

Original Research Article

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## Genetic Diversity Studies in Thermo Tolerant Genotypes of Tomato (*Solanum lycopersicum* L.)

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### ABSTRACT

#### Keywords

*Solanum lycopersicum*, Genetic diversity, D<sup>2</sup> analysis, Clustering pattern.

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Genetic diversity study involving twenty one thermo tolerant tomato genotypes was carried out for twelve physiological and biochemical characters at Indian Agricultural Research Institute, New Delhi during summer season of the year 2014. All the genotypes were grouped into 4 distinct clusters using D<sup>2</sup> statistics. Cluster I and cluster II comprised of 10 genotypes represented by heat tolerant genotypes while cluster III showed 4 heat sensitive genotypes. The clustering analysis of all genotypes showed that heat sensitive and heat tolerant genotypes were represented by distinct clusters. Maximum intra cluster distance was recorded in cluster IV (2.21), while the inter cluster distance was found maximum between cluster III and cluster IV (5.95). Cluster means of all genotypes showed that genotypes in cluster I exhibited minimum cluster mean value for chlorophyll b (0.24 mg/100g) and maximum for proline content (364µg/g). Principal component analysis showed that the first 4 PC's had proportionate contribution of 45.2%, 64.1%, 76.7% and 88.9% respectively.

### Introduction

Tomato is an herbaceous plant belongs to Nightshade family. It is an important Solanaceous vegetable crop grown worldwide. The nutritional value of tomato makes it useful for reducing cardiovascular risk associated with type-II diabetes (Freedman *et al.*, 2008). Tomato intake helps in weight loss and controlling obesity, eye disorders, night blindness, urinary tract infection and liver disorders. In any crop improvement programme, the proper selection of diverse parents is a prerequisite (Singh *et al.*, 2002). The assessment of genetic diversity

helps in differentiating well-defined population. Several methods have been proposed for diversity analysis; among them Mahalanobis generalized distance occupies a unique place and an efficient method to gauge the extent of diversity among genotypes, which quantify the differences among several quantitative traits. Therefore, the present investigation was undertaken involving various genotypes and popular varieties to assess the extent of genetic diversity in different thermo tolerant tomato genotypes.

## Materials and Methods

Genetic diversity analysis of twenty one thermo tolerant tomato genotypes was performed in the Research Farm of Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi during the summer season (March–June) of the year 2014. The experimental material consisted of 21 contrasting thermo tolerant tomato genotypes (Table 1) and the experiment was laid out in randomized block design with 3 replications. The physiological characters *viz.*, relative water content, membrane stability index and chlorophyll content (a, b and total chlorophyll, chlorophyll a/b ratio) were analysed according to method of Brass and Weatherley (1962), Premachandra *et al.*, (1990) and Hiscox and Israelstam (1979) respectively, whereas the biochemical parameters *viz.*, TSS, lycopene (as described by Ranganna, 1977), ascorbic acid and acidity (as described in A.O.A.C., 1975) and proline (as described by Bates *et al.*, 1973) were recorded for estimating the genetic diversity. Mahalanobis (1936)  $D^2$  analysis was used for assessing the genetic divergence among the test entries involving different characters. The genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

## Results and Discussion

Twenty one thermo tolerant tomato genotypes were analysed for genetic divergence following Mahalanobis  $D^2$  statistical procedure. Considering physiological and biochemical characters, 21 tomato genotypes were categorized into distinct clusters and their Euclidian distance using  $D^2$  statistics. 21 genotypes were grouped into 4 distinct clusters (Table 2). The grouping of genotypes into different clusters showed the presence of ample amount of genetic diversity among the genotypes under study. These results are in

close conformation with the findings of Sharma *et al.*, (2009), Basavaraj *et al.*, (2010), Evgenidis *et al.*, (2011), Iqbal *et al.*, (2014) and Dar *et al.*, (2015). Cluster I and cluster II comprised of 10 genotypes represented by heat tolerant genotypes while cluster III showed 4 heat sensitive genotypes namely, Pusa Ruby, Pusa 120, Pusa Rohini and Pusa Gaurav. All the wild genotypes and exotic collections were grouped into cluster IV. The clustering analysis of 21 genotypes showed that heat sensitive and heat tolerant genotypes were represented by distinct clusters.

