, D^2 statistics, Genetic diversity, Tomato, Genotypes.

INTRODUCTION

One of the important vegetable is tomato (*Solanum lycopersicum* L.) grown throughout the world for fruit yield. It belongs to Solanaceae family and its origin in the Peru-Ecuador-Bolvia area of the Andes (South American) (Vavilov, 1951). It is an important vegetable crop, which ranks next to potato in the world. Due to its high consumption rate in developed as well as developing countries, it is often referred to as a luxury crop. It is rich source of dietary fiber, vitamins A, C, minerals and antioxidants like lycopene (Frusciante *et al*. 2007). It is considered as a protective food because it contains of plenty of minerals, vitamins and organic acids (Hari, 1997). Tomato is one of the rich sources of lycopene, which imparts red colour to ripe tomatoes, reported to possess anti-cancerous properties (Bhuvaneswari and Nagini 2005).

The D^2 statistics concept was developed by P.C. Mahalonobis (1936). Assessment of genetic diversity among the different genotypes plays a vital role to select better genptypes. Keeping the above in view the importance of new varietal development, the promising germplasm collected from various sources was studied for genetic divergence.

MATERIAL AND METHODS

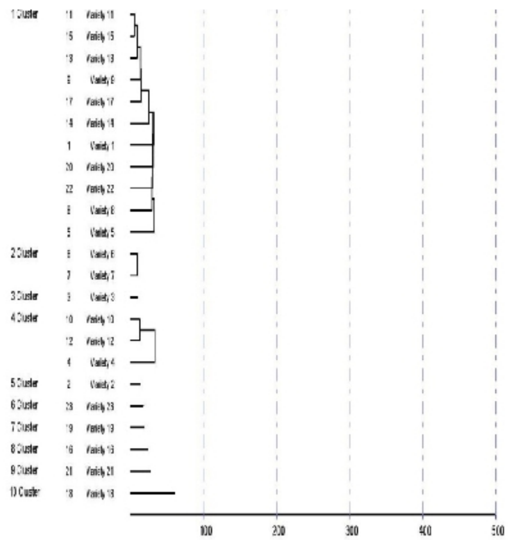
An experiment was carried in tomato (*Solanum lycopersicum* L.) at P.G Research Farm, College of Horticulture, SKLTSHU Rajendranagar, Hyderabad during *kharif*, 2018. It was laid out with twenty three genotypes of tomato in Randomized Block Design (RBD) with three replications maintaining a spacing of 60 × 45cm per replication. The observations were recorded on five randomly selected plants per replication for each genotype on fifteen characters *i.e.* plant height (cm), number of primary branches per plant, days to first flowering, days to 50% flowering, days to first fruit harvest, days to last fruit harvest, number of fruits per plant, fruit length (cm), fruit width (cm), average fruit weight (g), fruit yield per plant (kg), ascorbic acid (mg/100g), total soluble solids (ºBrix), lycopene content (mg/100g) and beta-carotene (mg/100g). The estimated of genetic diversity following Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Tocher (Rao 1952) suggested that the genotypes were grouped into clusters, based on D^2 values. Intra and inter cluster distances were calculated by the methods given by Singh and Chaudhary (1985).

RESULTS AND DISCUSSION

The quantitative assessment of genetic divergence of yield and its contributing characters was assessed by adopting D^2 Mahalonobis statistic.

A. Grouping of genotypes into different clusters (D^2 analysis)

Clustering of 23 genotypes under study is presented in Fig. 1. The D^2 values between any two genotypes was calculated as the sum of squares of the differences between the mean values of all the fifteen characters and used for the final grouping of the genotypes. Procedure suggested by Tocher (Rao 1952) has been used to group 23 genotypes into ten clusters by treating the estimated D^2 values as the square of the generalized distance. Based on D^2 values, the 23 genotypes were grouped into ten highly divergent clusters (Table 1). Few of the genotypes were so divergent in all the characters; hence each single genotype formed a separate cluster. Thus seven clusters *viz.*, III (Pant bahar), V (PKM-1), VI (AVTO-0101), VII (EC-620503), VIII (EC-620422), IX (AVTO-9804) and X (EC-631379) were solitary with one genotype in each cluster. The remaining three clusters were having maximum number of genotypes. Cluster I was biggest with eleven genotypes *viz.*, EC-620398, EC-620394, EC-620406, EC-620378, EC-631369, EC-620427, Pusa ruby, AVTO-9803, AVTO-1002, AVTO-1219 and EC-615055 followed by Cluster IV with 3 genotypes *viz.*, EC-620382, EC-620395 and Arka vikas then by Cluster II with 2 genotypes EC-620463 and EC-620428.



