Eco. Env. & Cons. 26 (3) : 2020; pp. (1208-1211)
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ISSN 0971–765X

Multivariate analysis for genetic diversity estimation among tomato (*Solanum lycopersicum* L.) Genotypes

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(Received 2 December, 2019; accepted 3 March, 2020)

ABSTRACT

A field experiment was conducted during the year 2017-18 at Department of Horticulture, Sikkim University to study the genetic diversity amongst thirteen genotypes for twelve polygenic traits in tomato (*Solanum lycopersicum* L.) in randomized block design with three replications. Considerable amount of variability was found for the twelve characters and D^2 analysis revealed total 4 clusters, maximum diversity was recorded between cluster II and cluster VI (2859.01), whereas maximum diversity within the cluster was obtained in cluster II (284.27) followed by cluster-I (216.91). The occurrence of divergence amongst genotypes was also assessed in cluster means by the appreciable amount of variability for different traits. Cluster- I had highest mean value for polar diameter (5.03). In cluster II the highest mean values are found in primary branches/plant (7.00), equatorial diameter (5.22), fruit weight (44.01), fruit yield/plant (669.59), ascorbic acid (30.73), protein content (0.29) and total phenol content (285.53). Total phenol content (69.23%) was reported to put maximum contribution towards total diversity.

Key words: *Tomato, Genotypes, Genetic diversity, Multivariate, D^2 analysis, cluster*

Introduction

Tomato is an important vegetable crop among the solanaceous vegetables grown throughout the globe. Though the tomato crop can be grown in varied range of soil and climate but being a warm season crop the most favorable range of temperature for its record yield is 20 to 24°C. In Sikkim it is grown organically in the warm season March to September. The crop gained importance among the vegetables because of its high contribution for human nutrition and multiple uses. Tomato has a wide range of variability which provides a tremendous scope of genetic improvement of economic traits (Khanna and Mishra, 1977). Genetic diversity is an important factor for improvement in heritability in the crops and its degree of variability is used in selecting desirable parents from available germplasms for a successful breeding programme. The present study was aimed to obtain information on the genetic diversity present amongst tomato genotypes and assessing their utility in developing hybrid

breeding for commercial utilization for organic cultivation in an organic land Sikkim.

Materials and Methods

The present investigation was conducted at Main Experiment Station, Department of Horticulture, Sikkim University, Gangtok located at 27°14′20″ N latitude and 88°18′15″ E longitude with an altitude of 1230 m above mean sea level during warm season, 2017. The total precipitation during the growing season was 1625 mm with a temperature ranging from 10-30 °C. Thirteen tomato genotypes from different geographic location of West Bengal covering Kalimpong, Kolkata, Coochbehar were collected and few genotypes maintained in department itself (Pusa Ruby, IIHR-2623, H-86, Arka Abha and Arka Vikas) utilized for present study. The seeds were sown in nursery and all the essential cares were taken to ensure proper growth of seedlings. The seedlings became ready for transplanting after 4 weeks of germination. Transplanting was done at 60x45 cm^2 spacing followed by light irrigation. The genotypes were statistically laid out in randomized block design with three replications. All other recommended improved organic package of practices including plant protection was followed for raising a healthy crop. The data was taken for three growth characters *viz*., plant height, number of primary branches/plant, days taken to 50% flowering, five yield characters *viz*., equatorial diameter, polar diameter, number of fruits/plant, average fruit weight, fruit yield/plant and four quality characters *viz*., total soluble solids (°Brix), ascorbic acid content (mg/100g), protein content (g/100g) and total phenol content (mg/100g). D^2 statistics is the efficient tool among multivariate analysis for measuring genetic diversity which gives the relationship between genotypes by measuring intra-cluster and inter-cluster. The concept of D^2 statistics for a measure of group distance based on multiple characters was developed by P. C. Mahalanobis in 1936. The data thus obtained are analyzed statistically for D^2 analysis.

