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ASSESSMENT OF BREEDING POTENTIAL OF TOMATO (*LYCOPERSICON ESCULENTUM* MILL.) GERMPLASM USING D^2 ANALYSIS

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ABSTRACT
The present investigation was carried out at Vegetable Research Farm, Department of Horticulture, SHIATS, Allahabad during 2012-13. All the genotypes were grouped into six clusters based on D^2 values, which exhibited no association between geographical and genetic divergence. The intra-cluster distance was maximum for cluster V (10192.68) and minimum for cluster III (0). The maximum distance at inter-cluster level was between cluster III and cluster VI (47922.37) followed by clusters I and VI (44098.14) which may serve as a potential genotypes for hybridization programme. On the basis of mean performance of different clusters, genotypes having maximum flower clusters/ plant (17.48), flowers/plant (97.62), fruit weight (55.94g) and radial diameter of fruit (55.62mm) were observed in cluster VI. Genotypes having maximum fruit yield (1920.98g) along with maximum polar diameter of fruit (48.85mm) and minimum leaf curl incidence per cent (25.68) were recorded in cluster III. The genotypes of the cluster III for highest mean yield per plant along with minimum leaf curl incidence percent can be utilized as donor parent for enhancing the yield and minimum leaf curl incidence percent of other accessions grouped in a cluster in F_1s and can be fixed by selecting transgressive segregants followed by continued selection in advance generations which may lead to development of high yielding varieties with desired component characters.

INTRODUCTION

Tomato (*Lycopersicon esculentum* Mill., 2n = 24) a member of family Solanaceae. It is an herbaceous, annual to perennial, prostrate and sexually propagated plant with bisexual flower. It is a typical day neutral plant and self-pollinated crop. Scientific information indicates that the cultivated tomato originated in a wild form in the Peru-Ecuador-Bolvia area of the Andes (South American) (Vavilov, 1951).

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 (Singh *et al.,* 2002). Success of crop improvement programme depends on the extent of genetic variability, choice of parents for hybridization and selection procedure. In plant breeding genetic diversity plays a very important role as it helps in selecting the suitable parents for hybridization programme resulting in superior hybrids and desirable recombinants (Rathi *et al.,* 2011). Multivariate analysis is a potent tool for measuring divergence among a set of populations based on multiple characters. D^2 statistic proposed by Mahalanobis (1936) has been generally used as an efficient tool in the quantitative estimation of genetic diversity for a rational choice of potential parent in a breeding programme. For the first time use of this technique for assessing the genetic variability in plants was suggested by Rao (1952). It is a very potent technique of measuring genetic divergence.

Tomato crop has wider adaptability, high yielding potential and multipurpose uses in fresh as well as processed food industries. It stands unique among vegetables because of its high nutritive values and myriad uses (Vitamin A, Vitamin C and Minerals). Tomato pulp and juice is digestible mild aperients, a promoter of gastric secretion and blood purifier. It is reported to have antiseptic properties against intestinal infestations. Apart from these, lycopene is valued for its anti-cancer property. It acts as an antioxidant (scavenger of free radicals), which is often associated with carcinogenesis. 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 (Reddy *et al.,* 2013).

Keeping in view the above facts present investigation was undertaken to its precision and versatility with an objective to study of genetic diversity in 30 genotypes of tomato based on fifteen important traits, to help the breeders in selecting promising and genetically diverse parents for desired improvement.

MATERIALS AND METHODS

The present investigation was carried out at Vegetable Research Farm, Department of Horticulture, SHIATS, Allahabad during 2012-13. The experimental materials comprised of

thirty indigenous genotypes of tomato collected from IIVR, Varanasi and VRS, JAU, Junagadh. The experiment was laid out in a randomized block design with three replications. Seeds were sown in the nursery bed on September, 30 and transplanting was done on 1st November, 2012. All the recommended agronomic package of practices was followed. The observation were recorded on five randomly selected plants per replication for each genotype on fifteen quantitative characters: (i) plant height (cm), (ii) no. of branches/plant, (iii) no. of leaves/plant, (iv) days to 50% flowering, (v) no. of flower clusters/plant, (vi) no. of flowers/plant, (vii) no. of fruits/plant, (viii) fruit set %, (ix) fruit weight (g), (x) radial diameter of fruit (mm), (xi) polar diameter of fruit (mm), (xii) fruit yield/plant (g), (xiii) leaf curl incidence %, (xiv) TSS^0B and (xv) ascorbic acid (mg/100g). Mean across three replications were calculated for each traits and the analysis of variation was carried out. Multivariate analysis was done utilizing Mahalanobis D^2 statistic (Mahalanobis, 1936) and genotypes were grouped into different clusters following Tocher's method.

