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PHENOTYPIC DIVERGENCE IN TOMATO GERMPLASM

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ABSTRACT

Phenotypic divergence was quantified by multivariate analysis among the 70 genotypes collected from different agro-climatic regions and was available in the gene bank of Energypac Agro Ltd., Gazipur, Bangladesh. Based on the phenotypic value of 11 characters, 70 genotypes were grouped into five clusters. The genotypes of tomato were distributed in different clusters suggesting that no association was found between geographical and phenotypic diversity. Cluster II consisted of maximum twenty three genotypes (32.86%) followed by cluster III of sixteen genotypes (22.85%). Cluster IV and Cluster V comprised of thirteen (18.57%) and ten genotypes (14.29%), respectively. Cluster I consisted of eight genotypes (11.43%). The highest intra-cluster divergence (0.061) for cluster I was invariably smaller than the lowest inter-cluster divergence between cluster IV and cluster V (2.83), thus authenticating the clustering pattern formed in this study. The intra-cluster divergence ranged from 0.007 to 0.061, whereas the inter-cluster divergence ranged from 2.83 to 8.34 between clusters IV and V and clusters III and V, respectively. The four characters that played the greatest role in differentiation were locule number per fruit, pericarp thickness, fruits per plant and days to 50% flowering. Twenty homozygous parents (15 female and five male) were selected from five clusters using range test among genotypes within cluster. From cluster I parents TM409, TM386 and TM528 and from cluster III parents TM403 and TM349 were selected as male. Parents TM356, TM361, TM368, TM371, TM377, TM384, TM422 and TM423 from cluster II; parents TM388, TM390, TM392 and TM410 from cluster IV and parents TM382, TM419 and TM360 from cluster V were selected as female.

Keywords: Tomato, Parent selection, Phenotypic value, Multivariate analysis

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INTRODUCTION

Tomato (*Solanum lycopersicum* L.) belongs to Solanaceae is one of the important and popular vegetable in the world. It is considered the second important vegetable in Bangladesh after potato because of its wider adaptability, high nutritional value, high yielding potential, multipurpose uses and commercial important (Reddy et al., 2013). Tomato is diploid (2n = 24) and self-pollinated annual crop. It is source of rich lycopene that acts as an antioxidant which is often colligated with carcinogenesis (Bai and Lindhot, 2007). In Bangladesh the average yield of tomato is very low (13.68 t ha^{-1}) compared to other tropical countries (BBS, 2018).

The knowledge of available genetic diversity is an important factor for any heritable improvement and selecting desirable parents from a germplasm for the successful breeding programe. Among the various methods identified/developed to study the genetic divergence in the genotypes. Mahalanobis D^2 (Mahalanobis, 1936) is reliable and the most frequently used. D^2 analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence, both at the inter and intra-cluster levels. The grouping of genotypes into different clusters is done by Tocher's method as described by Rao (1952). An improvement in yield and related traits in self-pollinated crops like tomato is normally achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridization (Reddy et al., 2013; Nalla et al., 2014). It is very useful technique of measuring genetic divergence as reported by various workers (Meena and Bahadur, 2015). Considering the above facts, the present studies had been planned with the objective to assess the extent of phenotypic diversity and identify promising accessions to use in future hybridization program from the available gene pool based on eleven quantitative traits.

MATERIALS AND METHODS

The present investigation was carried out R&D center, Energypac Agro Ltd., Gazipur. Seventy tomato genotypes were used as experimental materials (Table 1). Experiment was laid out in RCBD design with three replications during Rabi season of 2012-13. Seed sowing was carried out in October in the nursery. Thirty days old seedlings were transplanted in the field in Mid November with spacing of 40 cm between plants and 60 cm between rows. Necessary intercultural operations were carried out during cropping period for proper growth and development of the plants. Data were recorded on various morphological traits such as days to 50% flowering, flower per cluster, fruits per cluster, fruits per plant, plant height, fruit weight, fruit length, fruit diameter, pericarp thickness, locule number per fruit and fruit yield per plant. The means of characteristics per accessions of three replicates were subjected to D^2 and canonical analyzes for genetic divergence (Mahalanobis,1936; Rao, 1952).