Variety1-Pusa Ruby, Variety2-PKM-1, Variety3-Pant bahar, Variety4-ArkaVikas, Variety5- EC-615055, Variety6- EC-620463, Variety7- EC-620428, Variety 8- AVTO-1219, Variety9-EC-620378, Variety10-EC-620382, Variety11-EC-620389, Variety 12-EC-620395, Variety13-EC-620406, Variety14-EC-620427, Variety15-EC-620394, Variety16-EC-620422, Variety17-EC-631369, Variety18-EC-631379, Variety19-EC-620503, Variety20-AVTO-9803, Variety21- AVTO-9804, Variety 22- AVTO- 1002, Variety23-AVTO-0101

Fig. 1. Dendrogram showing clustering pattern for divergence of 23 tomato genotypes.

Table 1: Clustering pattern of twenty three genotypes of tomato by Tocher's method.

Cluster	Number of genotypes	Genotypes
I	11	EC-620389, EC-620394, EC-620406, EC-620378, EC-631369, EC-620427, Pusa Ruby, AVTO-9803, AVTO-1002, AVTO-1219, EC-615055
II	2	EC-620463, EC-620428
III	1	Pant bahar
IV	3	EC-620382, EC-620395, Arka vikas
V	1	PKM-1
VI	1	AVTO-0101
VII	1	EC-620503
VIII	1	EC-620422
IX	1	AVTO-9804
X	1	EC-631379

B. Cluster means of characters in cluster

The cluster means for the fifteen characters studied among tomato genotypes revealed considerable differences among them (Table 2). From the present study, it was evident that plant height was highest in cluster X (133.63 cm) and lowest in cluster VI (74.17 cm). Maximum number of primary branches was recorded in cluster X (8.13) whereas, minimum was recorded in cluster VI (4.03). The cluster IV had the early days to first flowering (29.92 days) followed by cluster III (30.02 days) whereas, cluster III had the early days to 50% flowering (32.80 days) followed by cluster V (35.51 days) whereas, cluster IX with more days to 50% flowering (44.50 days). The genotypes of cluster IV (70.27) have taken less number of days to first harvest followed by cluster III (71.27), while the genotype of cluster IX showed more number of days to first fruit harvest (82.90). Highest number of days taken to last fruit harvest was recorded in the genotypes of cluster III (133.07) followed by cluster IV (132.61). The lowest mean value was observed in cluster VIII (109.07). Number of fruits per plant was maximum in cluster X (48.63) and minimum in cluster VIII (14.47). The maximum fruit length was recorded by the genotype EC-620503 of cluster VII (5.34 cm) followed by cluster II (5.17 cm) whereas, minimum value was recorded in the genotype of cluster III (3.13 cm) followed by cluster IX (3.68 cm). The genotype of cluster VII registered more fruit width (5.94 cm) followed by cluster II (5.34 cm), while the genotype of cluster III (3.48 cm) observed less fruit width followed by cluster IX (4.14 cm). Average fruit weight was highest in cluster VII (87.15 g) and lowest in cluster III (34.43 g). Fruit yield per plant was highest in cluster II (2.28 kg) and lowest in cluster VIII (1.04kg). Ascorbic acid content was maximum in cluster X (36.11 mg/100g of fruit) and minimum value in cluster VI (19.37 mg/100g of fruit). The genotype of cluster X had maximum TSS value (7.47°Brix), whereas genotypes of the cluster II (3.69^{o}Brix) have minimum TSS. Lycopene content was maximum in cluster V (3.96 mg/100g of fruit) and minimum value in cluster IX (2.31 mg/100g of fruit), Beta-carotene content was highest in cluster VIII (2.16 mg/100g of fruit) and lowest in cluster II (1.00). Cluster mean values showed a wide range of mean values among the characters studied indicating presence of wide variation among the genotypes studies (Aveen *et al.*, 2018); Anuradha *et al*. (2020) in tomato and Chandrasekhar *et al*. (2018); Saidaiah *et al*. (2010, 2011); Pidigam *et al*. (2019) in other crops reported the similar kind of results.

Table 2: Mean values of clusters for fifteen characters in twenty three tomato genotypes.

