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GENETIC DIVERGENCE IN TOMATO

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Seventy one genotypes of tomato were evaluated during 1993-94 and 1994-95. Significant differences were observed for all the characters studied. Based on Mahalanobis D^2 values, genotypes were grouped into 9 clusters in 1993-94 & 10 clusters in 1994-95. Fruit weight showed maximum contribution to the genetic diversity in both years followed by plant height. Considering cluster distances and cluster means the genotypes KS-7, DVRT-2, Antey and PS-1 were recommended the best parents for hybridization.

Key words : *Lycopersicon esculentum* Mill, genetic, divergence, clustering, multivariate analysis, genetic drift, genetic existance, segregants

Tomato (*Lycopersicon esculentum* Mill.) is one of the most important vegetable grown in India. Selection of suitable variety for different use from the diverse group of tomato genotypes is of great importance. In plant breeding improvement over existing varieties is a continuous process. A plant breeder is constantly engaged in making an effective choice of desirable parents having high genetic variability so that the desirable character combination may be selected for higher yield. The genetically diverse parents are likely to produce heterotic effects and desirable segregants. Thus the gene diversity has obvious importance. Multivariate analysis using Mahalanobis (1936) D^2 statistics is a powerfull tool in quantifying the degree of divergence among the biological populations. The present study was carried out to identify suitable donors having wider genetic distance among tomato lines/genotypes for hybridization programme.

MATERIALS AND METHODS

Seventy one genotypes of tomato collected from different sources were grown during winter season of 1993-94 and 1994-95 at experimental tarm of project Directorate of Vegetable Research, Varanasi. The material was planted in a randomised block design having 3 replications. Each plot consisted of 5 rows of 3 m length with spacing of 60 cm from row to row and 45 cm from plant to plant. The recommended agronomic practices were followed to raise a good crop. The observations were recorded on plant height (cm), number of flowers per cluster, number of fruits per cluster, fruit set (%), node to fruit set, fruit length (cm), fruit diameter (cm), fruit size (cm2), fruit shape, number of fruits per plant, pericarp thickness (mm), number of locules per fruit, 10 fruit weight (g), fruit weight per plant (kg), number of nodes per branch, length of inter nodes (cm), and number of branches per plant. The multivariate analysis was done as suggested by Mahalanobis (1936) and genotypes were grouped into different clusters following. Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of the variance for both the years revealed significant differences among the genotypes for all the characters studied indicating the existence of genetic variability among the genotypes. Based on the relative magnitude of the D^2 values all the 71 genotypes were grouped into 9 clusters in 1993-94 and 10 cluster in 1994-95 (Table 1). The distribution pattern of population showed that cluster-1 was the largest comprising 60 genotypes in 1993-94 and 57 genotypes in 1994-95 followed by cluster-2 having 3 genotypes in 1993-94 and 4 genotypes in 1994-95. The clustering pattern was not same in both the year as the lines like Deogiri, Pant T-1 make distinct cluster in 1993-94 but were grouped in cluster-1 in 1994-95. It may be due to the influence of genotype × environment interactions. The genotypes did not cluster according to their geographical distribution. Similar results have also been observed by Singh and Singh (1980). This may be due to the fact that genetic drift and human selection in different environment have caused greater diversity than geographic distances. Among all the genotypes KS-7, Punjab Chhuhara, PDVR-2, Antey, PS-1 and Pusa Hybrid-2 (male), displayed their separate genotypic identity by constituting different clusters in both the years. This could be due to different genetic make up as compared to other genotype.

The statistical distances represents the index of genetic diversity among the clusters. The intra cluster distances ranged from 0.00 (monogenotypic cluster) to 11.04 (cluster-2) in 1993-94 and from 0.00 to 11.99 (cluster-2) in 1994-95. The highest intra cluster values were recorded for cluster-2 followed by cluster-1 in both the years. The inter cluster values ranged from 14.38 (cluster-5, cluster-7) to 39.16 (cluster-8 and cluster -9) in 1993-94 and from 14.15 to 29.96 in 1994-95. The lowest inter cluster values was observed between cluster-5 and cluster-7 in 1993-94. and between cluster-1 and cluster-7 in 1994-95 which indicated that the genotypes of these clusters were quite close to each other. On the other hand highest inter cluster value was observed between cluster-8 and cluster-9 in 1993-94 and between cluster-4 and cluster 10 in 1994-95, which revealed that the genotypes from these two clusters could be used as donors in hybridization programme for obtaining wide spectrum of variation among the Segregants.

