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Assessment of Genetic Diversity for Yield and its Attributing Traits in Tomato (*Solanum lycopersicum* L.) Genotypes for Protected Conditions

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ABSTRACT

Background: Tomato plant has high yield potential, although the yield is very low because of non-availability of superior cultivars for protected cultivation. Presence of diversity is an important for variety development. Hybridization among divergent parents is probably produce ample variability and helps to isolate superior recombinants. So, the study was carried out to assess of genetic diversity in tomato for choosing promising and genetically diverse parents for improvement in yield for protected cultivation.

Methods: Fourteen genotypes of tomato were planted inside naturally ventilated polyhouse during September 2018 to May 2019. The data were recorded for twenty-one characters from randomly five tagged plants from each genotype and genetic diversity was computed by utilizing Mahalanobis D^2 analysis.

Result: All genotypes were arranged into five highly divergent clusters in which cluster I contain maximum genotypes followed by cluster II. The intra cluster distance was highest in cluster I and inter-cluster distance was highest among cluster-II and V. Cluster means indicated that cluster II had high mean values for maximum traits. The highest contribution towards genetic diversity was shown by fruit yield/plant followed by number of fruits per plant. Based on breeding objectives, potential lines are selected as parents for utilization in hybridization programme.

Key words: Cluster distance, Cluster means, D^2 analysis, Genetic diversity, Protected conditions, Tomato.

INTRODUCTION

Protected cultivation helps to change the natural atmosphere to attain best possible plant growth and development. It helps to overcomes severe heat, high incidence of UV rays and reduces insect pest infestation which reduces the yield and quality of produce and provides good surroundings environment for increasing yield potential of crop thus protected cultivation best to achieve high yield and good quality of produce.

Tomato (*Solanum lycopersicum* L.) is originated from Peru-Ecuador-Bolvia region of South America (Vavilov, 1951) and widely cultivated throughout the country and has high yield potential, even though the yield is very low because of non-availability of superior cultivar. Presence of genetic diversity is an important for development of improved variety. In general, diverse plants are predictable to give more hybrid vigour (Harrington, 1940). Genetic divergence helps to recognize diverse genotypes from the base population which could be utilized in hybridization to achieve more recombinants in the segregating generation. The concept of D^2 statistics was developed by Mahalanobis's (1936) used to quantify the genetic diversity present among the population and to assess comparative contribution of different characters to the total divergence, both at the intra-cluster and inter-cluster levels. Hybridization among divergent parents is probably produce ample variability and helps to isolate superior recombinants. Generally, heterosis increases with the increase in parental diversity up to certain limit and decrease with further increase in parental diversity due to cross ability barriers. Matzinger and Werusman, (1958) suggested that the amount of heterosis cannot be projected alone on the basis of genetic diversity. Apart from the high level of diversity, the traits with maximum contribution towards diversity and the mean performance of genotypes should also be given due consideration. Keeping all these facts, the present investigation was carried out with an objective to assess of genetic diversity in fourteen genotypes of tomato for choosing promising and genetically diverse parents for desired improvement for protected cultivation.

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MATERIALS AND METHODS

The present study was conducted on fourteen diverse genotypes of tomato were collected from different sources (Table 1) and planted during September 2018 to May 2019 at spacing of 60×60 cm in double row planting in randomized block design inside the naturally ventilated polyhouse at Polyhouse Complex, Department of Horticulture (Veg. and Flori.), Bihar Agricultural College, Sabour, Bhagalpur. The observations were recorded from five arbitrarily selected plants for sixteen morphological traits and five biochemical parameters from each genotype. All the mean value of recorded data was used for statistical analysis. Mahalanobis D^2 statistic was used to measure genetic diversity between genotypes and the genotypes were group into different clusters by following Tocher's method (Rao, 1952). The average intra and inter cluster distances and character contribution towards genetic divergence were estimated by using formula given by Singh and Chaudhary (1985).

Table 1: List of genotypes.

Genotypes	Source of collection
Arka Abha	IIHR, Bangalore
Arka Rakshak	IIHR, Bangalore
Arka Samrat	IIHR, Bangalore
Arka Vikas	IIHR, Bangalore
Hawaii 7998	CSK HPAU, Palampur
Heemshikhar	Syngenta India Ltd.
NS 4266	Namdhari Seeds Pvt. Ltd.
Pant Polyhouse Tomato-2	GBPUAT, Pantnagar
Palam Tomato Hybrid 1	CSK HPAU, Palampur
Palam Pink	CSK HPAU, Palampur
San Marzano	NBPGR
TODINDVAR-5	AICRP on Vegetable Crops
TODINDVAR-6	AICRP on Vegetable Crops
TODINDVAR-8	AICRP on Vegetable Crops

Table 2: Grouping of fourteen genotypes of tomato on the basis of genetic divergence.