Table 1. List of tomato germplasm and their origin

Designation	Origin
TM341, TM342, TM343, TM344, TM354, TM355, TM356, TM382, TM383, TM384, TM388, TM390, TM392, TM393, TM403, TM404, TM405, TM406, TM407, TM408, TM423, TM425, TM445, TM429, TM385, TM399, TM491, TM497, TM395, TM360, TM510	India
TM361, TM368, TM369, TM370, TM371, TM374, TM375, TM376, TM377, TM426, TM428, TM427, TM386, TM357, TM400, TM467, TM470, TM372, TM462, TM463, TM458, TM460, TM465, TM466, TM412, TM394, TM349, TM514, TM521, TM524, TM508	Bangladesh
TM409, TM528	China
TM515	Italy
TM410, TM417, TM419, TM420, TM422	Thailand

RESULTS

Seventy tomato genotypes were used to study the genetic diversity among them. ANOVA showed the presence of significant variation among the tested genotypes in respect of the yield and yield related characters (Table 2).

PCA analysis

The results showed that the first principal axis largely accounted for the variation among the genotypes which alone contributed 25.31% of the total variation (Table 3). The first four axis of the principal component with eigen values above unity accounted for 73.59% of the total variation among the 11 axis. The rest seven axes contributed remaining 26.41% of total variation.

Table 2. Analysis of variances for yield and yield related characters of 70 genotypes in tomato

Variations	Df	MS										
		D50%F	FPC	FRPC	FPP	PH	FW	FL	FD	PT	LN	FYP
Rep	2	14.57	0.08	2.83	23.41	35.616	593.43	0.07	0.15	0.53	0.01	0.76
Var	69	162.58**	2.10**	2.64**	212.54**	593.15**	1437.91**	1.47**	0.87**	2.46**	4.76**	1.30**
Error	138	4.63	0.52	0.42	36.24	71.44	282.81	0.15	0.14	0.55	0.46	0.42

** >P 1%, DF= degrees of freedom, MS= mean sum of square, D50%F= days to 50% flowering, FPC= flower per cluster, FRPC= fruits per cluster, FPP= fruits per cluster, PH= plant height (cm), FW= Fruit weight (g), FL= Fruit length (cm), FD= Fruit diameter (cm), PT= Pericarp thickness (mm), LN= Locule number per fruit and FYP= Fruit yield per plant (Kg).

Table 3. Eigen values and percent contribution of 11 axis of 70 germplasm

Characters	Eigen values	Percent variation	Cumulative %
I	2.78	25.31	25.31
II	2.21	20.17	45.48
III	1.65	15.01	60.49
IV	1.44	13.10	73.59
V	0.94	8.55	82.14
VI	0.76	6.99	89.13
VII	0.65	5.92	95.05
VIII	0.30	2.78	97.83
IX	0.14	1.34	99.17
X	0.05	0.50	99.67
XI	0.03	0.33	100.00

Clustering and Cluster Distance

On the basis of nonhierarchical clustering, 70 tomato genotypes were grouped into five clusters (Table 4). Cluster II included of 23 genotypes (32.86%) and it was followed by cluster III of 16 genotypes (22.85%), cluster IV comprises 13 genotypes (18.57%), cluster V consisted of 10 genotypes (14.29%) while cluster I consisted eight genotypes (11.43%). The inter-cluster distance ranged from 2.83 to 8.34 (Table 5). The inter cluster D^2 values were maximum (8.34) between the cluster III and cluster V, followed by III and I (6.86) and III and IV (6.32). The intra cluster distance was highest in cluster I (0.061) followed by cluster III (0.016) and the lowest in cluster IV (0.008).

Table 4. Distribution of 70 tomato genotypes in five different clusters

Cluster no.	No. of Genotypes	Genotypes
I	8	TM342, TM344, TM370, TM409, TM425, TM386, TM357, TM528
II	23	TM341, TM354, TM355, TM356, TM361, TM368,TM371, TM376, TM377, TM384, TM405, TM406, TM422, TM423, TM426, TM427, TM385, TM491, TM463, TM465, TM510, TM521, TM524
III	16	TM343, TM369, TM374, TM403, TM404, TM417, TM420, TM428, TM462, TM466, TM412, TM394, TM349, TM514, TM515, TM508
IV	13	TM375, TM383, TM388, TM390, TM392, TM393, TM407, TM408, TM410, TM445, TM497, TM458, TM460
V	10	TM382, TM419, TM429, , TM400, TM399, TM395, TM467, TM470, TM360, TM372
	70	