Table 1. Grouping of 71 genotypes of tomato in different clusters

Cluster No.	No. of entries	Group of Genotypes (1993-94)	No. of entries	Group of Genotypes (1994-95)
1	60	NDT-1, PDVR-4, TC-104, H-36, BT-17, NDT-6, Ageta-1, DVRT-2, Sel-10, Ageta-2, Marglobe, ATV-2, Sel.No.4, PDVR-5, Punjab Kesari, Desi Local, ACE, Sel. No 6, IP-11, KS-2, Kalyani Eunish, Sioux, H-24, Roma, BT-3, NDT-11, NDT- 96, Dhanshree, Bhagyashree, BT-(12-2), NDT-4, Arka Saurabh, Pant-T- 4, Pusa Hyb-2 (female), IP-10, KT-15, NDT-120, IP-6, Sel-7, Arka Vikas, Sel-2, PDVR-1, Anand T-1, Arka Vishal, IP-8, TC-1, Sel-16, Pusa Sel-4, IP-2, Sel-32, IP-4, Pusa Ruby, Field King, PDVR-3, Pant Bahar, KS- 17, Solan Gola, Sel-4,D VRT-1, KT-10.	57	NDT-1, PDVR-4, IP-11, Sel No-6, H- 36, Punjab Kesari, Marglobe, NDT-6, BT-(12-2), BR-17, Pusa Sel- 4, Kalyani Eunish, KT-15, PDVR-3, Ageta-1, TC-1,Pant Bahar, DVRT- 1, Sel-17, Ageta-1, Bhagyashree, Sel-14, Arka Saurabh, TC-104, NDT- 11, IP10, H-24, IP-4, Dhanshree, Ageta-2, Arka Vikas, Sioux, Pusa Ruby, Desi Local, PDVR-5, KS-17, ACE, KT-15, Sel.No-4, NDT-120, Sel- 2, DVRT-1, Sel-16, Sel-32, Pant T-1, NDT-96, UP-6, Sel-18, Sel-4, Deogiri, NDT-4, IP-2, Solan Gola, Anand T-1, Field King, ATV-2, KS- 2, BT-3
2	3	Sel-18, Rutger, Floradale	4	KS-7, Punjab Chhuhara, KT-10, Pusa Hyb-2 (male)
3	2	KS-7, Punjab Chhuhara	1	Roma
4	1	PDVR-2	3	ATV-2, Rutger, Arka Vishal
5	1	Antey	1	Pant T-4
6	1	PS-1	1	DVRT-2
7	1	Pusa Hyb-2(male)	1	IP-8
8	1	Pant T-1	1	Antey
9	1	Deogiri	1	PS-1
10			1	PDVR-1

Apart from high genetic divergence the performance of genotypes and character with maximum contribution towards genetic divergence should also be given due consideration. The relative contribution of different characters towards the genetic divergence showed that 10 fruit weight had the maximum contribution in both the year (25.15% in 1993-94, 22.25% in 1994- 95) followed by plant height (15.2%, 14.37%). Cluster means were also calculated and compared which showed that in the year 1993- 94 cluster-2 and cluster-9 included the genotypes with dwarf in nature and high yield. Cluster-7 included single genotypes with dwarf and high yield. Though the cluster 4 and cluster-8 included tall genotypes but they showed poor yield.

Table 2a.. Intra and intercluster divergence in tomato in 1993-94

	Grp. 1	Grp. 2	Grp. 3	Grp. 4	Grp. 5	Grp. 6	Grp. 7	Grp. 8	Grp. 9
Grp.1	11.00	18.96	21.02	16.92	15.31	17.94	15.65	20.46	31.00
Grp.2		11.04	28.45	25.73	18.30	29.38	23.52	30.15	33.09
Grp.3			8.58	25.32	14.47	22.52	14.87	28.58	22.33
Grp.4				0.00	22.96	23.77	21.21	16.53	32.92
Grp.5					0.00	22.43	14.38	27.38	23.06
Grp.6						0.00	15.26	17.01	34.84
Grp.7							0.00	24.01	23.04
Grp.8								0.00	39.16
Grp.9									0.00

Table 2b. Intra and intercluster diversity in tomato in 1994-95

	Grp. 1	Grp. 2	Grp. 3	Gr. 4	Grp. 5	Grp. 6	Grp. 7	Grp. 8	Grp. 9	Grp. 10
Grp.1	11.43	16.695	14.747	19.279	15.718	17.056	14.148	15.742	17.992	18.988
Grp.2		11.991	16.422	25.562	21.373	18.92	23.405	14.768	17.681	19.052
Grp.3			0	26.367	16.263	20.295	19.222	18.977	16.584	17.084
Grp.4				10.887	26.58	26.217	19.569	20.377	28.221	29.945
Grp.5					0	15.784	14.466	24.742	20.926	16.343
Grp.6						0	18.478	21.448	19.992	12.741
Grp.7							0	21.924	22.221	22.395
Grp.8								0	19.811	21.939
Grp.9									0	15.814
Grp.10										0

Considering the cluster distances and cluster means the genotypes KS-7, DVRT-2, Aney and P.S-1 are recommended the best parents for hybridization owing to its high genetic distance. The other parents may be chosen from cluster-1, as per requirement. The choice of such diverse genotypes as donor hybridization is more important for varietal improvement.

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