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Estimation of genetic divergence among indigenous and exotic accessions of tomato (*Solanum lycopersicum* L.)

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Thirty genotypes of tomato, both indigenous and exotic were tested for the presence of diversity on the basis eighteen yield and quality traits. Mahalanobis's D^2 analysis was employed to estimate the distances between and within the clusters formed from the test genotypes. Ten clusters were formed using Tocher's method. Cluster I, III and X were having 16, 3 and 2 genotypes, respectively, rest of the seven clusters were solitary and having single genotype each. The highest inter-cluster distance was found between clusters IV and X whereas lowest distance was observed between cluster VI and VIII suggested a closer relationship between these clusters and low degree of diversity among the genotypes. The maximum contribution towards divergence was accounted by plant height, seed index and yield per plant (~15% each) followed by fruits per plant, juice-pulp ratio, pericarp thickness and flowers per cluster. Results also revealed that there was no association between clustering pattern and eco-geographical distribution of genotypes. On the basis of the divergence study the genotypes could be selected from the most divergent clusters for hybridization and further selection programme.

Key words : Diversity, Divergence, D^2 analysis, Tomato

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INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the economically important crops from the solanaceae family. Due to its wider adaptability and good yield potential it is grown on a commercial scale in most of the part of the world and in India. It is mostly used for fresh consumption as vegetable in various cuisines as well as on a very large scale in food processing industries for preparation of sauce, ketchup, soup etc. India stands second in production of tomato after China (FAOSTAT, 2013). Presence of genetic variability in the population for different traits is the prerequisite for the genetic improvement of this crop. The variability present among different genotypes of a species is known as genetic diversity. One of the powerful techniques for assessing genetic divergence is the D^2 – statistic proposed by P.C. Mahalanobis in 1928. This technique measures the forces of differentiation at two levels, namely, intra-cluster and inter-cluster levels, and thus helps in the selection of genetically divergent parents to be ordered in hybridization programme. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse genotype / origin generally display a greater heterosis than those between closely related strains. In addition to aiding in the selection of divergent parents for hybridization, D^2 – statistic also measures the degree of diversification and determines the relative proportion of each component character to the total divergence.

Genetic divergence studies between cultivars or accessions before any crossing programme would allow the breeder to concentrate efforts on those combinations which are more likely to be highly heterotic when different metric characters are avaible concerning a set of accessions. Mahalanobis's D^2 statistic based on multiple characters have been an efficient statistical tool for assessing genetic divergence among a set of genotypes which could be used for hybridization and thus the diverse genotypes incorporated in hybrids on selfing may be expected to throw desirable segregates with the accumulation of favorable genes into a single genetic background.

RESEARCH METHODOLOGY

The present study was carried out to evaluate the 30 germplasm lines (both indigenous and exotic) of tomato obtained from various sources including Indian Institute of Vegetable Research, Varanasi, U.P., India and National Bureau of Plant Genetic Resources, New Delhi, India with respect to yield and quality attributes. All the genotypes were grown in an experiment in Randomized Block Design with three replications in post-rainy season of 2012 at Vegetable Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (U.P.), India. Nursery was planted in second week of August and about 4 week old seedlings were transplanted during second week of September with row-to-row × plant-to-plant spacing maintained at 60 cm × 45 cm. Each plot consisted of 10 plants and represents a single entry in each replication. Standard agronomic practices were followed to raise a good crop.

Data were collected on eighteen yield and quality traits. Observations on days to first flowering, day to 50 per cent flowering and days to 50 per cent fruiting was taken on plot basis. Five plants, excluding border plants, were randomly selected for recording of data on various yield and fruit quality traits such as number of primary branches, number of secondary branches, plant height (cm), clusters per plant, flowers per cluster, fruits per cluster, fruits per plant, pericarp thickness (mm), locule number per fruit, average fruit weight (g), fruit shape index, juice-pulp ratio, total soluble solids and fruit yield per plant (kg). The data on total soluble solids was transformed using arc-sine transformation and transformed values were used for the data analysis. D^2 analysis of the data was done with Plant Breeding and Genetics programme of the software Windostat® ver. 8.5 for statistical data analysis. The genotypes were grouped into different clusters with the help of Tocher's method. Intercluster and intracluster distances and contribution of each trait towards total divergence among genotypes under investigation were estimated using Mahalanobis's D^2 analysis.

RESEARCH FINDINGS AND ANALYSIS

The simultaneous testing of significance of difference in mean value between thirty genotypes based on Wilk's lambda criterion (Λ) revealed highly significant differences (x^2 = 1684.559 with 522 d.f.) among the genotypes for the aggregate of the eighteen characters considered. Hence, genotypes were classified into different groups on the basis of the traits studied.

