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Genetic distances and divergence for heat tolerance as revealed in exotic germplasm of tomato (*Solanam lycopersicum* L.)

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Abstract
Genetic divergence was investigated in heat tolerant lines of tomato for yield and quality traits during *Kharif,* 2014 at Experimental Farm, Vegetable Research Station, ARI, Rajendranagar, Hyderabad using Mahalanobis's statistics. Based on twenty five quantitative and quality characters, the twenty germplasm both exotic and indigenous were grouped into five clusters based on the relative magnitudes of values following Tocher's method of cluster formation. Based on the rank totals, the characters which contributed maximum towards genetic divergence in the present study were chlorophyll content, relative water content, fruit length, ascorbic acid and total soluble solids.

Keywords: genetic distances, heat tolerance, exotic germplasm, tomato

Introduction
Tomato (*Solanum lycopersicum* L.) is universally treated as 'Protective Food' since it is rich in minerals like Ca, P and Fe vitamins A, C, B, small amounts of vitamin E, antioxidants such as carotenoids (mainly lycopene and *β*-carotene), organic acids (healthy acids) and phenolics in daily diets. It plays a vital role in maintaining health, vigor and very helpful in healing wounds because of the antibiotic properties found in the ripe fruit. Tomato belongs to the nightshade family Solanaceae and the cultivated tomato is widely grown around the world and constitutes a major agricultural industry and it is the second most consumed vegetable after potato.

Although tomato has a good potential to be cultivated every location in the universe but it confronts lots of abiotic stresses in which, high temperature is a crucial problem now-a-days. According to the Intergovernmental Panel on Climatic Change (IPCC), in each decade, worldwide average temperature will be enhanced by 0.3˚C (Jones *et al*., 1999) [8] and reached to around 1˚C and 3˚C higher than the current temperature by the years of 2025 and 2100, respectively and led to warming of the globe. This increased temperatures inhibit growth and development of tomato by adversely affecting plant morphological, physiological, biochemical, and molecular mechanisms (Singh *et al*., 2007) [22], eventually affecting yield (Bita and Gerats, 2013) [2].

The optimum temperature for tomato growth and development is 20–24°C. Temperatures above 34°C are considered super-optimal thermal stress. The optimum range of night temperature for fruit set is 15-20 °C (Thamburaj and Singh., 2004; Peter and Kumar., 2008) [25, 16], however above 18°C is likely to inhibit pollen production and fruit set (Peet and Bartholemew, 1996) [15]. With high day and night temperatures, the plant shows symptoms of irregular flower development, reduction in pollen production, pollen viability, fruit drop and ovule abortion, all of which ultimately lead to decreased yield (Dane *et al*., 1991; Hazara and Ansary, 2008) [4, 7]. In general, the level of heterosis increases with the increase in parental diversity up to some limit and decreases with further increase in parental diversity owing to crossing ability barriers. Thus maximum heterosis occurs at an optimal or intermediate level of parental diversity.

The use of Mahalanobis statistics for estimating genetic divergence had been emphasized by many workers (Murthy and Arunachalam, 1960) [13] because it permitted precise comparison among all possible pairs of population in any group before affecting actual crosses. In addition to aiding in the selection of divergent parents for hybridization, statistics measures the degree of diversification and determines the relative contribution of each component character to the total divergence (Singh, 1990) [24]. The utility of multivariate analysis in quantifying the degree of divergence between populations to understand the trend of evolutionary pattern,

to assess the relative contribution of different components to the total divergence and to determine the nature of forces operating on inter- and intra-cluster levels has greatly been emphasized (Sokal, 1959) [23]. Further, such studies have also permitted the choice of genetically divergent parents to obtain desirable recombinants in segregating generations (Ram and Panwar, 1970) [17].

Table 1: Mean values of clusters for twenty five characters of tomato germplasm (Tocher's method)

Cluster	Plant Height (cm)	Root Length (cm)	Root to Shoot Ratio	Primary Branches/ Plant	Days to 50% Flowering	No. of Flowers/ Cluster	No. of Clusters/ Plant	Stigma Exertion (%)	Fruit Set (%)	Days to First Fruit Harvest	Days to Last Fruit Harvest	No. of Fruits/ Cluster	No. of Fruits/ Plant
I	88.11	33.49	0.40	6.04	45.19	5.00	24.10	16.58	35.82	80.19	131.38	1.77	29.87
II	100.71	37.89	0.38	4.80	50.78	5.82	25.53	19.27	31.16	85.78	132.22	1.78	29.80
III	93.41	34.83	0.39	6.30	44.96	4.92	27.25	15.69	45.16	76.04	126.13	2.23	37.13
IV	98.52	34.03	0.35	8.00	46.00	5.07	19.27	17.89	31.75	80.00	126.67	1.60	27.73
V	129.07	37.77	0.29	5.60	46.00	5.33	40.00	17.00	46.01	81.00	130.67	2.47	41.20