Average intra (diagonal) and inter cluster ( $D^2$ ) distance of different clusters (Table 3) showed that maximum intra cluster distance was recorded in cluster IV (2.21), while the inter cluster distance was found maximum between cluster III and cluster IV (5.95), followed by cluster II and cluster III (5.42). The maximum inter cluster distance showed the presence of greater divergence within the cluster. Similar findings were also reported by Sekhar *et al.*, (2008) and Reddy *et al.*, (2013) in tomato.

Cluster means of all genotypes (Table 4) revealed that genotypes in cluster I exhibited minimum cluster mean value for chlorophyll b (0.24 mg/100g) and maximum for proline content (364 $\mu$ g/g). The lines fall in to same cluster having lowest degree of divergence (Fig. 1). Similarly genotypes in cluster IV recorded maximum cluster mean for proline (380 $\mu$ g/g). Similar trends were found for other clusters also. Low cluster mean value in all the clusters was recorded for acidity showed that there was least diversity among the 21 genotypes for this trait.

The Jaccard's similarity matrix was subjected to principal component analysis. PCA resolves complex relationships into interactions of fewer and simpler factors. First four PC's having eigen value greater than one

accounting for 88.9% of the total variation (Table 5, Fig. 2). This finding has the similarity with the findings of Glogovac *et al.*, (2012) based on biochemical fruit traits. The first 4 PC's had proportionate contribution of 45.2%, 64.1%, 76.7% and 88.9% respectively. PC-1 showed positive factor loading for RWC (0.37), Chlorophyll b (0.16), chlorophyll a/b ratio (0.014), lycopene (0.52), proline (0.07) and fruit yield

per plant (0.02). Contribution of lycopene was highest in PC-1 and indicated its role in total divergence. Similar result was also found by Lekshmi *et al.*, (2016).

Thus the present experiment clearly revealed that 21 tomato genotypes were categorized into 4 distinct clusters using D<sup>2</sup> statistics based on physiological and biochemical characters.

**Table.1** List of genotypes and standard released varieties included in this study

Sl. No.	Genotypes/Varieties	Tolerance level
1	Pusa Sadabahar	HT
2	Pusa Ruby	HS
3	Pusa 120	HS
4	Pusa Rohini	HS
5	Pusa Gaurav	HS
6	Pusa Sheetal	HT
7	Chikko	HT
8	LP-2	HT
9	PSH-3	HT
10	TH-348-T2	HT
11	Balkan	HT
12	TH-348-4-R	HT
13	TH-348-4-2	HT
14	TH-348-4-5-1	HT
15	Spr-1*	HT
16	Spr-2*	HT
17	Spm**	HT
18	SPM 1**	HT
19	SPM 2**	HT
20	SPM 3**	HT
21	SPM 4**	HT

(Where, HT- heat tolerant, HS- heat sensitive) (Where,\* *S. peruvianum*, \*\* *S. pimpinellifolium*)

**Table.2** Group constellation of twenty one tomato genotypes based on Mahalanobis D<sup>2</sup> statistics

Clusters	No. of genotypes	Name of genotypes
I	2	Chikko, PSH-3
II	8	Pusa Sadabahar, Pusa Sheetal, LP-2, TH-348-T2, Balkan, TH-348-4-R, TH-348-4-2, TH-348-4-5-1
III	4	Pusa Ruby, Pusa 120, Pusa Rohini, Pusa Gaurav
IV	7	Spr1, Spr2, Spm, SPM1, SPM2, SPM3, SPM4

**Table.3** Estimates of average intra (diagonal) and inter cluster distance for different clusters for twenty one tomato genotypes

Clusters	I	II	III	IV
I	1.434			
II	3.375	2.084		
III	4.500	5.427	1.392	
IV	4.584	3.168	5.951	2.217