Cluster	Number of genotypes	Genotypes
1	9	TODINDVAR-6
		Palam Pink
		Heemshikhar
		Arka Samrat
		Arka Rakshak
		Arka Abha
		Arka Vikas
		San Marzano
		TODINDVAR-5
2	2	NS 4266
		Palam Tomato Hybrid-1
3	1	Pant Polyhouse Tomato-2
4	1	Hawaii 7998
5	1	TODINDVAR-8

RESULTS AND DISCUSSION

Based on D^2 value, all genotypes were arranged into five highly divergent clusters (Table 2 and Fig 1) which represent sufficient amount of genetic diversity in the population for choosing superior and diverse parents which can be utilized in breeding programme. Cluster I contain maximum genotypes (9) *viz.* TODINDVAR-6, Palam Pink, Heemshikhar, Arka Samrat, Arka Rakshak, Arka Abha, Arka Vikas, San Marzano, TODINDVAR-5 which corresponds to 64% of the total population followed by cluster II which contain two genotypes *viz.*, NS 4266, Palam Tomato Hybrid-1 representing 14% of the total population whereas cluster III, cluster IV and cluster V contain only one genotype each *viz.*, Pant Polyhouse Tomato-2, Hawaii 7998 and TODINDVAR-8, respectively. The clustering of genotype showed that the genotypes were distributed among the different clusters randomly regardless of their geographic origin and it may be due to the continuous interchange of breeding material from one place to another place. The genotypes in solitary clusters (cluster III, IV and V) indicate their independent identity and importance. These results agree with those of Iqbal *et al.* (2014) and Vargas *et al.* (2020) reported five clusters in tomato. Different clustering patterns in tomato were also confirmed by Chernet *et al.* (2014) which found six clusters and Naveen *et al.* (2018) and Kumar *et al.* (2018) reported eight clusters.

The average intra-cluster distance varied from 0.00 to 1467.61 (Table 3). The intra cluster distance was highest in cluster I (1467.61) and also has highest number of genotypes which indicate significant genetic diversity among genotypes within cluster followed by cluster II. Cluster III (0.00), IV (0.00) and V (0.00) had least intra-cluster distance since these clusters consisted of only one genotype. In general inter-cluster distances were higher than intra-cluster distances, signifying wider genetic diversity of the genotypes within and among the clusters respectively. The inter-cluster distance varied from 10527.69 to 1746.81. It was highest among cluster-II and V (10527.69) after that cluster II and III (5711.51) which indicated that genotypes from these clusters were more diverse and can be utilized in hybridization program. Average inter-cluster distance was lowest among cluster-III and IV (1746.81) which indicated close association between the genotypes. These relationships were also shown in the scatter diagram (Fig 2). Crosses made between genotypes from distant cluster give a wide range of variation among the segregates. Analogous results are also reported by Meena and Bahadur (2015), Prajapati *et al.* (2015), Lekshmi and Celine (2016) and Naveen *et al.* (2018) and Debnath *et al.* (2020).

The cluster means (Table 4) indicated considerable differences all the characters. It was observed that cluster II had lower values for days to first flowering (27.33), days to 50% flowering (31.20), days to first fruiting (44.27), titratable acidity (0.55%) and maximum values for number of flowers per truss (9.10), no. of fruits per truss (4.30), plant height at 60 DAT (159.57 cm), equatorial diameter of fruit (4.95 cm),

pericarp thickness (4.61 mm), β-carotene (1.22 mg/100 g) and lycopene (3.76 mg/100 g). Cluster III showed lower values for days to first picking (115.13) and no. of locules per fruit (2.00) and higher values for titratable acidity (1.20%) and ascorbic acid (35.19 mg/100 g). Cluster IV exhibited higher values for total soluble solid (4.91°Brix), plant height at final harvest (390.67 cm), no. of fruit /plant (101.87). Cluster V showed lower values for node to first flowering (7.60) and higher values for polar diameter of fruit (4.78 cm), average fruit weight (99.73 g). Thus, genotypes of above cluster may be selected for transfer of one or more character having high mean values through hybridization programme.