Table 1: Cont…

Cluster	Fruit Length (cm)	Fruit Width (cm)	Avg. Fruit Weight (g)	Fruit Yield/ Plant (kg)	No. of Seeds/ Fruit	No. of Locules/ Fruit	Ascorbic Acid (mg/100g)	Total Soluble Solids (°Brix)	Lycopene Content (mg/100 g)	Stomatal Diffusive Resistance (sec/cm)	Relative Water Content (%)	Chlorophyll Content (%)
I	4.46	4.71	59.03	1.77	37.02	3.22	20.47	4.96	5.56	7.46	47.74	1.01
II	6.52	4.95	51.57	1.52	34.09	3.38	22.22	4.97	5.88	7.81	57.98	0.91
III	4.21	4.69	52.80	1.88	34.45	3.42	20.04	5.14	6.34	5.23	36.97	1.00
IV	4.88	5.55	82.07	2.31	33.47	3.47	19.72	4.17	5.06	8.96	43.73	1.46
V	3.71	4.06	25.57	1.06	34.73	3.33	19.30	5.90	4.78	4.75	36.67	0.74

Material and methods

The experimental material comprising of a set of fifteen heat tolerant testers and five lines of tomato which were obtained from World Vegetable Centre, Taiwan (previously, AVRDC) and Indian Institute of Horticultural Research, Bangalore respectively, were systematically evaluated for quantitative and quality traits. Germplasm were evaluated in a Randomized Block Design with three replications during *Kharif,* 2014 at Experimental farm of Vegetable Research Station, Agricultural Research Institute, Rajendranagar, Hyderabad. In each replication, each entry was grown in a single row plot of 4.5 m length. Each plot consisted of one ridge alternating with furrow accommodating only one row of germplasm line. Row-to- row spacing of 60 cm and plant-to-plant spacing of 45 cm was maintained. The recommended package of practices and necessary prophylactic plant protection measures were carried out to safeguard the entire germplasm from pests and diseases. The data on quantitative and quality characters were recorded on five competitive and randomly selected plants in each replication for all the characters under study except days to 50% flowering and fruit yield per plant which were recorded on whole plot basis. Mahalanobis statistics (1936) [9] was used to estimate genetic divergence among the 20 germplasms. The germplasm were grouped into clusters according to Tocher's methods by Rao (1952) [18].

Results and discussion

Grouping of genotypes in to various clusters

Procedure suggested by Tocher (Rao, 1952) [18] was used to group twenty genotypes into five clusters by treating estimated D^2 values as the square of the generalized distance. The pattern of distribution of twenty genotypes in to various clusters is indicated (Table 1). Out of five clusters formed, cluster II was the largest group comprising of seven genotypes, followed by cluster I with four genotypes, cluster III, cluster IV and cluster V with three genotypes each.

Average intra and inter cluster distances

The mean intra and inter cluster D^2 values among the five clusters are presented (Table 2). The intra cluster distance varied from nil to 321.67. Cluster III recorded maximum D^2 value (321.67) followed by cluster II (234.32) and cluster I (198.37). Intra cluster distance observed in cluster IV and cluster V. The inter cluster D^2 values revealed that highest inter cluster distance (1813.95) was between cluster IV and cluster V while the lowest (290.89) was between cluster I and cluster II.

The inter cluster distance was minimum between cluster I and II indicating narrow genetic diversity whereas maximum recorded between clusters IV and V followed by II and IV indicating wider genetic diversity in these groups. Selection of parents from these diverse clusters for hybridization would help in achieving novel recombinants. Similar type of observations are reported by Reddy *et al*. (2013) [19] and Meena and Bahadur (2015) [11].