Table 5. Intra (bold) and inter-cluster divergence (D^2 values) among five clusters of tomato

Clusters	I	II	III	IV	V
I	0.061 (0.246)	5.27 (2.30)	6.86 (2.62)	4.29 (2.07)	6.06 (2.46)
II		0.005 (0.070)	3.73 (1.93)	3.11 (1.76)	5.18 (2.28)
III			0.016 (0.126)	6.32 (2.51)	8.34 (2.89)
IV				0.007 (0.084)	2.83 (1.68)
V					0.011 (0.105)

D value in parenthesis

Cluster mean analysis

Minimum days to 50% flowering were observed in cluster I (53.92) (Table 6). Maximum (6.47) flowers per cluster were observed in cluster III. Genotypes in cluster III had the highest mean (5.99) for fruits per cluster. Maximum fruits per plant (32.10) and plant height (119.14) were observed in cluster III and cluster I, respectively. Cluster V and cluster IV had the maximum average fruit weight (123.35) and fruit length (5.99), respectively. Highest fruit diameter (6.29) and pericarp thickness (8.20) both were recorded in cluster V. Minimum locule number per fruit was observed in cluster III (2.80). A highest fruit yield per plant was recorded by the genotype making up cluster I (2.51).

Table 6. Cluster mean values of 11 characters of 70 genotypes

Characters	I	II	III	IV	V
Day to 50% flowering	53.92	54.51	63.98	56.95	59.97
Flower per cluster (no.)	5.81	6.15	6.47	5.85	5.99
Fruit per cluster (no.)	5.88	5.24	5.99	5.05	5.59
Fruits per plant (no.)	28.11	25.58	32.10	19.50	17.80
Plant Height (cm)	119.14	82.70	87.23	89.76	80.27
Average fruit weight (g)	90.81	82.94	59.88	102.45	123.35
Fruit length (cm)	5.61	5.47	5.27	5.99	5.97
Fruit diameter (cm)	5.70	5.43	4.93	5.77	6.29
Pericarp thickness (mm)	7.33	7.70	7.23	7.84	8.20
Locule number per fruit	3.85	3.23	2.80	3.55	3.87
Fruit yield per plant (Kg)	2.51	2.05	1.92	1.99	2.16

Table 7. Relative contributions of eleven characters of 70 genotypes

Characters	Principal Component	
	Vector-1	Vector-2
Day to 50% flowering	0.0156	0.0262
Flower per cluster (no.)	-0.1173	0.0811
Fruit per cluster (no.)	0.3464	-0.3603
Fruits per plant (no.)	0.0738	0.0226
Plant Height (cm)	-0.0420	-0.1169
Average fruit weight (g)	-0.1248	0.0229
Fruit length (cm)	0.1940	-0.2653
Fruit diameter (cm)	0.0546	-0.8500
Pericarp thickness (mm)	0.0925	0.4530
Locule number per fruit	0.4192	0.2609
Fruit yield per plant (Kg)	-0.6675	0.4550

Selection of parents

The genotypes of cluster I best in terms of early flowering, high yielder and tall plant (Table 11). The genotypes of cluster II produced early maturing and medium yielder. The genotype of cluster III possessed highest flower and fruit per cluster and highest fruit per plant. The genotypes of cluster IV produced longer fruit and higher fruit weight and the cluster V possessed highest fruit weight, more fruit diameter, pericarp thickness and locule number per fruit**.** To select potential homozygous parents from each cluster, DMRT was done within each cluster. That`s why mean values with DMRT of studied traits are presented in Table 8-10.

