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SELECTION OF DIVERSE PARENTS USING MULTIVARIATE ANALYSIS IN TOMATO (*LYCOPERSICON ESCULENTUM* Mill.)

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*Evaluation of genetic diversity within germplasm collection is important to plant breeders who desire source of genes for particular traits. The twenty five genotypes of tomato (*Lycopersicon esculentum* Mill.) collected from various countries were evaluated for quantitative characteristics in an attempt to differentiate among the lines. The genotypes could be grouped into seven clusters of phenotypic diversity. There was no correspondence between the geographic collection sites of genotypes and their inclusion in particular cluster. Analysis was useful for identification of potentially different sources of desired traits. It was noticed that the entries of the cluster III and VII showed the maximum distance and the crosses between genotypes in these clusters will produce heterotic hybrids. The use of these genotypes in future breeding programme should greatly help to cross the yield plateau in this crop.*

Genetic diversity among parental lines is an important factor for obtaining heterotic hybrids (Moll *et al.*, 1962). Statistical techniques such as D^2 analysis which quantify the differences among the quantitative traits is an efficient method to evaluate genetic diversity. It is generally agreed that genetically diverse parents will show maximum heterosis and offer the maximum chances of isolating transgressive segregants. Therefore, the present

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study was carried out using D^2 analysis to classify twenty five lines into groups on the basis of quantitative characters.

MATERIALS AND METHODS

The experimental material comprised of twenty five exotic lines of tomato from Australia, Canada, Czekoslovakia, Denmark, England, France, Iraq, Japan, USA, Russia and Yugoslovia were grown at Defence Agricultural Research Laboratory, Hawalbagh during 1990, in randomized block design with three replications. The plots were three meters long and one meter wide, each of them comprising two rows spaced at 50 cm. Plant density was six plants per linear meter. Days to 50 per cent flowering and yield were recorded on plot basis. Five competitive plants were selected from each genotype in each replication to record the observations on plant height, number of clusters per plant, number of fruits per cluster and number of fruits per plant. Mahalanobis (1936) D^2 analysis was used for assessing the genetic divergence between the populations. The genotypes were grouped into a number of clusters by Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The twenty five genotypes were highly significant for the characters studied. The coefficient of variation was the maximum for number of fruits per plant followed by yield per plant (Table 1). The coefficient of variation at environmental level also showed

Table 1 : **Means and coefficient of variation for different characters**

Characters	Days to 50% flowering	Plant height (cm)	No. of clusters per plant	No. of fruits per cluster	No. of fruits per plant	Yield Q/ha
General Mean	55.92 ±0.74	51.27 ±1.34	16.40 ±2.70	3.21 ±0.42	23.20 ±4.88	117.80 ±15.40
C.V. (%)	2.31	4.55	8.52	2.79	12.74	12:47
C.D. 5%	2.12	3.83	7.67	1.20	13.89	43.98
C.D. 1%	2.83	5.12	10.24	1.60	18.53	58.68

similar pattern but magnitude of the values were less than corresponding genotypic values. The genotypes were grouped into seven clusters (Table 2). Cluster I contained the maximum number of genotypes (8). These genotypes were of early to medium flowering duration. Cluster II comprised five genotypes of similar duration of flowering to that of Cluster I but comparatively higher number of fruits and yield per plant. Four genotypes of cluster III were dwarf in comparison to genotypes in other clusters but having the highest number of fruits per plant thereby producing the highest yield too. Cluster IV and V each contained three genotypes of medium duration and plant height. Cluster VI and VII comprised of single genotype by and large of late duration, tall type with large number of fruits per cluster.