Cluster pattern :

The 30 genotypes were grouped in 10 clusters following Tocher's method (Table 1). Cluster I constituted of 16 genotypes and was the largest one followed by cluster III consisting of 5 genotypes. Cluster X was consisted of 2 genotypes, whereas rest of the seven clusters (cluster II, IV, V, VI, VII, VIII and IX) were solitary, *i.e.* consisted one genotype each. The average intra- and inter-cluster distances were calculated and presented in Table 2. The maximum intra-cluster distance was found in cluster X followed by cluster III and cluster II. The most divergent clusters indicated highest inter-cluster distance which was found between clusters IV and X, whereas lowest distance was between cluster VI and VIII suggested a closer relationship between these two clusters and low degree of diversity among the genotypes.

Table 1 : Distribution of 30 genotypes of tomato into different clusters by Tocher's method

Cluster	No. of genotypes in cluster	Genotype
I	16	EC - 20510
		EC - 538148
		EC - 538422
		EC - 62025
		EC - 620530
		EC - 620536
		EC - 620538
		EC - 620578
		Co-3
		H-86
		Kajela
		Kashi Amrit
		Kashi Sharad
		PM-1
		Punjab Upama
		Superbug
II	1	EC - 620541
III	5	EC - 538419
		Azad T-5
		DT-10
		Selection-7
		Shalimar-2
IV	1	Pant T-3
V	1	EC - 168283
VI	1	Angurlata
VII	1	Swarna Naveen
VIII	1	EC - 538408
IX	1	EC - 538423
X	2	EC - 538380
		EC - 538455

Cluster means :

A comparison of the mean values for eighteen characters of different clusters has been presented in Table 3. Cluster means showed considerable differences among the clusters.

Cluster I containing 16 genotypes were characterized by genotypes/cultivars having moderate values for most of the characters. Cluster II having single genotype and was characterized by late flowering genotypes, *i.e.* having highest value for days to first flowering. Cluster II was having highest mean values for seed index and total soluble solids content and minimum values of number of primary branches, locule number and juice-pulp ratio. Cluster III comprising 5 genotypes was characterized by lowest mean for days to 50 per cent flowering, fruits per plant and seed index. Cluster IV was solitary cluster, which can be characterized by highest mean value for juice-pulp ratio and lowest values for days to first flowering, days to 50 per cent fruiting, plant height, fruits per cluster, fruit shape index and total soluble solids. Maximum number of primary branches, secondary branches and highest mean value for plant height was the characteristic of the cluster V which consisted of single genotype. This cluster also exhibited minimum number of clusters per plant along with lowest values for pericarp thickness, average fruit weight and minimum fruit yield per plant. Cluster VI, which was also a solitary cluster, was characterized by maximum locule number, highest average fruit weight and highest yield per plant, whereas this cluster also exhibited minimum value for juice-pulp ratio which was same as cluster II. Another solitary cluster *i.e.* cluster VII exhibited genotype with late flowering and fruiting owing to highest values for days to first flowering, days to 50 per cent flowering and days to 50 per cent fruiting. This cluster was also having highest value for fruit shape index, whereas a minimum number of flowers per cluster and locules was observed in this cluster. Maximum thickness of pericarp was the characteristic feature of the genotype present in cluster VIII. A maximum number of flowers per cluster and minimum number of secondary branches was recorded for cluster IX which was also having single genotype. Cluster X consisted of 2 genotypes and having maximum mean values for clusters per plant, fruits per cluster and fruits per plant. For yield improvement genotype contained in cluster VI which exhibited highest yield per plant would be promising if taken for hybridization programmes.

Contribution of traits in divergence :

The contribution of different characters towards the expression of genetic divergence was calculated (Table 4) on the basis of number of first rank earned by every character out of 1 to 18 in each combination of genotypes (total no. of combination in present study were 435) during the calculation of D^2 values. Each character was ranked on the basis of $d_i = Y_i^j - Y_i^k$ values, where d_i represents the mean difference between the same character for two different genotypes and Y_i^j and Y_i^k represents the mean value of i^{th} character for genotype j and k. Rank 1^{st} was given to the highest mean difference and rank 18^{th} to the lowest mean difference. Per cent contribution was calculated by taking total number of combination as 100 per cent, *i.e.* 435 = 100 per cent. By the above stated method it was found that plant height, seed index and yield per plant (~15%) contributed maximum towards total divergence followed by fruits per plant, juice-pulp ratio, pericarp thickness and flowers per cluster. The contribution of plant height in divergence had been also observed by Rai *et al.* (1998) and Joshi and Kohli (2003), pericarp thickness by Rai *et al.* (1998), fruit yield and pericarp thickness by Sharma and Verma (2001), fruits per plant and average fruit weight by Mohanty and Prusti (2001) and locule per fruit and fruit yield by Mehta *et al.* (2007). The contribution of fruits per cluster to the divergence was found to be nil in the selected set of genotypes and the total soluble solids contributed minimum towards the total divergence. The contribution of various characters towards the expression of genetic divergence should be taken into account as a criterion for choosing parents for crossing programme for the improvement in such characters.