Table 8. Mean performance for 11 traits of genotypes of cluster I & V

Cluster	Genotype	DFPF	FPC (no.)	FRPC (no.)	FPP (no.)	PH (cm)	FW (g)	FL (cm)	FD (cm)	PT (mm)	LN	FYP (Kg)
I	TM342	52.00b	5.67ab	5.83-ac	33.11a	111.46ab	83.16bc	5.86bc	5.11b	7.72b	2.33c	2.76a
	TM344	52.67b	6.22a	6.67ab	29.83ab	112.74ab	104.86ab	7.15a	5.50b	8.83a	2.00c	3.13a
	TM370	54.00ab	6.67a	5.56a-d	34.22a	137.38a	62.52c	5.16d-f	5.19b	6.29e	3.42b	2.12ab
	TM409	52.33b	4.78bc	5.35cd	14.50c	118.17ab	93.50b	5.14ef	5.75ab	7.58bc	4.00ab	1.38b
	TM425	49.33c	5.89ab	4.44d	34.35a	103.07ab	84.16bc	5.52cd	5.51b	7.33b-d	2.22c	2.94a
	TM386	52.67b	6.56a	5.96a-c	21.50bc	87.16b	118.78a	5.49de	6.38a	6.84c-e	4.76a	2.53a
	TM357	55.67a	6.11a	6.75a	24.67ab	117.33ab	94.85b	5.03f	5.81ab	6.75de	4.17ab	2.36ab
	TM528	48.00c	3.78c	5.44b-d	29.63ab	115.94ab	84.39bc	5.99b	5.73ab	8.13ab	3.67ab	2.49ab
V	TM382	57.00d	5.11c	4.67bc	22.67a-c	73.73c	112.53a	6.17b	6.17bc	7.95a	4.67b	2.58a

Cluster	Genotype	DFPF	FPC (no.)	FRPC (no.)	FPP (no.)	PH (cm)	FW (g)	FL (cm)	FD (cm)	PT (mm)	LN	FYP (Kg)
	TM419	67.33b	7.33a	7.00a	24.53a	137.00a	119.07a	5.00c	7.03a	5.99b	9.00a	2.90a
	TM429	75.33a	5.22c	5.35bc	15.50c-e	79.17bc	115.28a	7.08a	5.68c	9.00a	2.00c	1.70a
	TM400	54.67d	6.78ab	7.00a	15.82b-e	83.00bc	124.04a	5.92bc	6.17bc	8.14a	4.37b	1.96a
	TM399	56.67d	6.00bc	6.67a	21.83a-c	87.00b	122.50a	5.51bc	6.33a-c	8.08a	4.00bc	2.70a
	TM395	60.33c	6.00bc	4.22c	15.11c-e	74.67c	130.20a	5.87bc	6.33a-c	7.92a	3.17bc	1.99a
	TM467	62.00c	6.22a-c	5.44b	9.67e	77.67bc	133.68a	5.87bc	6.42a-c	8.17a	4.17bc	1.26a
	TM470	62.67c	6.22a-c	4.67bc	18.00a-d	81.00bc	123.08a	6.18b	6.93ab	9.28a	4.11bc	2.22a
	TM360	61.33c	6.33a-c	7.11a	24.00ab	80.00bc	113.86a	5.95bc	5.92c	8.17a	2.83bc	2.77a
	TM372	61.00c	5.78bc	5.35bc	11.50de	73.83c	143.55a	5.94bc	6.74ab	9.17a	3.83bc	1.65a