Results and Discussion

Mahalanobis (1936) generalized distance estimated by D^2 statistics has been proven as an important tool in the numeric estimation of genetic diversity for a rational selection of potent parents in hybrid breeding programme. Based on D^2 values, genotypes were classified into four highly divergent clusters (Table 1 and Figure 1). Cluster III contained maximum number of genotypes (6) comprising IIHR-2623, Arka Vikas, ST-52, ST-42, Pusa Ruby and Arka Abha, followed closely by cluster I contained 4 genotypes comprising ST-62, ST-72, ST-82, H-86, cluster II contained 2 genotypes namely ST-92, ST-102 and cluster IV was found to be monogenotypic contained only single genotype named ST-112, which shows no parallelism is there between genetic diversity and geographical distribution in tomato crop. This finding was in agreement with the study by Prakash *et al*. (2019), Lekshmi and Celine (2016) and Khapte and Jansirani (2014). The cluster divergence was proved by the high inter cluster and low intra cluster D^2 values. The intra and inter cluster D^2 values among thirteen genotypes presented in Table 2 revealed that the intra-cluster was maximum in cluster -II(284.27) reveals maximum genetic diversity followed by cluster-I (216.91), cluster III exhibited intra-cluster distance of 177.96 and cluster IV revealed 0.00 distance since it contains only single genotype. It was clear from the table that maximum inter-cluster generalized distance (2859.01) was ascertained between cluster II & IVexhibited maximum divergence in between groups followed by cluster II & III (1640.01). While, the lowest (589.15) was obtained between cluster I & III. Inter-cluster distance was higher than intra-cluster distances in table revealing appreciable amount of genetic divergence amongst the genotypes studied. The finding was in close concordance with the report by Kumar *et al.* (2010); Sharma *et al.* (2006); Joshi and Kohli (2003) and Dharmatti *et al.* (2001).

Table 1. Clustering patterns of thirteen genotypes of tomato on the basis of genetic divergence

	Number	Cluster members
1-Cluster	4	ST-62, ST-72, ST-82, H-86
2-Cluster	2	ST-92, ST-102
3-Cluster	6	IIHR-2623, Arka Vikas, ST-52, ST-42, Pusa Ruby, Arka Abha
4-Cluster	1	ST-112

Cluster means for twelve characters are present in Table 3. The existence of diversity amongst the genotypes was assessed by the appreciable amount of variability in cluster means too for different characters. The Cluster- I had highest mean values for

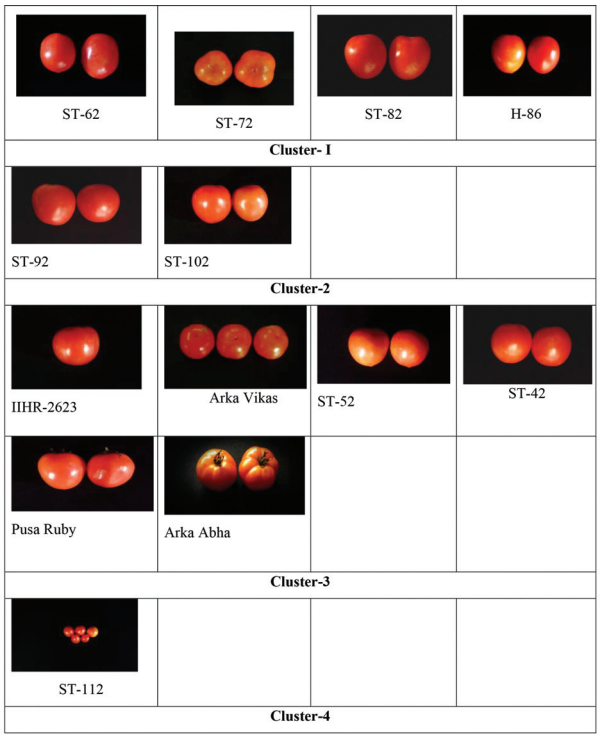

Fig. 1. Clustering patterns of thirteen genotypes of Tomato on the basis of genetic divergence

plant polar diameter (5.03). In cluster II highest mean values are obtained for primary branches per plant (7.00), equatorial diameter (5.22), fruit weight (44.01), fruit yield/plant (669.59), ascorbic acid (30.73), protein content (0.29) and total phenol content (285.53). In cluster III highest mean value reported for plant height (161.05). In cluster IV highest mean values recorded for days taken to 50 %