Cluster	Plant height (cm)	No of primary branches per plant	Days to first flowering	Days to 50% flowering	Days to first fruit harvest	Days to last fruit harvest	No of fruits per plant	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	Fruit yield/plant (kg)	Ascorbic Acid content (mg/100g)	TSS (^{0}Brix)	Lycopene (mg/100g)	Beta-carotene (mg/100g)
I	85.38	5.01	34.43	37.68	73.95	118.33	22.64	4.57	4.77	64.73	1.44	27.32	4.08	3.09	1.68
II	85.53	5.50	35.17	39.78	74.03	127.10	27.90	5.17	5.34	81.78	2.28	34.08	3.60	2.50	1.00
III	83.23	5.67	30.02	32.80	71.27	133.07	37.10	3.13	3.48	34.43	1.27	23.56	4.00	2.89	1.70
IV	109.49	7.33	29.92	35.51	70.27	132.61	47.63	3.91	4.31	42.73	2.01	30.89	4.60	3.61	1.42
V	86.07	6.20	33.03	39.30	77.47	128.73	34.78	4.07	4.34	45.90	1.60	26.05	5.20	3.96	1.68
VI	74.17	4.03	36.73	41.17	71.90	116.13	26.27	4.74	4.89	73.55	1.92	19.37	4.80	3.67	1.19
VII	96.47	6.67	35.63	38.43	74.93	124.13	24.23	5.34	5.94	87.15	2.10	35.70	4.90	2.26	2.05
VIII	86.43	4.87	31.67	42.00	74.07	109.07	14.47	4.94	4.30	72.44	1.04	20.69	4.63	2.96	2.16
IX	102.97	5.60	42.33	44.50	82.90	117.90	25.77	3.68	4.14	48.01	1.24	33.73	4.23	2.31	1.46
X	133.63	8.13	35.00	39.90	74.07	130.80	48.63	4.68	4.25	45.32	2.20	36.11	7.47	3.45	1.55

C. Average intra and inter cluster distances

The mean intra and inter cluster D^2 values among the ten clusters are given in the Table 3 (Fig. 2). The intra cluster D^2 values ranged from nil (Cluster III, V, VI, VII and VIII, IX, X) to 102.28 (Cluster III). The cluster III had the maximum D^2 value (102.28) followed by Cluster I (83.88) and Cluster II (25.78). The inter cluster D^2 values of the ten clusters revealed that highest inter cluster generalized distance (597.76) was between cluster X and VIII followed by cluster X and VI (485.59), while the lowest (67.39) was between cluster VI and cluster V. The inter cluster distance was minimum between cluster VI and V indicating narrow genetic diversity, whereas maximum recorded between clusters X and VIII indicating wider genetic diversity between these groups. Similar findings are reported by Reddy *et al*. (2013); Nitish Kumar *et al*. (2017); Patel *et al*. (2017); Naveen *et al.* (2018); Anuradha *et al*., 2020 in tomato.

Table 3: Average intra (bold) and inter-cluster D^2 values for ten clusters in twenty three genotypes of tomato.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**83.88**	182.00	118.72	258.37	103.20	108.69	158.04	121.37	141.86	458.63
II		**25.78**	237.25	170.66	222.46	214.65	132.70	408.51	162.53	362.56
III			**0.00**	162.10	75.75	143.88	258.98	197.42	176.53	428.15
IV				**102.28**	163.32	283.33	237.08	466.43	244.53	217.74
V					**0.00**	67.39	207.78	159.18	164.27	299.23
VI						**0.00**	285.84	164.85	234.83	485.59
VII							**0.00**	236.76	123.01	277.65
VIII								**0.00**	227.55	597.76
IX									**0.00**	312.36
X										**0.00**

* Bold diagonal values indicate intra cluster distance, rest of the values show the inter cluster distances

