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Genetic Divergence and Cluster Analysis in Tomato (*Solanum lycopersicum* L.)

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Abstract A study was conducted on 44 genotypes of tomato collected to assess the value and magnitude of genetic divergence among the genotypes using Mahalanobis D^2 statistics. The results revealed wide genetic diversity among the 44 evaluated genotypes which were grouped into 9 clusters based on 12 important characters in tomato. The cluster VIII was the largest containing 9 genotypes followed by cluster 1 with 8 genotypes. The diversity among the cluster was measured by inter-cluster distance, highest being observed between cluster III and cluster VI (D^2 = 317.456) followed by cluster III and cluster V (D^2 = 299.872). Therefore, selection of divergent parents of tomato based on these cluster distances would be useful in formulating a comprehensive strategy to develop superior hybrids or better segregants in tomato. On the the basis of the present study, superior hybrids or variety (s) may be expected by crossing parents selected from cluster III (BT-12-2, BT-507-2-2, BT-506-1, BT-112-1, BT-508-1-1, Megha tomato and BT-21-2) with parents of cluster VI (BT-17-2 (5) and Utkal (Deepti).

Keywords *Solanum lycopersicum*, Clustering pattern, Genetic divergence, Mahalanobis D^2 statistics, Multivariate analysis.

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Introduction

Tomato (2n = 24) belonging to the family Solanaceae is an important vegetable crop of the world, which ranks next to potato in importance. Systematic study and evaluation of germplasm is of great importance for current and future agronomic and genetic improvement of the crop. Furthermore, if an improvement program is to be carried out, evaluation of germplasm is imperative, in order to understand the genetic background and breeding value of the available germplasm [1]. Landraces are often heterogeneous and composed of different genotypes which are mostly homozygous and usually exhibit considerable genetic variation for quantitative and qualitative characteristics [2]. Tomato crop has wider adaptability, high yielding potential and multipurpose uses in fresh as well as processed food industries. An improvement in yield and quality in self pollinated crops like tomato is normally achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridization. Mahalanobis D^2 multivariate analysis [3] treated as one of the most valuable tools for

Table 1. Clustering pattern of 44 tomato genotypes.

Cluster No.	Number of genotypes	Name of genotypes
I	8	BT-442-2, BT-437-1-2, BT-429-2-2, BT-413-1-2, BT-429-1-1, BT-215-3-3-1, BT-317 and BT-106
II	3	BT-22-4-1, BT-19-1-1-1 and BT-207-2
III	7	BT-12-2, BT-507-2-2, BT-506-1, BT-112-1, BT-508-1-1, Megha Tomato and BT-21-2
IV	6	BT-433-2-1, Arka Vikash, BT-17-2, BT-433-3-2, BT-18 and Utkal Pragyan
V	2	BT-21 and BT-17
VI	2	BT-17-2 (5) and Utkal Deepti
VII	2	BT-12-3-2 and Utkal Kumari
VIII	9	IIVR Sel-2, BT428-3, BT-306-1-2, BT-224-3-1, BT-305-2-4-2, BT-3, BT-101, Arka Saurabh and BT-136
IX	5	Utkal Pallavi, Utkal Urbashi, Utkal Raja, BT-218 and BMZ-21

obtaining quantitative estimates of genetic divergence between plant populations / biological populations. Moreover, grouping of different genotypes of a particular crop by adopting Tochers method will be more useful in choosing suitable parents for heterosis breeding. Therefore, an attempt was made in the present study to assess the nature as well as magnitude of genetic divergence and clustering pattern of 44 genotypes in tomato.

Materials and Methods

The experimental materials for the present study consisted of 44 genotypes of tomato provided by and evaluated under AICRP on Vegetable Crops, Orissa University of Agriculture and Technology, Bhubaneswar, Odisha during *rabi*, 2013. The experiment was laid out in the randomized block design with three replications at spacing of 60 cm × 45 cm. The crop was raised by adopting recommended package of practices uniformly. Observations were recorded from five randomly selected plants (excluding border rows) of each genotype in each replication, for twelve characters. Mean values of five plants were used for statistical analysis. The data of 44 genotypes of tomato were analyzed utilizing multivariate analysis (D^2 statistic) (Mahalanobis, 1936). The original measurements were transformed to standardized

Table 2. Intra (diagonal) and inter cluster average (D^2) corresponding D ($\sqrt{D^2}$) values (in parentheses) among groups.