Table 4. Contribution of various characters towards total genetic divergence

S. No.	Characters	Contribution %	Times ranked first
1	PH	1.28%	1
2	PB/P	0.00%	0
3	DTT50%F	0.00%	0
4	ED	8.97%	7
5	F/P	0.00%	0
6	FW	0.00%	0
7	PD	0.00%	0
8	FY/P	0.00%	0
9	TSS	11.54%	9
10	ASC	8.97%	7
11	PRO	0.00%	0
12	TPhC	69.23%	54

PH= Plant height (cm)
PB/P= Number of primary branches/plant
DTT50%F= Days taken to 50% flowering
FW= Average fruit weight (g)
ED= Equatorial diameter of fruit (cm)
F/P= Number of fruits/plant
FY/P= Fruit yield/plant (g)
PD= Polar diameter of fruit (cm)
TSS= Total soluble solid (°BRIX)
ASC= Ascorbic acid content (mg/100g)
PRO= Protein content (g/100g)
TPhC= Total phenol content (mg/100g)

Table 2. Average clusters distance of thirteen genotypes of tomato

	1 Cluster	2 Cluster	3 Cluster	4 Cluster
1- Cluster	216.91	698.98	589.15	1400.29
2- Cluster		284.27	1640.01	2859.01
3- Cluster			177.96	762.29
4- Cluster				0.00

Table 3. Cluster wise mean values of twelve characters in tomato

	PH	PB/P	DTT50%F	ED	F/P	FW	PD	FY/P	TSS	ASC	PRO	TPhC
1 Cluster	111.25	6.25	35.08	4.69	15.25	29.55	5.03	445.93	4.44	21.27	0.18	182.55
2 Cluster	149.33	7.00	36.33	5.22	15.33	44.01	4.61	669.59	5.01	30.73	0.29	285.53
3 Cluster	161.05	6.61	32.38	4.93	13.77	31.96	4.76	444.76	4.65	20.46	0.17	82.65
4 Cluster	123.33	5.00	32.33	1.86	16.00	15.25	1.90	245.55	6.40	19.41	0.18	57.20

PH= Plant height (cm)
PB/P= Number of primary branches/plant
DTT50% F= Days taken to 50% flowering
FW= Average fruit weight (g)
ED= Equatorial diameter of fruit (cm)
F/P= Number of fruits/plant
FY/P= Fruit yield/plant (g)
PD= Polar diameter of fruit (cm)
TSS= Total soluble solid (°BRIX)
ASC= Ascorbic acid content (mg/100g)
PRO= Protein content (g/100g)
TPhC= Total phenol content (mg/100g)

flowering (32.33), number of fruits per plant (16.00) and TSS (6.40). The percentage contribution of different characters towards genetic divergence is depicted in Table 4. The ranking was done character wise and ranks were added for each trait for all the entries identified the different variables, which actually contributed towards the total divergence. Total phenol contributed maximum (69.23%) towards total divergence and this was followed TSS (11.54%), equatorial diameter and ascorbic acid (8.97%) and plant height (1.28%), whereas primary branches/plant, no. of days taken for 50% flowering, no. of fruits/plant, average fruit weight, polar diameter, fruit yield/plant and protein content have zero (0.00%) contributions. This study was in accordance with Singh and Singh (1980); Jogi *et al.* (2018) and Bhattacharya *et al*. (1979).

Acknowledgement

All the necessary facilities for morphological and biochemical analysis of the samples were provided by Department of Horticulture, Sikkim University.

Conclusion

From the above study it might be concluded that present set of material exhibited wide range of variation for different morpho-biochemical traits which resulted in distant clustering of the genotypes. Clustering pattern of the genotypes could be utilized in choosing potent parents for cross combination towards organic hybrid breeding in the organic land Sikkim.

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