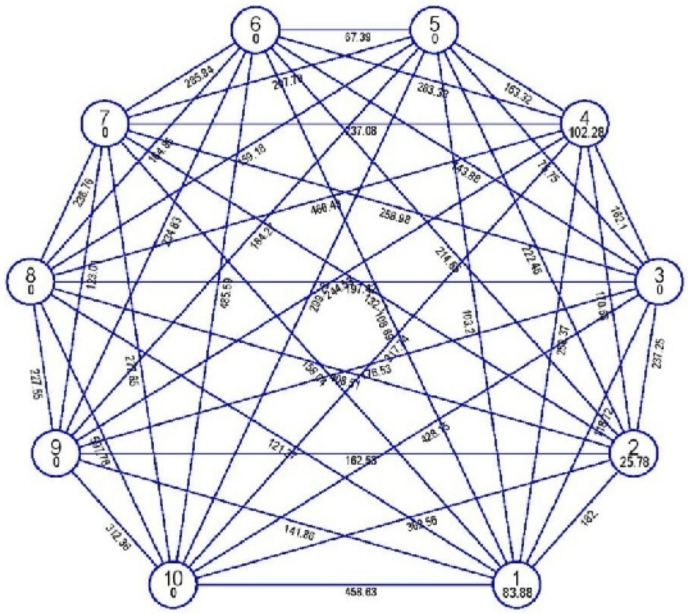


Fig. 2. Cluster diagram showing average intra and inter-cluster D^2 values of tomato genotypes.

D. Relative Contribution of different characters towards divergence

Number of times each of fifteen traits appeared in first rank and its respective percent contribution towards genetic divergence are presented in Table 4. The results showed that the number of fruits per plant contributed maximum (28.06 %) towards diversity by taking 71 times first ranking followed by ascorbic acid (16.60%) by 42 times, lycopene content (14.23%) by 36 times, total soluble solids (13.44%) by 34 times, beta-carotene (11.86%) by 30 times, fruit yield per plant (9.49%) by 24 times, number of primary branches per plant (2.77%) by 7 times, fruit length (2.37%) by 6 times, plant height (0.79%) by 2 times, fruit width (0.4%) by one time. In contrast, the remaining traits *viz*., days to first flowering, days to 50 per cent flowering, days to first fruit harvest, days to last fruit harvest and average fruit weight did not contribute to the total divergence. Apart from the high divergence, the performance of the genotypes and the characters with maximum contribution towards divergence should also be given due consideration which appears as desirable for inclusion in tomato improvement. Similar results are reported in tomato Khaidem *et al*. (2014); Meena and Bahadur (2015); Sunil *et al*. (2015); Ullah *et al*. (2015); Amarjeet *et al*. (2017); Naveen *et al*. (2018); Chandrasekhar *et al*. (2018) Anuradha *et al*. (2020); Saidaiah *et al*. (2010, 2011); Pidigam *et al*. (2019) in other crops.

Table 4: Percent contribution of different characters towards genetic divergence in twenty three genotypes of tomato.

Sr. No.	Source	Times ranked 1st	Contribution (%)
1.	Plant height (cm)	2	0.79
2.	Number of primary branches per plant	7	2.77
3.	Days to first flowering	0	0.00
4.	Days to 50% flowering	0	0.00
5.	Days to first fruit harvest	0	0.00
6.	Days to last fruit harvest	0	0.00
7.	Number of fruits per plant	71	28.06
8.	Fruit length (cm)	6	2.37
9.	Fruit width (cm)	1	0.40
10.	Average fruit weight (g)	0	0.00
11.	Fruit yield/plant (kg)	24	9.49
12.	Ascorbic acid content (mg/100g)	42	16.60
13.	TSS (°Brix)	34	13.44
14.	Lycopene content (mg/100g)	36	14.23
15.	Beta-carotene (mg/100g)	30	11.86

CONCLUSION

While maximum intra cluster distance was recorded in cluster IV and this might be due to limited gene exchange or selection practices among the genotypes for diverse characters. The maximum inter cluster distance was observed between cluster X and VIII are farthest, indicating wider genetic diversity. Hence, they should be selected for making cross combinations to deliver heterotic crosses to exploit yield.

FUTURE SCOPE

The present experiment would help in creating a base line for future work. Selection of parents from these diverse clusters for hybridization programme would help in achieving novel recombinants.

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Conflict of Interest. None.

REFERENCES

Amarjeet, K. R., Amit, V., Manish, K., Meenu, G., & Dogra R. K. (2017). Genetic divergence and its implication in breeding tomato (*Solanum lycopersicum*) suitable for mid-hills of Himachal Pradesh. *Indian Journal of Agricultural Sciences*, *87*(5): 657–662.

Anuradha, B., Saidaiah, P., Harikishan S., Geetha, A., & Ravinder R. K. (2020). Genetic divergence for yield and yield attributes in tomato (*Solanum lycopersicum* L.). *Green Farming*, *11*(4-5): 293-298

Bhuvaneswari, V. & Nagini, S. (2005). Lycopene: a review of its potential as an anticancer agent. *Current Medicinal Chemistry Anti-Cancer Agents*, *5*(6): 627-635.