The mean values of clusters for twenty five characters of tomato germplasm were presented in table 4. The genotypes belonging to cluster V (129.07 cm) recorded highest plant height followed by cluster II (100.71 cm). Root length was highest in the cluster II (37.89 cm) followed by cluster V (37.77 cm), while cluster I showed lowest root length (33.49 cm) followed by cluster IV (34.03 cm) and cluster III (34.83). The root to shoot ratio was maximum in the cluster I (0.40) followed by cluster III (0.39) and cluster II (0.38). The character numbers of primary branches per plant were highest in cluster IV (8.00) followed by cluster III (6.30), while less number of primary branches was observed in genotypes of cluster II (4.80) followed by cluster V (5.60). Days to fifty per cent flowering recorded minimum value in the genotypes of cluster III (44.96 days) followed by cluster I (45.19 days).

The genotypes of cluster II (5.82) recorded more number of flowers per cluster followed by cluster V (5.33) whereas. More number of clusters per plant was recorded in cluster V (40.00) followed by cluster III (27.25), while less number of clusters per plant was recorded in cluster IV (19.27) followed by cluster I (24.10). Lowest percentage of stigma exertion was exhibited by the genotypes of cluster III (15.69 %) followed by the cluster I (16.58 %), while highest percentage of stigma exertion was exhibited by cluster II (19.27) followed by the cluster IV (17.89). Fruit set per cent was recorded highest in the genotypes of cluster V (46.01 %) followed by cluster III

(45.16 %). Least number of days to first fruit harvest was recorded in the genotypes of the cluster III (76.04 days) followed by the cluster IV (80.00 days) and cluster I (80.19 days). The mean values for days to last fruit harvest was most in the genotypes of the cluster II (132.22 days) followed by the cluster I (131.38 days) and cluster I (130.67 days) whereas, the genotypes of cluster III (126.13 days) took least number of days to last fruit harvest followed by the cluster IV (126.67 days).

More number of fruits per cluster was recorded in the genotypes of the cluster V (2.47) followed by the cluster III (2.23). The mean values for maximum number of fruits per plant were recorded by the genotypes of the cluster V (41.20) followed by cluster III (37.13), while minimum number of fruits per plant was recorded by the genotypes of the cluster IV (27.73) followed by the cluster II (29.80) and cluster I (29.87).

The genotypes of the cluster II (6.52 cm) recorded highest fruit length followed by the cluster IV (4.88 cm) whereas, the genotypes of the cluster V (3.71 cm) recorded lowest fruit length followed by cluster III (4.21 cm) and cluster I (4.46 cm). Highest fruit width was recorded in the genotypes of the cluster IV (5.55 cm) followed by the cluster II (4.95 cm) whereas, lowest fruit width was recorded in the genotypes of the cluster V (4.06 cm) followed by the cluster I (4.71 cm) and cluster II (4.95 cm). Maximum fruit weight was observed in the genotypes of the cluster IV (82.07 g) followed by the cluster I (59.03 g), while the genotypes of the cluster V (25.57 g) recorded minimum fruit weight followed by the cluster II (51.57 g) and cluster III (52.80). The character fruit yield per plant was recorded maximum in the genotypes of the cluster IV (2.31 kg) followed by the cluster III (1.88 kg) and cluster I (1.77 kg), while the genotypes of the cluster V (1.06 kg) recorded minimum fruit yield per plant followed by the cluster II (1.52 kg).

More number of seeds per fruit were recorded in the genotypes of the cluster I (37.02), while less number of seeds per fruit were recorded in the genotypes of the cluster IV (33.47) followed by the cluster II (34.09), cluster III (34.45) and cluster V (34.73). Most number of locules per fruit was recorded in the genotypes of the cluster IV (3.47) followed by the cluster III (3.42), while least number of locules per fruit was recorded in the genotypes of the cluster I (3.22) followed by the cluster V (3.33) and cluster II (3.38). The character ascorbic acid content in the fruit was highest in the genotypes of the cluster II (22.22 mg/100 g) followed by cluster I (20.47 mg/100 g) and cluster III (20.04 mg/100 g) whereas, lowest ascorbic acid content was recorded in the genotypes of the cluster V (19.30 mg/100 g) followed by the cluster IV (19.72 mg/100 g). Highest total soluble solids were recorded in the genotypes of the cluster V (5.90 °Brix) followed by the cluster III (5.14 °Brix), while lowest total soluble solids were recorded in the genotypes of the cluster IV (4.17 °Brix) followed by the cluster I (4.96 °Brix) and cluster II (4.96 °Brix).

