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Assessment of morphological diversity among hybrids of tomato (*Solanum lycopersicum* L)

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Abstract

Using Mahalanobis D^2 statistics method, the 8 hybrids were grouped into five clusters, indicating the presence of diversity for different traits. The maximum contribution to the total divergence was made by average fruit weight followed by fruit yield per plant, number of fruits per cluster. Cluster mean analysis revealed that the cluster IV and V had high yielding hybrids. Maximum intracluster distance exhibited in Cluster I followed by cluster II indicating within cluster divergence. The highest intercluster distance was found to be between clusters III and V indicating more divergence. Genotypes from divergent clusters can be used to produce hybrids.

Keywords: Mahalanobis D^2 , genetic diversity and tomato

Introduction

Tomato is the second most economically important and consumed vegetable worldwide and a well-studied crop species in terms of genetics, genomics, and breeding. Tomato is a rich source of minerals, vitamins and organic acid, essential amino acids and dietary fibers. It is rich source of vitamin A and C and contains minerals like iron and phosphorus. Tomato is rich source of minerals, vitamins, organic acid, essential amino acids and dietary fibres.

Genetic diversity analysis assists in interpreting the genetic background and breeding value of the genotypes. It was also said that plant breeders use a much less diverse genetic pool than the overall available genetic diversity within the crop (Joshi *et al.*, 2012) [4]. Heterogeneous local population of the genus forms an important source of genetic variation (Zeven, 1998) [6]. For the selection of parents in hybridization, diversity among parents for the character of interest, estimation of genetic distance is most important as diverse plants are supposed to give high hybrid vigour (Harrington, 1940) [3]. Estimation of genetic divergence also allows breeders to eliminate some parents in downsizing the gene pool available and concentrate their efforts in a smaller number of hybrid combinations (Fuzzato *et al.*, 2002) [2]. Diversity relative to its use and production environments is high. However, the genetic base of cultivated tomato is narrow (Bai & Lindhout 2007) [1]. The multivariate analysis provides valuable information on the extent of variation present in the crop under improvement and usually helps a plant breeder in choosing desirable parents for breeding programme. Also inclusion of genetically diverse parents in any breeding programme is essential to generate new variability and desirable recombinants.

Materials and Methods

Eight single cross hybrids were (TSH-1, TSH-2, TSH-3, TSH-4, TSH-5, TSH-6, TSH-7 and TSH-8) were sown under RBD design with three replications and spacing of 60 cm x 60 cm. The observations were recorded on twelve quantitative characters *viz.*, plant height (cm), number of primary branches, number of clusters per plant, number of fruits per cluster, number of fruits per plant, average fruit weight (g), polar length of fruit (mm), equatorial length of the fruit (mm), fruit yield per plant (kg), number of locules per fruit, total soluble solids (TSS) ($^{\circ}$ Brix), rind (pericarp) thickness (mm).

Mahalanobis (1936) [5] D^2 -statistic was used for assessing the genetic divergence among the promising genotypes. The original correlated un-standardized variables (X_i) were transformed to standardized uncorrelated variables (Y_i) so that the computation of D^2 values reduce to simple summation of squares of the differences between values of transformed variables of the two accessions *i.e.*, D^2_i .

Results and Discussion

Among the 12 quantitative characters studied, the maximum contribution to the total divergence was made by average fruit weight followed by fruit yield per plant, number of

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fruits per cluster, fruit length and number of locules indicating more variability in these characters (Table 1).

Five divergent clusters were formed using Tochers method (Table 2 and Fig 1). Analysis of cluster means (Table 3) indicated substantial variation among the five clusters grouped according to D² analysis. Based on the cluster means, it is possible to know the characters influencing divergence. In the present study the cluster IV and V had high yielding hybrids, whereas clusters III was comprised of less yielding hybrids.

Cluster I followed by cluster II had maximum intracluster distance (Table 4) indicating that the hybrids in these clusters were more divergent than other clusters. The clusters I had least intra cluster distance indicating less divergence.

Similarly highest inter cluster distance was observed between III and V clusters. Therefore, the hybrids falling in these two clusters may have wider variability. It was observed that hybrids producing maximum yield per plant, higher number of fruits, higher number of clusters, more pericarp thickness and TSS fall in cluster II while hybrids having lower values for all these characters including plant height in cluster III. The highest intercluster distance was found to be between clusters III and V. Hence, it could be expected that the cross combinations involving hybrids from each of these clusters as parents might produce maximum heterosis. Also the probability of isolating superior or transgressive segregants in advanced generations could be high.

Table 1: Per cent contribution of twelve characters towards divergence in eight Tomato hybrids (*Solanum lycopersicum* L.)