**Table.4** Cluster means of physiological and biochemical traits of twenty one tomato genotypes under heat stress

Sl. No.	Cluster Traits	I		II		III		IV	
		Mean	SE±	Mean	SE±	Mean	SE±	Mean	SE±
1	RWC (%)	75.9	3.21	76.94	3.13	66.38	2.22	77.66	3.52
2	MSI %	77.83	2.59	81.73	2.33	68.01	3.48	80.38	4.15
3	chl a (mg/g)	0.92	0.23	1.31	0.2	1.02	0.25	1.45	0.25
4	chl b (mg/g)	0.24	0.06	0.39	0.03	0.24	0.05	0.38	0.05
5	Total chl (mg/g)	1.16	0.29	1.7	0.2	1.27	0.3	1.82	0.27
6	chl a/b ratio	3.89	0.06	3.41	0.59	4.2	0.3	3.91	0.71
7	TSS (°Brix)	5.7	0.09	5.79	0.48	5.22	0.15	7.81	0.42
8	Lycopene (mg/100g)	1.7	0.25	1.86	0.26	1.11	0.09	1.98	0.12
9	Ascorbic Acid (mg/100g)	16.85	2.33	16.82	3.58	17.23	1.46	21.5	1.41
10	Acidity (%)	0.42	0.03	0.36	0.03	0.34	0.01	0.37	0.05
11	Proline (µg/g)	364.34	10.36	361.6	27.66	276.02	8.15	380.34	24.88
12	Yield/plant (g)	182.20	11.59	295.00	15.2	165.20	9.36	579.00	18.31

**Table.5** Principal component analysis for physiological and biochemical traits of twenty one tomato genotypes under heat stress

Parameters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Eigen value (root)	5.42	2.27	1.50	1.48	0.47	0.37	0.19	0.15	0.11	0.02	0.02	0.00
Cumulative eigen value	5.42	7.69	9.20	10.67	11.15	11.51	11.71	11.86	11.98	11.99	12.00	12.00
Explained variation (%)	45.20	18.9	12.56	12.29	3.93	3.05	1.65	1.26	0.96	0.17	0.01	0.00
Cumulative explained variation (%)	45.20	64.1	76.69	88.98	92.91	95.96	97.61	98.87	99.83	100	100.01	100.01
Eigen vectors												
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
RWC (%)	0.37	0.38	0.29	0.35	0.326	-0.09	0.26	0.37	0.18	0.14	0.36	0.08
MSI %	-0.19	-0.19	0.28	-0.03	0.226	0.38	0.33	-0.13	0.41	-0.10	-0.05	-0.59
chl a (mg/g)	-0.07	0.02	-0.35	0.14	-0.257	-0.59	0.24	-0.07	0.35	-0.41	0.20	-0.18
chl b (mg/g)	0.16	0.06	-0.33	-0.42	-0.373	0.12	0.28	0.22	0.17	0.58	0.12	-0.16
Total chl (mg/g)	-0.18	0.26	0.03	0.02	0.028	0.08	-0.52	-0.36	0.61	0.29	0.16	0.15
chl a/b ratio	0.14	0.16	-0.02	-0.33	-0.089	0.39	0.08	-0.28	-0.11	-0.42	0.61	0.18
TSS (° Brix)	-0.61	-0.30	0.07	0.10	0.084	-0.09	0.38	-0.08	-0.09	0.29	0.33	0.38
Lycopene (mg/100g)	0.52	-0.64	-0.03	0.05	0.007	0.04	0.07	-0.11	0.35	-0.02	-0.09	0.40
Ascorbic Acid (mg/100g)	-0.29	0.24	-0.02	-0.19	-0.057	0.21	0.15	0.43	0.35	-0.33	-0.36	0.45
Acidity (%)	-0.14	-0.40	0.07	-0.16	0.025	-0.04	-0.47	0.59	0.07	-0.12	0.39	-0.16
Proline (µg/g)	0.07	0.03	0.45	-0.68	0.205	-0.51	0.07	-0.12	0.09	0.01	-0.08	0.04
Yield/plant (g)	0.02	-0.01	-0.63	-0.18	0.759	-0.06	0.01	-0.02	0.01	0.02	0.01	0.01