Table 9. Mean performance for 11 traits of genotypes of cluster II

Cluster	Genotype	DFPF	FPC (no.)	FRPC (no.)	FPP (no.)	PH (cm)	FW (g)	FL (cm)	FD (cm)	PT (mm)	LN	FYP (Kg)
	TM341	55.00d-f	8.11a	6.33a-d	25.33b-d	78.01c-f	76.08a-c	5.97a-c	5.00de	7.75a-f	2.33gh	1.94a-e
	TM354	48.33g-j	6.74b	4.44g	20.67b-d	79.53b-f	85.98a-c	5.20c-f	5.75a-c	7.97a-e	3.50c-f	1.84a-e
	TM355	61.33bc	5.89b-d	4.22g	16.67cd	84.31a-e	74.96bc	5.80a-e	4.88e	7.56b-g	2.33gh	1.25de
	TM356	51.67e-i	6.44b	5.44c-g	28.08a-c	83.86a-e	91.99ab	5.75b-e	5.77a-c	7.30c-g	4.00b-d	2.58a-c
	TM361	53.67e-g	4.89cd	4.67fg	23.67b-d	87.13a-d	84.38a-c	5.32c-f	5.68a-d	7.00d-g	4.67b	2.04a-e
	TM368	53.00e-h	6.56b	7.11a	33.58ab	79.74b-f	68.34c	5.09ef	5.25b-e	6.30g	3.27c-g	2.29a-e
	TM371	47.33h-j	6.78b	5.78b-f	33.22ab	78.66b-f	86.88a-c	5.23c-f	5.72a-c	8.90a	3.27c-g	2.87a
II	TM376	57.00c-e	6.33b	6.22a-e	20.67b-d	68.97f	95.32a	5.33c-f	5.97ab	7.67a-f	4.67b	1.98a-e
	TM377	64.33b	5.78b-d	6.75ab	15.33cd	73.33ef	92.07ab	5.57b-f	5.37a-e	6.56fg	3.78b-e	1.38c-e
	TM384	50.33f-j	6.44b	4.44g	21.60b-d	74.81d-f	84.93a-c	5.49c-f	5.56a-e	8.19a-d	2.71e-h	1.83a-e
	TM405	55.33d-f	6.67b	5.00e-g	20.34b-d	90.13a-c	86.12a-c	5.33c-f	5.33a-e	8.38a-c	2.00h	1.45c-e
	TM406	46.00ij	5.78b-d	5.00e-g	15.78cd	77.82c-f	87.30a-c	5.19c-f	5.50a-e	6.79e-g	4.33bc	1.38c-e
	TM422	50.00f-j	6.11bc	4.44g	22.73b-d	92.32ab	70.83c	5.93a-d	5.27b-e	8.17a-d	2.33gh	1.61b-e
	TM423	50.33f-j	4.67d	6.67a-c	33.50ab	88.42a-d	82.28a-c	5.38c-f	5.52a-e	7.83a-f	3.00d-h	2.76ab
	TM426	52.33e-h	4.89cd	4.22g	38.44a	78.66c-f	75.65a-c	5.31c-f	5.12c-e	8.00a-e	2.33gh	2.90a
	TM427	51.33ei	6.67b	4.67fg	32.48ab	84.33a-e	72.04bc	5.18d-f	5.27b-e	7.09c-g	3.33c-g	2.34a-d
	TM385	56.67c-e	6.56b	5.35d-g	25.89a-d	89.78a-c	84.68a-c	5.51c-f	5.48a-e	8.39a-c	2.55f-h	2.20a-e
	TM491	45.33j	5.56b-d	4.44g	12.77d	79.40b-e	82.49a-c	4.92f	5.56a-e	5.19h	6.87a	1.05e
	TM463	71.00a	6.22bc	5.78b-f	26.00a-d	87.33a-d	81.37a-c	6.48a	4.89e	8.89a	2.00h	2.11a-e
	TM465	59.33b-d	6.22bc	5.96a-e	23.00b-d	95.67a	75.12a-c	4.86f	5.26b-e	7.50b-g	2.58f-h	1.74a-e
	TM510	60.33b-d	5.44b-d	7.00ab	21.00b-d	82.21a-f	84.83a-c	6.29ab	5.13c-e	8.67ab	2.00h	1.81a-e
	TM521	56.33c-e	6.14bc	4.44g	33.00ab	84.06a-e	76.80a-c	5.57b-f	5.17c-e	7.18c-g	2.67f-h	2.56a-c
	TM524	53.33e-g	5.78b-d	4.22g	32.33ab	84.33a-e	85.24a-c	4.81f	6.04a	7.33c-g	4.00b-d	2.79ab

Values with same letter(s) are statistically identical at 5% level of probability