	I	II	III	IV	V	VI	VII	VIII	IX
I	142.925 (11.955)	187.844 (13.706)	147.017 (12.125)	170.13 (13.043)	180.86 (13.448)	196.5 (14.018)	166.138 (12.889)	159.946 (12.647)	155.172 (12.457)
II		152.609 (12.354)	274.536 (16.569)	125.918 (11.221)	113.582 (10.657)	127.564 (11.294)	110.545 (10.514)	200.748 (14.169)	144.842 (12.035)
III			118.779 (10.899)	269.085 (16.404)	299.872 (17.317)	317.456 (17.817)	242.096 (15.559)	155.058 (12.452)	218.755 (14.790)
IV				67.759 (8.232)	39.907 (6.317)	46.487 (6.818)	74.82 (8.650)	233.199 (15.271)	98.591 (9.929)
V					19.374 (4.402)	24.653 (4.965)	64.409 (8.026)	249.621 (15.799)	92.361 (9.610)
VI						23.317 (4.829)	60.339 (7.768)	269.276 (16.410)	101.673 (10.083)
VII							23.963 (4.895)	163.357 (12.781)	92.251 (9.605)
VIII								133.485 (11.554)	189.085 (13.751)
IX									137.678 (11.734)

Table 3. Cluster wise mean values of 12 characters of tomato genotypes. Days to 50% flowering- (1), Plant height (2), Number of primary branches per plant (3), Number of bunches per plant (4), Number of fruits per bunch (5), Number of fruits per plant (6), Average fruit weight (7), Number of locules per fruit (8), Total soluble solids (9), Length of fruit (10), Girth of fruit (11), Fruit yield per plant (12). Figures in the parentheses indicate number of cultivars in a cluster, * and **indicate lowest and highest values respectively.

Character Cluster	1	2	3	4	5	6
I. (8)	70.554**	76.196	6.97**	15.274	4.768	39.729
II. (3)	65.096	48.725	5.457	15.227	4.519	39.195
III. (7)	66.021	86.516**	6.54	10.401*	4.351	29.055
IV. (6)	64.893	54.387	6.171	15.232	5.092	47.467
V. (2)	66.383	50.2	6.837	15.483	5.130**	51.072**
VI. (2)	65.598	45.6	5.818	15.978**	5.052	46.988
VII. (2)	64.528*	39.857*	4.74*	12.205	4.373	33.137
VIII. (9)	65.959	63.672	6.044	10.65	3.795*	24.497*
IX. (5)	65.745	58.251	6.471	12.331	5.079	37.569

Table 3. Continued.

Character Cluster	7	8	9	10	11	12
I. (8)	62.41	3.368	4.933	7.052	4.922	1.36
II. (3)	69.703	3.398	4.531	7.334	5.019	1.672**
III. (7)	56.534	3.544	5.135**	7.21	4.691	1.057
IV. (6)	49.071	2.702	4.32	7.284	4.438	1.292
V. (2)	46.21	3.195	4.043*	7.175	4.595	1.467
VI. (2)	34.118*	2.385*	4.797	5.957*	4.118*	1.09
VII. (2)	45.422	3.91	4.152	6.375	4.6	0.723*
VIII. (9)	74.097**	4.203**	4.476	7.629**	5.504**	1.034
IX. (5)	53.195	2.826	4.304	7.373	4.489	1.085

uncorrelated variables by pivotal condensation [4]. Grouping of genotypes into different clusters was carried out by adopting Tochers method [4] and the relative contribution of different characters towards total divergence was calculated [5].

Results and Discussion

On the basis of Mahalanobis D^2 analysis, 44 genotypes were grouped into 9 clusters (Table 1). Cluster VIII, the largest group included 9 genotypes followed by cluster I comprising of 8 genotypes, cluster III comprising of 7 genotypes, cluster IV having 6 genotypes, cluster IX with 5 genotypes and cluster II with 3 genotypes. Cluster V, VI and VII comprised of 2 genotypes each. When the clusters were compared for divergence, maximum inter-cluster distance was observed between clusters III and VI followed by III and V, clusters II and III, clusters VI and VIII (Table 2). Each of the clusters III, IV and VIII contained genotypes which originated from different eco-geographic regions of India. Moreover, the genotypes with BT as prefix were developed at AICRP on Vegetable Crops, OUAT, Bhubaneswar. But all such genotypes were distributed among divergent clusters. This indicated that geographic distribution and genetic divergence did not follow the same trend.