S. No.	Characters	Contribution percentage
1	Plant height (cm)	0.00
2	No. of clusters	0.00
3	Number of fruits per cluster	7.14
4	Number of fruits per plant	0.00
5	Number of branches	0.00
6	Fruit length(cm)	6.62
7	Fruit diameter(cm)	0.00
8	No. of locules	3.57
9	Pericarp thickness(mm)	0.00
10	TSS	0.00
11	Average fruit weight(g)	53.57
12	Fruit yield per plant(kg)	35.71

Table 2: Clustering pattern of eight Tomato hybrids based on D² analysis

Cluster	No of genotypes	Genotypes
I	3	TSH-3, TSH-4, TSH-7
II	2	TSH 1, TSH-5
III	1	TSH-8
IV	1	TSH-6
V	1	TSH-2

Table 3: Average intra-cluster and inter-cluster D² values of eight hybrids observed in Tomato

Cluster	I	II	III	IV	V
I	20.27	39.42	34.46	26.72	35.18
II		19.52	44.52	53.79	56.22
III			0.00	44.53	60.53
IV				0.00	27.36
V					0.00

Table 4: Cluster means for twelve characters in eight hybrids of Tomato.

S. No.	Characters	I	II	III	IV	V
1	Plant height (cm)	89.47	91.15	101.53	64.20	98.87
2	No. of clusters	23.20	23.70	16.70	23.17	32.67
3	Number of fruits per cluster	3.88	3.73	2.60	4.26	8.17
4	Nmuber of fruits per plant	53.96	62.41	26.37	81.30	93.80
5	Nnumber of branches	2.62	2.93	2.57	3.00	2.83
6	Fruit length(cm)	4.34	4.43	4.43	4.42	4.77
7	Fruit diameter(cm)	5.55	5.45	4.11	4.91	5.36
8	No. of locules	3.84	4.07	5.10	3.58	2.47
9	Pericarp thickness(mm)	0.63	0.71	0.39	0.77	0.66
10	TSS	5.84	6.65	5.43	5.33	5.80
11	Average fruit weight(g)	79.25	114.09	76.23	58.59	77.70
12	Fruit yield per plant(kg)	4.56	6.95	1.95	5.91	4.15

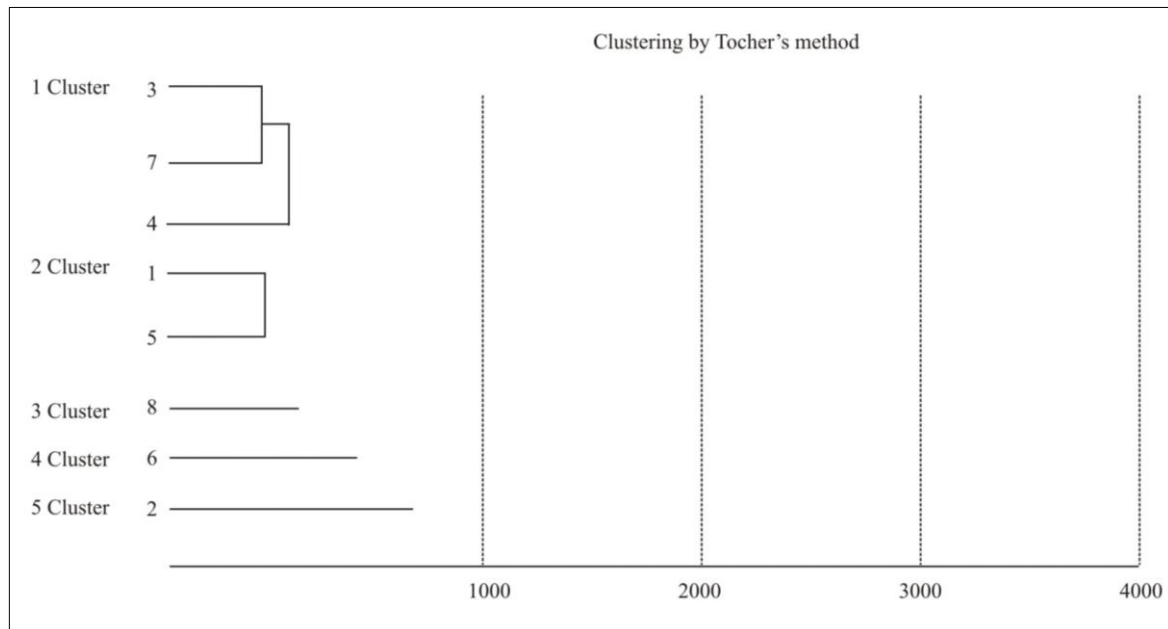


Fig 1: Dendrogram showing clustering of 8 hybride of tomato by Tocher's method

References

1. Bai Y, Lindhout P. Domestication and breeding of tomatoes: What have we gained and what can we gain in the future? *Ann. Bot.* 2007; 100:1,085-1,094.
2. Fuzzato SR, Ferreira DF, Ramalho PMA, Ribeiro PHE. Genetic divergence and its relationship with diallel crossing in maize crop. *Ciencia-e-Agrotechnologia.* 2002; 26:22-32.
3. Harrington JB. Yielding capacity of wheat crosses as indicated by bulk hybrid tests. *Canadian J. Res.* 1940; 18:578-84.
4. Joshi BK, Gardner RG, Dilip RP. Diversity Analysis of Tomato Cultivars Based on Coefficient of Parentage and RAPD Molecular Markers. *J. Crop Imp.* 2012; 26:177-196.
5. Mahalanobis PC. On the generalized distance in statistics. *Proc. Nat. Inst. Sci. India.* 1936; 2:49-55.
6. Zeven AC. Landraces: A review of definitions and classifications. *Euphytica*, 1998; 104:127-139.