RESULTS AND DISCUSSION

On the basis of D^2 values, the 30 genotypes were grouped into six highly divergent clusters (Table 1). The cluster divergence was proved by the high inter-cluster and low intra-cluster D^2 values. Cluster II was the largest and consisted of thirteen genotypes followed by cluster IV with six genotypes. Cluster III, V and VI each had three genotypes, whereas cluster I had two genotypes. The grouping pattern did not show any relationship between genetic divergence and geographic diversity, which has been a point of debate in the past.

A perusal of the Table 1 clearly showed the genotypes usually did not cluster according to geographical distributions. This is an agreement with results of Basavaraj *et al*. (2010), Joshi and Kohli (2003) and Mohanty and Prusti (2001). One of the possible reasons may be the fact that it is very difficult to establish the actual location of origin of a genotype. The free and frequent exchange of genetic material among the crop improvement programmes in the country makes it difficult to maintain the real identity of the genotypes. Moreover, breeding progenies incorporate genes from varied sources, thus losing the basic geographical identity of the genotype. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, nature and artificial selection are responsible for genetic diversity. It may also be possible that causes for clustering pattern were much influenced by environment and genotype x environment interaction resulting in differential gene expression. Another possibility may be that estimates might not have been sufficient to account for the variability caused by some other traits of physiological or biochemical nature which might have been important in depicting the total genetic diversity in the population.

The divergence within the cluster (intra-cluster distance) indicates the divergence among the genotypes falling in the same cluster. On the other hand, inter cluster divergence suggests the distance (divergence) between the genotypes of different clusters. The intra and inter cluster D^2 values among 30 genotypes presented in Table 2 revealed that cluster III showed minimum intra-cluster D^2 value (0) followed by cluster IV (5898.27), whereas, maximum intra-cluster D^2 value (10192.68) was shown by cluster V followed by cluster I (7231.35) indicated that genotypes included in this cluster are very diverse and was due to both natural and artificial selection forces among the genotypes. Minimum inter-cluster D^2 value was observed between the cluster I and II (13570.16) indicated close relationship among the genotypes included in these clusters. Maximum inter-cluster D^2 value was observed between the cluster III and VI (47922.37) followed by cluster I and VI (44098.14) indicated that the genotypes belonging to these groups were genetically most divergent and the genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregating population (Mehta and Asati, 2008). Several authors also reported profound diversity in the germplasm of tomato by assessing genetic divergence on the basis of quantitative traits following Mahalanobis D^2 statistics (Basavaraj *et al.*, 2010 and Evgenidis *et al.*, 2011). Average inter and intra-cluster distances revealed that, in general, inter-cluster distances were much higher than those of intra-cluster distances, suggesting homogeneous and heterogeneous nature

Table 1: Distribution of 30 tomato genotypes into different clusters

Cluster No.	No. of Genotypes	Genotypes Included
I	2	2012/TODVAR-01, 2012/ATL- 08-21
II	13	2011/TODVAR-01, 2012/TODVAR-02, 2012/TODVAR-05, 2012/TODVAR-06, 2012/TODVAR-08, EC-620438, EC- 620514, EC- 620533, 2012/JTL- 08-07, 2012/JTL- 08-35, 2012/AT-03, Arka Alok, H-86.
III	3	2011/TODVAR-03, 2012/TODVAR-07, 2012/JT-03.
IV	6	2012/TODVAR-04, EC- 620452, EC- 620598, F- 3-1, 2012/JTL- 08-062012/ATL- 08-81.
V	3	2011/TODVAR-06, EC- 620545, 2012/ATL- 01-19.
VI	3	2011/TODVAR-05, 2012/TODVAR-03, 2012/JTL- 08-14.