If genotypes possessing high genetic divergence are involved in hybridization programes, it is expected that more heterotic hybrids and transgressive segregants may be produced in segregating generations. Present results are in agreement with the findings of Veershety [6], Mahesh et al. [7] and Singh et al. [8]. It is evident from Table 2 that cluster V had the minimum intra-cluster distance (4.402) whereas

Table 4. Relative contribution of different characters to genetic divergence in tomato genotypes.

Names of characters	Number of times ranked 1st	Percent contribution
Days to 50% flowering	0	0.000
Plant height (cm)	237	23.939
Number of primary branches/plant	23	2.323
Number of bunches/ plant	62	6.263
Number of fruits/bunch	6	0.607
Number of fruits/plant	172	17.374
Average fruit weight (g)	167	16.869
Number of locules/fruit	126	12.727
Total soluble solids	35	3.535
Length of fruit (cm)	16	1.616
Girth of fruit (cm)	6	0.606
Fruit yield /plant (kg)	140	14.141
Total	990	100

maximum intra-cluster distance (12.354) was observed in cluster II.

Since improvement in yield and other related traits is a basic objective in any breeding program, cluster means for fruit yield plant^{-1} and its major components need to be considered for selection of parents. The cluster means of 12 quantitative characters for groups of tomato genotypes are presented in Table 3. Cluster I containing eight tomato genotypes showed the highest values in respect of days to 50% flowering (70.554) and number of primary branches plant^{-1} (6.97). Cluster II contains 3 tomato genotypes with highest value in yield plant^{-1} (1.672). Cluster III with 7 genotypes showed the highest values in plant height (86.516 cm) and TSS (5.135), where as lowest value in number of bunches plant^{-1} (10.401). Cluster V containing 2 genotypes, showed the highest values in respect of number of fruits bunch^{-1} (5.130) and number of fruits plant^{-1} (51.072).Cluster VI with two genotypes had the lowest values of average fruit weight (34.118), number of locules fruit^{-1} (2.385), length of fruit (5.957 cm) and girth of fruit (4.118 cm), whereas it had highest value in respect of number of bunches plant^{-1} (15.978). Cluster VIII containing 9 genotypes showed the lowest values in number of fruits bunch^{-1} (3.795) and in number of fruits plant^{-1} (24.497).Highest values of cluster VIII were observed in average fruit weight (74.097 g), number of locules fruit^{-1} (4.203), length of fruit (7.629 cm) and girth of fruit (5.504 cm).

The relative contribution of 12 quantitative traits to genetic divergence among the 44 genotypes of tomato have been presented in Table 4, by rank average of individual character over all 990 paired combinations. Among the yield contributing characters, the maximum contribution towards divergence was made by plant height (23.939%) followed by number of fruits plant^{-1} (17.374%). Rest of the characters contributing to divergence in descending order were average fruit weight (16.869%), yield plant^{-1} (14.141%), number of locules fruit^{-1} (12.727%), number of bunches plant^{-1} (6.263%), TSS (3.535%), number of primary branches plant^{-1} (2.323%), length of fruit (1.616%), number of fruit bunch^{-1} (0.607%) and girth of the fruit (0.606%). It was observed that in the character days to 50% flowering contribution to divergence was 0%.

Previous workers [6—8] had also obtained high contribution of plant height towards divergence. Average fruit weight was shown to have substantial contribution to divergence by several researchers [6, 8]. Singh et al. {8] corroborated the importance of number of fruits/plant while numerous researchers [7, 8] confirmed high contribution of fruit yield plant^{-1} towards divergence. The characters like plant height and number of fruits plant^{-1} will offer a good scope for improvement through selection and direct selection can be adopted effectively for achieving desirable results. In order to achieve high heterosis or superior recombinants in future, hybridization between genotypes in clusters III and VI or between clusters III and would be more desirable.

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