Table 10. Mean performance for 11 traits of genotypes of cluster III & IV

Cluster	Genotype	DFPF	FPC (no.)	FRPC (no.)	FPP (no.)	PH (cm)	FW (g)	FL (cm)	FD (cm)	PT (mm)	LN	FYP (Kg)
III	TM343	52.33g	8.33a	7.00a	34.11b-d	76.25e	60.98cd	6.16b	4.73b-d	7.78a-d	2.00f	2.09b-e
	TM369	68.67cd	7.33ab	5.35c-e	32.17b-e	91.73b-d	47.06d	4.15f	4.90b-d	6.50d-f	3.33cd	1.51de
	TM374	56.00ef	5.67c-f	5.00c-f	20.22ef	85.70c-e	119.37a	5.64b-d	6.07a	7.50a-e	4.67b	2.40b-d
	TM403	54.00fg	7.00a-c	5.56cd	22.58d-f	75.01e	83.41bc	5.86bc	5.56a-c	8.46ab	2.58d-f	1.88c-e
	TM404	56.00ef	6.33b-e	5.78bc	21.33d-f	75.18e	61.39cd	5.20cd	5.07b-d	8.00a-c	2.00f	1.24de
	TM417	67.00d	7.45ab	6.75ab	30.19b-f	79.50de	54.26d	4.09f	5.14b-d	7.18b-f	4.00bc	1.59de
	TM420	77.67a	6.12b-e	6.67ab	33.75b-e	75.50e	63.43b-d	4.00f	5.48a-d	6.18ef	5.67a	2.15b-e
	TM428	52.67g	5.22ef	5.44c-e	25.33c-f	93.68bc	58.50cd	5.00de	5.03b-d	6.33ef	2.00f	1.50de
	TM462	69.33cd	7.34ab	5.56cd	21.67d-f	84.00c-e	61.72cd	4.32ef	4.87b-d	6.00f	3.17c-d	1.23de
	TM466	71.33bc	5.67c-f	6.75ab	40.78ab	82.93c-e	71.56b-d	7.03a	4.90b-d	7.89a-c	2.00f	2.85bc
	TM412	57.00ef	5.56d-f	6.67ab	42.83ab	79.67de	71.15b-d	6.91a	4.70cd	7.78a-d	2.44ef	3.18b
	TM394	73.67b	6.22b-e	4.44ef	37.50a-c	89.67b-d	60.59cd	5.05de	5.07b-d	6.83c-f	3.33cd	2.29b-d
	TM349	55.00eg	4.67f	4.22f	17.33f	105.67a	56.01cd	5.37cd	4.67cd	7.50a-e	2.00f	0.98e
	TM514	69.00cd	6.67b-d	5.44c-e	39.33ab	109.50a	49.01d	5.53b-d	4.60d	8.57a	2.00f	1.91c-e
	TM515	73.00b	7.11ab	6.67ab	39.44ab	98.22ab	54.25d	5.87bc	4.63d	8.44ab	2.00f	2.12b-e
	TM508	57.67e	6.41b-e	4.67d-f	48.82a	86.72b-e	89.79b	5.00de	5.63ab	7.96a-c	3.67c	4.31a
IV	TM375	56.33c	4.33d	5.35bc	22.83a-d	93.49bc	109.24a	5.75d	5.78a-d	8.17b-d	4.00ab	2.51ab
	TM383	54.33c-e	5.11cd	4.78bc	18.67b-e	89.04bc	98.55a	5.32d	5.73a-d	7.33c-e	4.11ab	1.80b-d
	TM388	55.33cd	5.56cd	4.22c	22.67a-d	105.09a	108.99a	5.53d	6.11a	6.50e	4.89a	2.49ab
	TM390	54.33c-e	5.33cd	4.78bc	23.92a-c	79.76de	99.51a	5.63d	5.68a-d	6.88de	3.92ab	2.35a-c
	TM392	55.33cd	5.67c	4.67bc	19.17a-e	86.36cd	97.96a	5.38d	5.95a-c	6.83de	4.17ab	1.88b-d
	TM393	53.67c-e	7.11ab	5.00bc	26.00a	93.78bc	96.78a	6.78bc	5.40cd	9.71a	2.42d	2.53ab
	TM407	52.33e	5.67c	4.33c	17.50c-e	85.88cd	111.49a	5.34d	6.14a	7.19c-e	4.83a	1.94a-d
	TM408	52.67de	5.78c	4.67bc	15.75de	93.32bc	102.58a	5.59d	5.79a-d	7.33c-e	4.40ab	1.62cd
	TM410	66.00a	7.33a	5.96ab	15.67de	75.33e	100.16a	5.72d	5.80a-d	7.17c-e	3.50bc	1.52d
	TM445	56.00c	6.00bc	7.11a	14.00e	92.50bc	104.88a	7.41a	5.36d	8.40a-c	2.33d	1.48d
	TM497	56.33c	6.44a-c	4.44bc	16.23de	95.63b	90.67a	5.69d	6.02ab	8.50a-c	2.89cd	1.42d
	TM458	64.67ab	6.11a-c	5.00bc	25.44ab	86.26cd	108.70a	7.23ab	5.81a-d	9.37ab	2.00d	2.75a
	TM460	63.00b	5.56cd	5.35bc	15.67de	90.50bc	102.34a	6.53c	5.50b-d	8.50a-c	2.75cd	1.60cd