Table 2 : **Grouping of 25 entries of tomato in different clusters**

Cluster	No. of entries	Accessions (with source country)
I	8	Red star UFN (Canada), Fire ball (Canada) Heinz (Canada), Mountain Pride VF (Canada) EC 10303 (Japan), EC 6199 (USA), New York Speical (USA), EC 13553 (USA)
II	5	EC 8590 (England), EC 9689 (France), EC 8973 (England), Star Shot (Canada), EC 7787 (Yugoslavia)
III	4	EC 16787 (Australia), EC 16788 (Australia) Cold Set (Canada), EC 7261 (Iraq).
IV	3	Pilgrim VF (Canada), Lemon boy (Canada), EC 8821 (Denmark)
V	3	EC 10302 (Japan), EC 10310 (Japan), EC 14167 (Russia).
VI	1	Olympic Pink (Canada)
VII	1	EC 11847 (Czekoslovakia)

The genetic divergence of the genotypes is in no way influenced by geographic distribution. In this experiment, there are various examples of genotypes having same origin but falling in different groups. Similarly the genotypes namely 'Red Star VFN' from Canada, 'EC 10303' from Japan, 'New York Special' from USA having different origin fell in the same group. These results are in agreement with the findings of Balasch *et al.* (1984).

The intra-cluster distance varied from 0 to 4.83, while inter-cluster distance ranged from 6.18 to 25.86 (Table 3). Intra-cluster distances were smaller than the inter-cluster distance which revealed that the genotypes within cluster had greater similarity. High inter-cluster distance between III and VII and I and VII indicated greater divergence between the genotypes belonging to these clusters. Character means (Table 4) showed appreciable variation among the seven clusters grouped according to D^2 analysis. The differences among cluster means though observed for all characters but were more pronounced for plant height, number of clusters per plant, number of fruits per plant and yield per plant. The cluster III showed the highest yield and number of fruits per plant. The genotypes belonging to cluster VII were late in flowering but had highest number of clusters per plant. Twenty five genotypes included in this experiment exhibited wide genetic variation for all six characters studied especially for number of fruits per plant confirming earlier report by Singh *et al.* (1978). The genotypes in the present experiment were not well adapted to the environment in which the study was conducted.

Table 3 : **Inter and intra-cluster value in tomato accessions**

Clusters	Accessions						
	I	II	III	IV	V	VI	VII
I	2.30	6.83	7.71	6.18	8.04	10.30	18.05
II		3.52	8.58	10.13	6.49	6.80	16.71
III			3.03	7.86	9.48	13.95	22.21
IV				4.29	7.98	14.79	18.36
V					4.83	15.99	20.92
VI						0	25.86
VII							0

Table 4 : **Cluster means for different clusters**

Characters	I	II	III	IV	V	VI	VII
Days to 50% flowering	51.62	54.74	54.33	55.44	48.78	60.33	60.00
Plant height (cm)	55.03	65.99	37.73	38.03	52.47	70.97	73.47
No. of cluster per plant	14.76	16.67	16.33	17.67	19.00	12.00	25.33
No. of fruits per cluster	2.67	3.20	3.42	3.64	3.45	3.67	4.33
No. of fruits per plant	18.91	23.27	25.08	23.89	24.34	10.67	23.33
Yield (Q/ha)	93.24	138.42	182.52	78.60	134.33	123.33	84.33

The utility of classifying germplasm for selection of diverse parents for hybridization has long been appreciated (Bhatt, 1970, Arunachalam, 1981). It was noticed that the lines of the cluster III and VII (D = 19,18) and I and VII (D = 15.75) showed the maximum distance. Obviously, the crosses between genotypes in these clusters might be useful for fixing transgressive segregants. However, the selection of more than one genotypes from cluster III may pose some other problems. In that context, apart from genetic distance, the performance of genotypes for yield and yield contributing characters should be given due consideration. It was found expedient to select parental entries with considerable genetic distance between them especially for the characters, viz., number of fruits per plant for heterosis breeding. In this study, genotypes EC 16787, 16788, Cold Set and EC 11847 appeared to be desirable for further improvement programme. Inclusion of these parents in crossing programme is expected to prove more rewarding.

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