Lycopene content recorded its highest mean value in the genotypes of cluster III (6.34 mg/100 g) followed by cluster II (5.88 mg/100 g) and cluster I (5.56 mg/100 g), while the lowest mean value was recorded in the genotypes of cluster V (4.78) followed by cluster IV (5.06 mg/100 g). Stomatal diffusive resistance recorded its highest mean value in the genotypes of the cluster IV (8.96 sec/cm) followed by the cluster II (7.81 sec/cm) and cluster I (7.46 sec/cm), while the lowest mean value was recorded in the cluster V (4.78 sec/cm) followed by the cluster III (5.23 sec/cm). The character relative water content was recorded maximum values in the genotypes of the cluster II (57.98 %) followed by cluster I (47.74 %) and cluster IV (43.73 %) whereas, the minimum values were recorded in the cluster V (36.67 %) followed by the cluster III (36.97 %). The character chlorophyll content was recorded maximum values in the genotypes of the cluster IV (1.46 %) followed by cluster I (1.01 %) and cluster III (1.00 %) whereas, the minimum values were recorded in the cluster V (0.74 %) followed by the cluster II (0.91 %).

The results of Mahalanobis's D^2 statistics revealed substantial and desirable genetic diversity among twenty germplasm lines included in the present study for all the twenty five characters under consideration collectively. 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) [1, 6]. Murthy and Arunachalam (1960) [13] pointed that Mahalanobis D^2 statistics is an important breeding tool to evaluate the clustering pattern. Average inter and intra cluster distances revealed that, in general, intercluster distances were much higher than those of intracluster distances, suggesting homogeneous and heterogeneous nature of the germplasm lines within and between the clusters, respectively. These results are in accordance with the findings of Parthasarathy and Aswath (2002) [14], Mahesha *et al.* (2006) [10] and Sekhar *et al.* (2008) [20] in tomato.

Mahalanobis D^2 statistic was found to be a useful tool to assess the relative contribution of different characters to the total divergence both inter and intracluster levels. In general, the characters responsible for discrimination between populations can narrow down the problem of selecting divergent parents for breeding programme. Amongst the yield contributing characters, the fruit weight, number of fruits per plant and plant height were the major contributors towards divergence. Mohanty and Prusti (2001) [12] also observed such maximum contribution of fruit weight and number of fruits per plant to total divergence of tomato germplasm. De *et al.* (1988) [5] opined that traits contributing maximum towards the D^2 values need to be given more emphasis for deciding the clusters to be taken for the purpose of choice of parents for hybridization. The characters that predominantly contributed to divergence in this study also happen to be the main components of yield. The results of the present study point out a positive contribution of genetic divergence and yield components; this can be of considerable help in selecting for yield and other economic traits. It can be concluded that there was more divergence for these characters offering greater scope while making selection of horticulturally superior genotypes of tomato.

In general, the genotypes grouped together in one cluster are less divergent than those which are placed in a different cluster. Further, higher intracluster distance indicates high degree of divergence within that cluster. Mahalanobis's D^2 statistics revealed that considerable genetic diversity exists within and among five clusters. The characters fruit weight, fruit set per cent, number of fruits per plant and plant height were the potent factors in differentiating the germplasm of tomato under study.

Relative contribution of characters towards diversity

Number of times each of twenty five traits appeared in first rank and its respective per cent contribution towards genetic divergence (Table 3). The results showed that the character

chlorophyll content contributed maximum (42.11 %) towards diversity by taking 80 times ranking first followed by relative water content (21.05 %) by 40 times, fruit length (9.47 %) by 18 times, ascorbic acid (8.42 %) by 16 times, total soluble solids (5.26 %) by 10 times, days to first fruit harvest (4.21 %) by 8 times, stomatal diffusive resistance (2.11 %) by 4 times, fruit yield per plant (2.11 %) by 4 times, average fruit weight and number of clusters per plant (1.58 %) by 3 times, fruit width (1.05 %) by 2 times. Apart from high divergence, performance of the genotypes and characters with maximum contribution towards divergence should also be given due consideration which appears as desirable for inclusion in tomato improvement.

The choice of parents for heterosis breeding depends on genetic diversity of parents. The expression of heterosis is influenced by genetic diversity of parents. Cress (1966) [3] demonstrated that 'genetic diversity' is necessary for significant heterosis but not sufficient to guarantee it'. Several reports are available to show that hybrids between genetically diverse parents manifest greater heterosis than those between more closely related parents (Singh and Sharma, 1989) [21].

Hence, apart from selecting genotypes from the clusters which have high inter- cluster distance for hybridization, one can also think of selecting parents based on extent of genetic divergence in respect to a particular character of interest. This means that, if breeders' intention is to improve fruit yield, he can select parents which are highly divergent with respect to these characters.

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