Frusciante L, Carli P, Ercolano M. R, Pernice R, Di Matteo A, Fogliano V. & Pellegrini, N. (2007). Antioxidant nutritional quality of tomato. *Molecular nutrition & food research*, *51*(5): 609-617.

Hari, H. R. (1997). Vegetable Breeding Principles and Practices, *Kalyani Publications*. India.

Khaidem, M. M., Bora, G. C., Senjam, J. S. & Anjan, K. S. (2014). Morphology based genetic variability analysis and identification of important characters for Tomato (*Solanum lycopersicum* L.). *American-Eurasian Journal Agriculture & Environmental Science*, *14* (10): 1105-1111.

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

Meena, O. P. & Bahadur, V. (2015). Breeding potential of indeterminate tomato (*Solanum lycopersicum* L.) accessions using D^2 analysis. *Sabrao Journal of Breeding and Genetics*, *47*(1): 49-59.

Naveen, B. L, Ravinder R. K. & Saidaiah, P. (2018). Genetic divergence for yield and yield attributes in tomato (*Solanum lycopersicum* L.). *Indian Journal of Agricultural Sciences*, *88*(7): 1018-1023.

Nitish Kumar, Bhardwaj, M. L., Sharma, A. & Kumar, N. (2017). Assessment of Genetic Divergence in Tomato (*Solanum lycopersicum* L.) through Clustering and Principal Component Analysis under Mid Hills Conditions of Himachal Pradesh, India. *International Journal of Current Microbiology and Applied Sciences*, *6*(5): 1811-1819.

Patel, P., Udit, K., Thakur, G. & Pankaj, K. M. (2017). Assessment of genetic diversity through D^2 analysis in tomato (*Solanum lycopersicum* L.). *Bulletin of Environment, Pharmacology and Life Sciences*, *6*(1): 219-224.

Rao, C. R. (1952). Advanced statistical methods in biometrical research. *Jhon Wiley and Sons*, Inc. New York. 357–363.

Reddy, B. R., Reddy, M. P., Begum, H. & Sunil, N. (2013). Genetic diversity studies in tomato. *Journal of Agriculture and Veterinary Science*, *4*(4): 53-55.

Pidigam, S., Suchandranath, B. M., Srinivas, N., Narshimulu, G., Srivani, S. A., Hari, Y., Lavanya, B., & Geetha, A, (2019). Assessment of genetic diversity in yardlong bean (*Vigna unguiculata* (L.) Walp subsp. sesquipedalis Verdc.) germplasm from India using RAPD markers. *Genetic Resouces and Crop Evolution*, *66*: 1231–1242.

Saidaiah, P., Ramesha, M. S., Sundaram, R. M. & Hari, Y. (2010). Molecular profiling of parents of some released rice hybrids using SSR markers. *Indian Journal of Plant Genetic Resources*, *23*(3): 269-273.

Saidaiah, P., Kumar, S. S., & Ramesha, M. S. (2010). Variability for yield and yield component attributes in rice. *Crop Research (Hisar)*, *39*(1/2/3): 91-93.

Saidaiah, P., Ramesha, M. S., Suresh, J., Sudheer, K. S. & Geetha, A. (2011). Genetic divergence among maintainers and restorer lines of rice. *Oryza - An International Journal on Rice*, *4*(48): 283-287.

Chandrashekhar T., Vijaya, M., Saidaiah, P., Joshi, V. & Pandravada, S. R. (2018). Genetic variability, heritability and genetic advance for yield and yield attributes in bottle gourd (*Lagenaria siceraria* (mol) Standl.) germplasm. *Journal of Pharmacognosy and Phytochemistry*, *7*(6): 2085-2088.

Singh, R. K. & Chaudhary, B. D. (1985). Biometrical methods in quantitative genetic analysis. *Kalyani Publishers, New Delhi*, 239-266.

Sunil, P., Raghuwanshi, O. & Avtar, S. D. (2015). Genetic divergence studies for fruits yield and quality components in diverse tomato (*Solanum lycopersicum* L.) genotypes. *The Ecoscan- An International Quarterly Journal of Environmental Sciences*, *7*.

Ullah, M. Z., Hassan, L., Sonia, B. S. & Patwary, A. K. (2015). Variability and inter relationship studies in tomato (*Solanum lycopersicum* L.). *Journal of Bangladesh Agricultural University*, *13*(1): 65–69.

Vavilov, N. I. (1951). The origin, variation, immunity and breeding of cultivated plants. *Chronica Botany*, *13*: 1-366.

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