The highest contribution towards genetic diversity (Table 5) was shown by fruit yield/plant (36.26%) followed

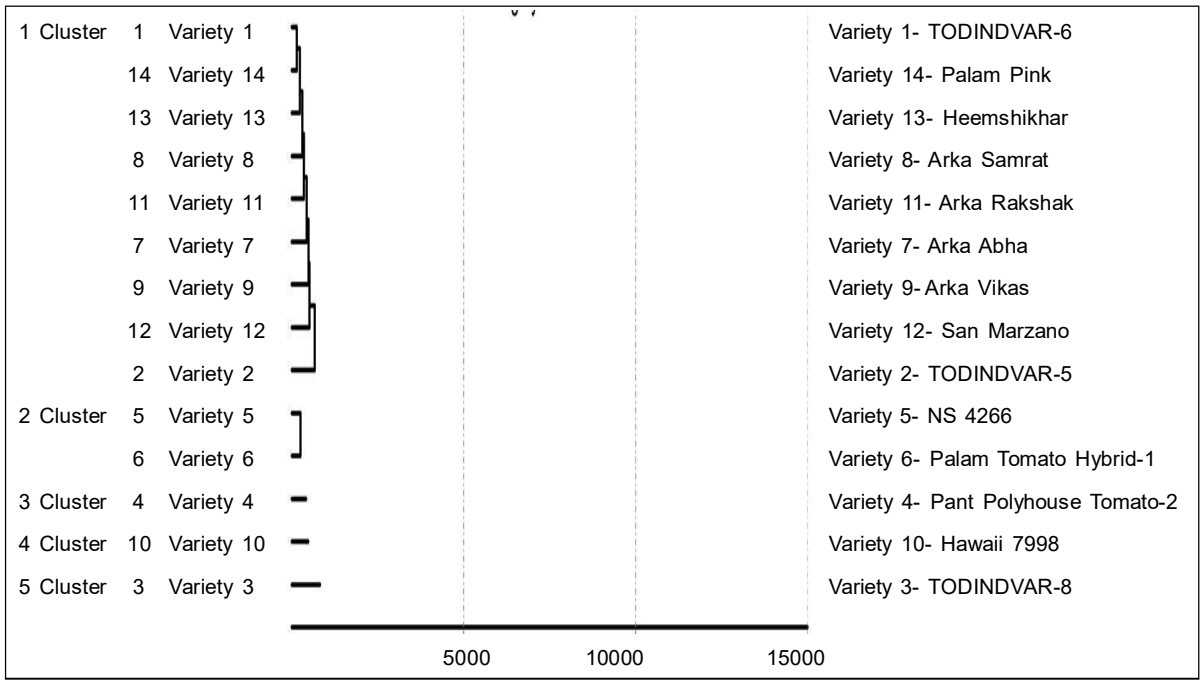

Fig 1: Dendrogram showing clustering of fourteen genotypes of tomato by tocher method.

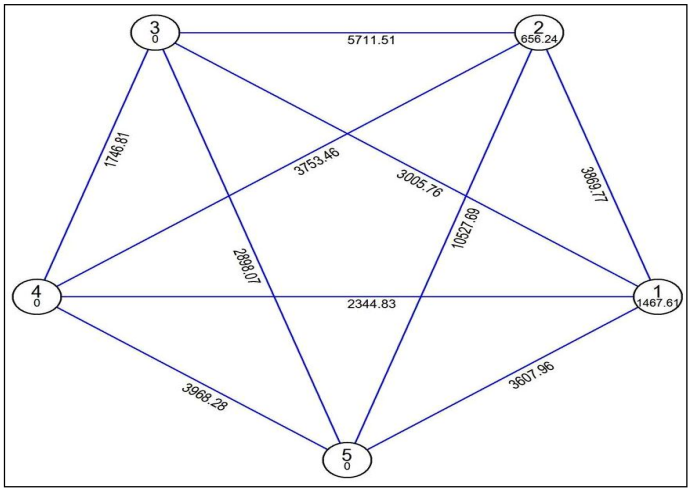

Fig 2: Diagram showing the inter cluster distance and intra-cluster (within circle) distances.

Table 3: Average inter and intra cluster distance in tomato.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	1467.61				
Cluster II	3869.77	656.24			
Cluster III	3005.76	5711.51	0.00		
Cluster IV	2344.83	3753.46	1746.81	0.00	
Cluster V	3607.96	10527.69	2898.07	3968.28	0.00

Table 4: Cluster means for fourteen genotypes of tomato.

Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Days to first flowering	33.88	27.33	37.93	43.40	41.80
Node to first flowering	09.52	08.63	10.00	11.40	07.60
Days to 50% flowering	38.41	31.20	42.87	47.47	45.00
No. of flowers per truss	06.49	09.10	04.90	07.07	05.70
Days to first fruiting	51.13	44.27	49.33	58.93	69.45
No. of fruits per truss	03.46	04.30	03.97	02.93	01.67
Plant height at 60 DAT (cm)	126.45	159.57	106.67	126.60	116.40
Days to first picking	119.21	115.87	115.13	120.67	135.10
No. of locules per fruit	02.97	02.53	02.00	02.33	05.20
Polar diameter of fruit (cm)	04.72	04.35	04.26	03.51	04.78
Equatorial diameter of fruit (cm)	04.67	04.95	04.38	04.01	04.85
Pericarp thickness (mm)	04.41	04.61	04.55	04.03	05.47
Total soluble solid (%)	04.35	03.94	04.21	04.91	04.42
Titratable acidity (%)	00.63	00.55	01.20	00.77	00.92
Ascorbic acid (mg/100 g)	25.21	20.40	35.19	16.68	18.84
β-carotene (mg/100 g)	00.55	01.22	00.85	00.57	00.32
Lycopene (mg/100 g)	01.58	03.76	02.64	01.73	00.99
Plant height at final harvest (cm)	299.18	368.87	384.67	390.67	300.33
Average fruit weight (g)	68.30	70.23	66.80	32.40	99.73
No. of fruits per plant	48.03	85.63	60.00	101.87	25.28
Fruit yield per plant (kg)	03.18	05.27	03.30	03.29	02.14

Table 5: Contribution of different attributes towards genetic diversity.

Characters	Times ranked first	Contribution %
Days to first flowering	0	0.00%
Node to first flowering	0	0.00%
Days to 50% flowering	0	0.00%
No. of flowers per truss	0	0.00%
Days to first fruiting	0	0.00%
No. of fruits per truss	0	0.00%
Plant height at 60 DAT (cm)	0	0.00%
Days to first picking	0	0.00%
No. of locules per fruit	0	0.00%
Polar diameter of fruit (cm)	0	0.00%
Equatorial diameter of fruit (cm)	0	0.00%
Pericarp thickness (mm)	0	0.00%
Total soluble solid (°Brix)	0	0.00%
Titratable acidity (%)	3	3.30%
Ascorbic acid (mg/100 g)	10	10.99%
β-carotene (mg/100 g)	8	8.79%
Lycopene (mg/100 g)	11	12.09%
Plant height at final harvest (cm)	5	5.49%
Average fruit weight (g)	0	0.00%
No. of fruits per plant	21	23.08%
Fruit yield per plant (kg)	33	36.26%

by number of fruits per plant (23.08%), Lycopene (12.09%), ascorbic acid (10.99%), β-carotene (8.79%), plant height at final harvest (5.49%), titratable acidity (3.30%) and remaining traits had 0.00% contribution. The inheritance of these characters is nearly zero. The characters that highly contributed to genetic diversity are selected for enhancing yield and other economic traits. The genotypes with character having higher contributions towards diversity can be incorporated in breeding programme for further improvement as they show rich amount variability. Reddy *et al.* (2013) reported higher contribution of fruit weight, plant height and number of fruits per plant to total divergence. Higher contribution towards genetic diversity were reported for lycopene, yield per plant, β-carotene, fruits per plant by Lekshmi and Celine (2016). Naveen *et al.* (2018) observed maximum contribution of plant height, number of fruits per plant, lycopene, days to fruit set, TSS, titratable acidity, ascorbic acid, days to first flowering and average fruit weight towards divergence in tomato.

CONCLUSION

Extensive genetic diversity was observed among the genotypes, which were grouped into five clusters. Cluster II had higher performance for yield. The intra-cluster distance highest in cluster I and inter-cluster distance highest between cluster II (Palam Tomato Hybrid-1 and NS 4266) and cluster V (TODINDVAR- 8) and highest contribution towards genetic diversity was shown by fruit yield/plant followed by number of fruits per plant. So, based on cluster distance, mean performance of cluster and contribution toward genetic divergence, parents may be selected to get more recombinants in the segregating generations in tomato under protected conditions for further improvements.

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