**Figure.1** Dendrogram showing clustering pattern among twenty one genotypes of tomato

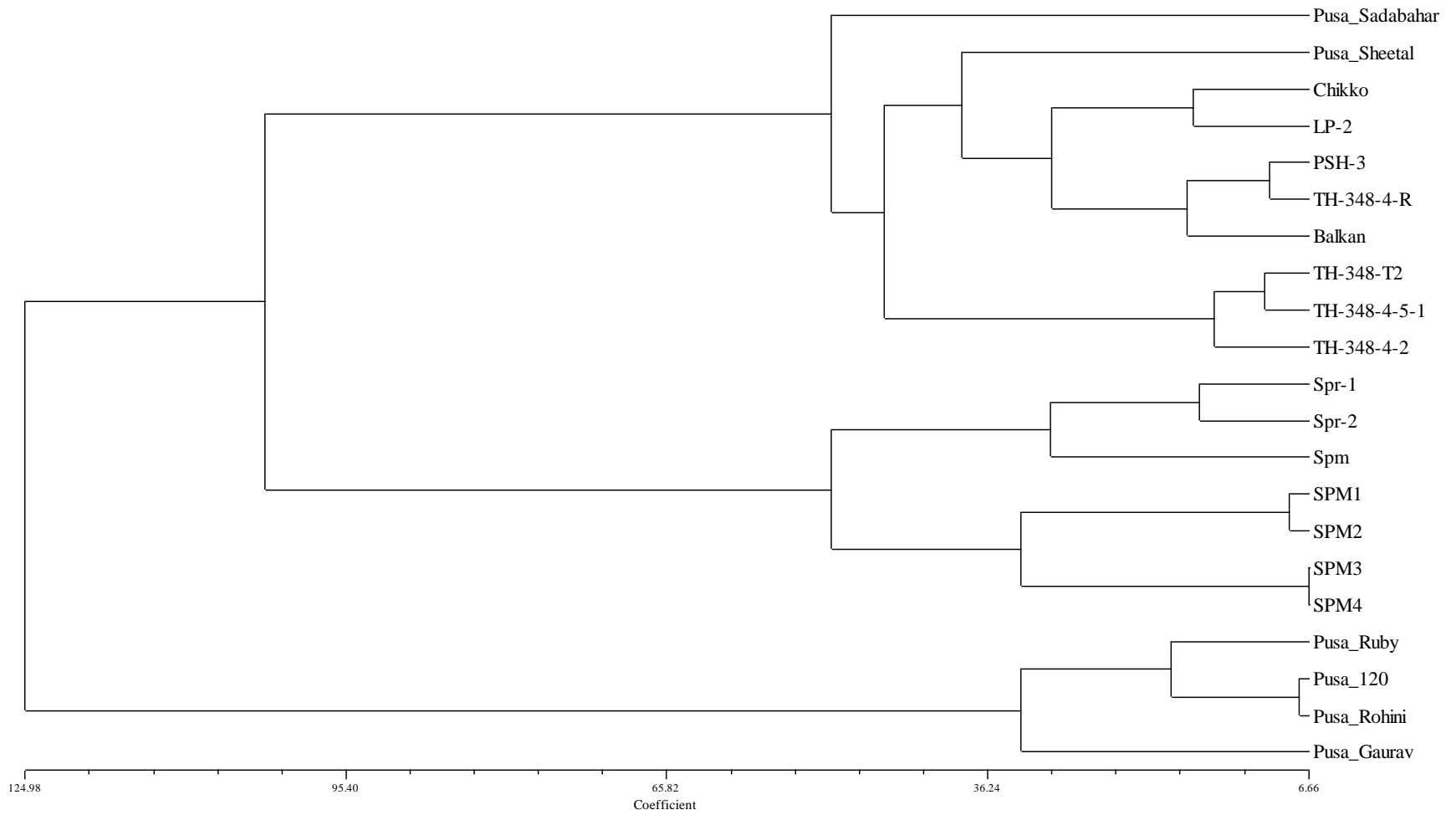
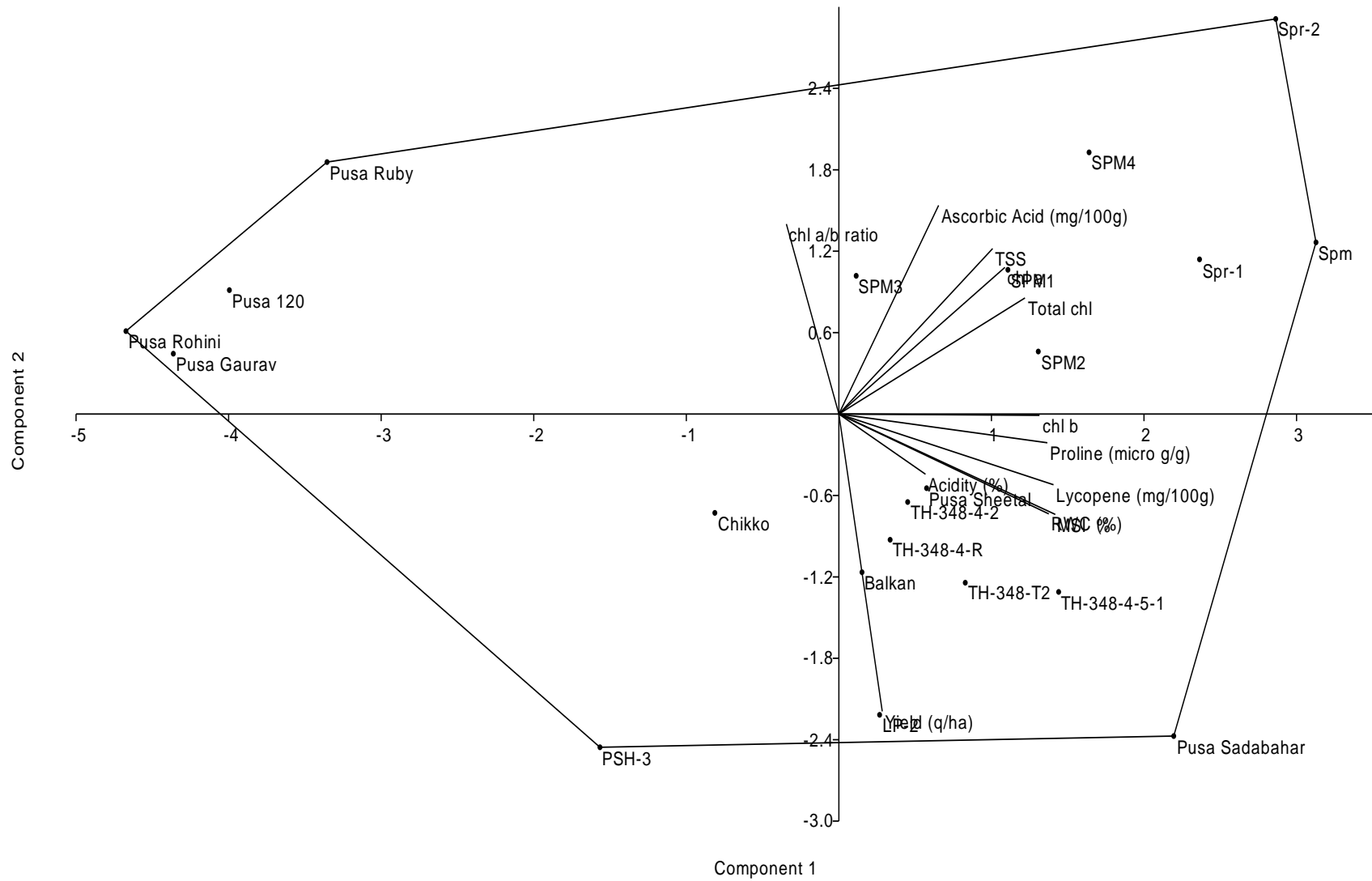


Figure.2 Principal component analysis of twenty one tomato genotypes revealed by physiological and biochemical traits



All the wild genotypes and exotic collections were grouped into two different clusters. 10 heat tolerant genotypes, namely Pusa Sadabahar, Pusa Sheetal, Chikko, LP-2, PSH-3, TH-348-T2, Balkan, TH-348-4-R, TH-348-4-2, TH-348-4-5-1 were represented by same cluster, while 4 heat sensitive genotypes, namely Pusa Ruby, Pusa 120, Pusa Rohini and Pusa Gaurav were grouped into another cluster. This showed that clustering was done effectively.

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