Table 2: Intra (Diagonal) and Inter-cluster distance (D^2) among clusters in tomato

Clusters	I	II	III	IV	V	VI
I	7231.35	13570.16	20789.41	14164.14	29873.14	44098.14
II		6273.82	20555.58	13203.4	14714.56	17185.39
III			0	18795.94	27599.07	47922.37
IV				5898.27	14227.94	38783.39
V					10192.68	24466.37
VI						6734.35

Table 3: Cluster mean of thirty tomato genotypes for fifteen traits

Clusters	Plant Height at120 DAT	Branches /Plant at 120 DAT	Leaves/ plant at 120 DAT	Days to 50% flowering	Flower clusters/ plant	Flowers/ plant	Fruits/ plant	Fruit Set %	Fruit Weight	Radial Diameter of Fruit	Polar Diameter of Fruit	Fruit Yield/ plant	Leaf Curl Incidence	TSS^0 B	Ascorbic Acid
I	146.94	15.86	199.90	57.90	14.30	70.96	35.46	49.97	38.45	49.29	37.75	1365.02	54.56	4.40	35.28
II	66.74	10.65	155.48	61.89	15.41	78.16	37.47	47.80	50.35	49.11	46.31	1853.95	30.68	4.06	30.41
III	60.54	9.11	137.20	62.91	16.91	81.57	34.86	43.03	55.52	51.45	48.85	1920.98	25.68	4.10	27.77
IV	79.30	12.01	170.18	66.11	14.61	73.75	34.40	46.85	48.95	45.45	45.29	1673.76	41.70	4.37	27.83
V	100.68	12.44	182.71	54.88	15.42	83.37	30.68	36.81	51.90	48.29	46.61	1592.83	34.93	4.95	36.56
VI	65.93	10.22	159.53	58.28	17.48	97.62	27.60	28.63	55.94	55.62	47.83	1540.66	35.75	3.52	21.372

of the germplasm lines within and between the clusters, respectively. These results are in accordance with the findings of Mahesha *et al*. (2006) and Sekhar *et al*. (2008) in tomato.

The cluster mean of 30 genotypes (Table 3) showed that the mean value of clusters varied in magnitude for all the fifteen characters. Genotypes in cluster I showed maximum performance for plant height (146.94cm), number of branches per plant (15.86), number of leaves per plant (199.90), fruit set per cent (49.97) and leaf curl incidence per cent (54.56). Cluster II showed maximum mean value for number of fruits per plant (37.47). Cluster III recorded high mean performance for polar diameter of fruit (48.85mm) and fruit yield per plant (1920.98g), whereas low mean performance for leaf curl incidence per cent (25.68). Cluster IV showed minimum performance for radial diameter of fruit (45.45mm). Cluster V recorded minimum days to 50% flowering (54.88days), whereas high mean performance for TSS ºBrix (4.95ºB) and ascorbic acid (36.56mg/100g). It reveals that genotypes included in this cluster are useful in inducing earliness and improve quality in tomato varieties. Cluster VI registered maximum performance for flower clusters per plant (17.48), number of flowers per plant (97.62), fruit weight (55.94g) and radial diameter of fruit (55.62mm). Depending upon the aim of breeding, the potential lines to be selected from different clusters as parents in a hybridization programme should based on genetic distance. In accordance to the findings, Edang *et al*. (1971) and Hazra *et al*. (2010) reported that the clustering pattern could be utilized in choosing parents for cross combinations likely to generate the highest possible variability for various economic characters.

In a plant breeding programme aimed at crop improvement, the choice of parents is quite important and only component character of yield should be taken into account for selecting genetically divergent parents. For generating wide spectrum of variability intercrossing of genotypes of cluster II for fruits per plant; cluster III for polar diameter of fruit, fruit yield per plant and low leaf curl incidence per cent; cluster V for minimum days to 50% flowering, high TSS ºBrix and ascorbic acid and cluster VI for flower clusters per plant, flowers per plant, fruit weight and radial diameter of fruit. The genotypes of the cluster III for highest mean yield per plant along with minimum leaf curl incidence percent can be utilized as donor parent for enhancing the yield and minimum leaf curl incidence percent of other accessions grouped in a cluster in F_1s and can be fixed by selecting transgressive segregants followed by continued selection in advance generations which may lead to development of high yielding varieties with desired component characters. The genotypes of highly divergent cluster may also be utilized in a breeding programme for development of high yielding varieties with desirable attribute and can also be utilized in heterosis breeding programme for development of F_1 hybrids with superior yield and quality characters.

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