Table 11. Parent selection from different clusters and their saline features

Cluster	Salient features	Selected parent genotypes
I	Early flowering Tall plant High fruit yield	TM409, TM386, TM528 as male
II	Early flowering Medium yielder	TM356, TM361, TM368, TM371, TM377, TM384, TM422, TM423 as female
III	High flower and fruit per cluster High fruits per plant	TM403, TM349 as male
IV	Longer fruit Higher fruit weight	TM388, TM390, TM392,TM410 as Female
V	Highest fruit weight More fruit diameter More pericarp thickness More locule number per fruit	TM382, TM419, TM360 as Female

DISCUSSION

The clustering pattern indicates that there was no association between geographical distribution of genotypes and genetic divergence. This result suggests that the factor(s) other than geographical separation is responsible for divergence. Singh et al. (2008) reported eight clustering in tomato, Sharma et al. (2006) studied with 60 genotypes of tomato and had 10 clusters and Prasanth (2003) had seven clusters for 67 tomato genotypes. The present genotypes were grouped into five clusters. Among the five clusters, cluster II was the biggest with 23 genotypes, followed by III and IV with 16 and 13 genotypes. This result supported to the Mahesh et al. (2006) results, they reported 11 genotypes in cluster II and Singh et al. (2008) reported 10 each in cluster I & II.

The maximum inter cluster distance recorded between III and V clusters (8.34) indicate to obtain wide variability of the genotypes in these clusters. The moderate distance was between cluster I and II (5.27). It was apparent that the genotypes included cluster III was far diversed from cluster V and where genotypes belonging to V and IV were the least diversed followed by IV and II. Genotypes of cluster III-IV, III-I and I-V were moderately diversed from each other. Therefore, the genotypes present in the clusters III and V or I and II could be utilized for successful hybridization progarmme. Inter cluster distance was observed maximum between cluster V and VI by Prasanth (2003). Considerable diversity between clusters was noticed by Dharmatti et al. (2001). Hybridization among the genotypes drawn from widely divergent clusters with high yield potential would likely to manifest maximum heterotic combinations as well as new recombination with desired traits. The intra cluster distance was maximum in cluster I (0.061) was invariably smaller than the lowest inter cluster divergence between clusters IV and V (2.83), thus authenticating the clustering pattern formed in this study. The maximum intra-cluster distance was reported by Prasanth (2003) in cluster IV. The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related.

First principal component axis contributed maximum (25.31%) each towards total divergence followed by 2nd PCA (20.17%), 3rd PCA (15.01%), 4th PCA (13.10%), 5th PCA (8.55%) and 6th PCA (6.99). These results were almost in accordance with the studies of Prasanth (2003).

Cluster I mainly an early flowering genotype e.g. it produced the lowest values for 50% flowering. They possessed the highest mean values for plant height and yield. This findings support to the result of Arun et al. (2003) for these traits. The genotypes under cluster II were also early flowering and higher yielder. Cluster III has late flowering and maximum flowers and fruits per cluster, fruits per plant and the lowest fruit weight, fruit length, fruit diameter, pericarp thickness, locule number per fruit. The genotypes belong to the cluster IV were oblong fruit and lowest number of fruits per cluster. The genotypes of the cluster V were shorter plant statue and the least number of fruits per plant. They also had larger fruit size along with most fruit diameter and pericarp thickness. In general, cluster V had maximum mean for most of the characters followed by cluster I including yield in the present study.

Selection of parents

From five clusters twenty parents were selected based on mean value within each cluster. From cluster I the genotypes TM409, TM386 and TM528 and from cluster III genotypes TM403 and TM349 were selected as male (tester) parent. Other hand, the female (line) parents were selected as TM356, TM361, TM368, TM371, TM377, TM384, TM422 and TM423 from cluster II; genotypes TM388, TM390, TM392 and TM410 from cluster IV; and genotypes TM382, TM419 and TM360 from cluster V for line x tester (15 x 5) cross.

CONCLUSION

Parent selection is an important step in any breeding program. In the present study, 20 genotypes out of 70 were selected using cluster analysis and mean performance. Cluster analysis developed uniform group and mean separation helped in selection parent from each uniform group. Genetic potentiality of the selected parents could be evaluated by combining ability and heterotic hybrid.

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