Table 2 : Intra and inter-cluster distance (D-value) of clusters formed with 30 genotypes of tomato

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	7.12	8.83	8.97	8.68	10.94	8.67	9.34	9.12	8.97	13.20
II		0.00	13.30	10.08	15.12	10.23	10.87	11.40	9.60	16.35
III			7.42	9.64	9.29	10.14	9.87	10.70	11.01	13.02
IV				0.00	14.52	7.52	13.17	10.77	12.17	17.05
V					0.00	13.62	7.66	13.81	11.59	10.90
VI						0.00	10.97	6.71	11.56	14.02
VII							0.00	10.98	9.34	9.53
VIII								0.00	10.37	11.97
IX									0.00	10.96
X										8.15

*Values shown as bold are intra-cluster distances.

*Intra-cluster distance as '0.00' is for solitary clusters.

Table 3 : Cluster means for eighteen yield attributes in 30 genotypes of tomato

Traits / Cluster	Days to first flowering	Days to 50% flowering	Days to 50% fruiting	Primary branches	Secondary branches	Plant height	Clusters/ plant	Flowers/ cluster	Fruits/ cluster	Fruits/ plant	Pericarp thickness	Locule number	Seed index	Average fruit weight	Fruit shape index	Juice-pulp ratio	Total soluble solids	Fruit yield / plant
I	40.46	47.85	60.63	3.41	6.04	77.29	4.63	5.10	3.37	28.04	0.52	2.99	0.30	38.14	1.02	0.63	12.38	1.28
II	49.00	56.00	67.33	2.73	3.77	62.35	4.37	4.53	3.81	35.00	0.49	2.00	0.36	43.00	1.08	0.43	13.52	1.63
III	38.20	45.93	57.13	3.56	7.03	85.86	4.51	4.91	3.16	26.74	0.45	3.17	0.19	36.67	0.92	0.81	12.34	1.20
IV	37.67	46.33	54.00	3.70	4.20	46.17	5.40	4.75	2.95	30.53	0.46	4.30	0.28	45.00	0.69	0.82	11.68	1.70
V	42.67	50.33	64.67	4.40	13.03	116.20	4.03	4.80	4.00	33.00	0.33	3.00	0.28	21.00	0.89	0.71	13.05	0.75
VI	38.00	49.00	56.67	3.90	5.50	72.45	5.30	4.50	3.94	41.00	0.52	4.40	0.27	71.67	0.77	0.43	12.34	3.20
VII	49.00	56.33	68.00	3.00	10.50	99.17	6.40	3.93	3.56	50.67	0.42	2.00	0.24	32.50	1.12	0.63	12.95	1.80
VIII	41.00	47.00	61.67	3.00	2.77	77.30	6.50	3.60	4.27	36.07	0.62	3.13	0.21	44.67	1.07	0.38	12.39	2.70
IX	42.00	49.67	66.67	3.27	2.43	68.67	4.53	8.85	4.84	33.52	0.44	2.33	0.20	46.67	0.98	0.44	12.00	1.55
X	41.00	48.67	62.17	3.23	5.53	106.47	6.83	7.73	5.12	54.64	0.55	3.08	0.22	39.83	0.94	0.70	12.70	2.18

Table 4 : Per cent contribution of each character toward the total divergence in 30 genotypes of tomato

Sr. No.	Characters	Number of times appearing first in the ranking	Per cent contribution
1.	Days to first flowering	19	4.37
2.	Days to 50% flowering	5	1.15
3.	Days to 50% fruiting	5	1.15
4.	Primary branches	2	0.46
5.	Secondary branches	4	0.92
6.	Plant height	68	15.63
7.	Clusters / plant	8	1.84
8.	Flowers / cluster	34	7.82
9.	Fruits / cluster	0	0.00
10.	Fruits / plant	42	9.66
11.	Pericarp thickness	38	8.74
12.	Locule number	13	2.99
13.	Seed index	65	14.94
14.	Average fruit weight	3	0.69
15.	Fruit shape index	26	5.98
16.	Juice-pulp ratio	39	8.97
17.	Total soluble solids	1	0.23
18.	Fruit yield / plant	63	14.48

It is observed from the clustering pattern (Table 1), that distribution of exotic and indigenous genotypes into clusters occurred randomly irrespective of their geographical origin. Similar type of results was obtained in the studies of Rai *et al.* (1998), Sharma and Verma (2001), Mohanty and Prusti (2001), Joshi and Kohli (2003) and Basavaraj *et al.* (2010). Murthy and Arunachalam (1966) showed that genetic drift and selection in different environments could cause greater diversity among genotypes than their geographical distances. So, selection of parental material for hybridization simply based on geographical diversity may not be rewarding. It could be inferred from the present study that genotypes showing greater divergence may be considered for utilization in crossing programme, irrespective their exotic or indigenous origin.

It is worthy to note that in calculating cluster mean, the superiority of a particular genotype with respect to a given character could be get diffused by other genotypes that are grouped in the same cluster but are inferior or intermediate for the character in question. Hence, apart from selecting genotypes from the clusters which have an increased inter-cluster distance for hybridization, one can also think of selecting parents based on the extent of divergence with respect to a character of interest within a cluster.

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