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ORIGINAL ARTICLE

Evaluation of Breeding Potential of Tomato Germplasm using D^2 analysis

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ABSTRACT

The present investigation was carried out to evaluate the breeding potential of tomato germplasm. All the genotypes were grouped into six clusters based on D^2 values, which exhibited no association between geographical and genetic divergence. The intra cluster distance was the minimum for cluster II (0.000) and maximum for cluster IV (4.111). The maximum distance at inter-cluster level was between clustering II and IV (25.331) indicated that the genotypes belongings to these groups were genetically most divergent. Genotypes included in cluster V were important for % of brix in tomato fruit whereas secondary branches per plant and yield per plant was remarkable feature for cluster II. Cluster VI was important for vit.-C, chlorophyll % of leaf and pH of tomato juice. Considering diversity pattern, genetic status and others agronomic performance BD-7285 form cluster II, BD-9011 form cluster I, BD-7759 form cluster IV, BD-10124 form cluster III, BARI Tomato -11 form cluster IV and BARI Tomato 15 form Cluster VI, might be considered better parents for efficient hybridization programme. Involvement of such diverse genotypes in crossing programme may produce desirable segregants.

Key words: *Genetic diversity, germplasm, Multivariate analysis*

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INTRODUCTION

Tomato (*Solanum lycopersicum*L, 2n=24) a member of family Solanaceae. It is a herbaceous, annual to perennial, prostrate and sexually propagated plant with bisexual flower. It is a typical day neutral plant and self-pollinated crop. Tomato ranking 1st in the world for vegetables, accounts for 14% of world vegetable production [4]. Systematic study and evaluation of germplasm is of great importance for current and future agronomic and genetic improvement of the crop. Furthermore, if an improvement program is to be carried out, evaluation of germplasm is imperative, in order to understand the genetic background and breeding value of the available germplasm [13]. Diversity and evaluation of tomato germplasm are necessary in the context of genetics against, disappearance, as well as, a rich source of genetic variability. For this characterization of data are the first requirements, for particularly plant breeders, have also emphasized the need for improved evaluation of accessions. It is worth emphasizing that both characterization and evaluation data provide an effective source of information for genetic diversity studies and ultimately that will play an important role for identify the suitable parents in the future hybridization program.

MATERIALS AND METHODS

Experimental Site

The present research work was carried out in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during September 2013-May 2014. The location of the site is 23° 74' N latitude

and 90° 35' E longitude with an elevation of 8.2 meter above sea level. The experimental site was situated in the subtropical zone. The soil of the experimental site lies in Agroecological region of "Madhupur Tract" (AEZ No. 28). Its top soil is clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 6.1 and organic carbon content is 0.82%.

Plant Materials

Forty eight genotypes of tomato were used for the present research work. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Genetic Resources Centre of Bangladesh Agricultural Research Institute and land races were collected from farmer's field.

Field Experiment

The experimental plot was prepared by ploughing with proper tiller. The weeds and other unwanted plant materials were removed from the field during the land preparation. Proper laddering was done to bring the soil at proper tilth condition. A Randomized Complete Block Design was used in the experiment with three replications. The field was divided into three blocks; the blocks were subdivided into 48 plots. Genotypes were randomly assigned into 48 plots in each block. The unit plot size was 37.71m×15m and block to block distance was 1.00 m.

The seed sowing was carried out on 13 November 2013 in the seedbed. After 25 days seedlings were transplanted into the main field. Intra and inter row distance were maintained @ 0.6 m and 0.5 m, respectively.

The Urea, Triple Super Phosphate, Muriate of Potash @ 550, 450, 250 kg/ha and Cowdung 10 ton/ha were used in the experiment. Total TSP and Cowdung were applied in final land preparation. Half of Urea and half muriate of potash were applied after three weeks and remaining were applied in the plot after five weeks of transplanting.

When the seedlings were well established, 1st mulching and weeding were done uniformly in all the plots. 2nd weeding was done after 20 days of the first one. Mechanical support was provided to the growing plants by bamboo sticks to keep them erect. During early stages of growth, pruning was done by removing some leaves to allow the plants to get more sunlight and to reduce the self-shading and incidence of increased insect infestation. Several weeding mulching were done as per requirement. After transplanting the seedlings were properly irrigated for 3 consecutive days. Then flood irrigation was given to the plants after each top dressing of urea. Final irrigation was given during active fruiting stage.

Ripcord 10EC (Cypermethrin) was used for 6 times at an interval of 7 days from 06 January to 11 February 2014 to prevent pest infestation. There were different types of weeds which were controlled effectively by hand weeding. Harvesting continued from 04 March to 20 April, 2014 because fruits of different lines matured progressively at different dates. Fruits were picked on the basis of maturity, size, color and age.

The observations were recorded on various growth and yield traits from 10 randomly selected plants in each replication as per standard procedure.

Statistical analysis

The data were analyzed by GENSTAT program. However, genetic diversity was measured through Mahalanobi (1936) generalized distance (D^2) extended by Rao (1952).

RESULTS AND DISCUSSION

On the basis of D^2 values, the 48 genotypes were grouped into six highly divergent clusters (Table 1).The clusters divergence was proved by the greater amount of inter-cluster and low intra clusters D^2 values. Cluster III was the largest and consisted sixteen genotypes followed by cluster VI with twelve genotypes. Cluster V, I, IV and II had eleven, five, three and one genotypes respectively. The germplasms were collected different regions of Bangladesh particularly where the tomato plants are growing well. So, our prediction was that the genotypes could have the little variation and also that variation would not able to create more clusters. Unfortunately our assumption was wrong and the grouping of the clusters did not show any relationship considering the genetic diversity and the geographical area of Bangladesh (Table 1.). This is an agreement with results of [1, 6, 9, 11].

One of the possible reasons for this may be the fact that it is very difficult to establish the actual location of the origin of genotypes. The country wise free and frequent exchange of genetic material among the crop improvement programmes makes it difficult to maintain the exact identity of the genotypes.

Table 1: Distribution of 48 genotypes of tomato in different clusters

Cluster	No. of genotype	Name of genotypes	Numbering of genotypes
I	5	BD-7270, BD-7287, BD- 7291, BD-7748, BD- 9011	14, 16, 17, 36, 37
II	1	BD-7285	13
III	16	BD-10122, BD-10124, BD-7750, BD-7752, BD-7754, BD-7755, BD-7751, BD-7760, BD-7761, BD-7292, BD-10125, BD-10126, BD-10127, BARI Tomato 11, BD-10123, Local Jossore 3	1,2,3,4,5,6,7,11,12,18,21,22,23,29,35,48
IV	3	BD-7759,BARI Tomato-2,BARI Hybrid-4	10,26,27
V	11	BARI Tomato-14, BD-7258, BD-7289, BARI Tomato – 8, BD-7276, Local Kustia -1, BD- 7279, BD-10321, BARI Tomato-7, BARI Tomato-9, Local Jessore -2	30,31,32,33,34,38, 41,42,44,46,47
VI	12	BD-7756, BD-7757, BD-7281, BD-7298, BD-7301, BD-10128, BD-9010, BARI Hybrid-5, BD-7290, BD-7762, BARI Tomato-3, BARI Tomato-15	8,9,15,19,20,24,25,28,39,40,43,46

Table 2: Average intra (bold) and inter-cluster distances (D^2) for 48 tomato genotypes

Cluster	I	II	III	IV	V	VI
I	**1.737**					
II	13.950	**0.000**				
III	4.327	17.314	**1.8415**			
IV	7.235	8.978	10.098	**4.111**		
V	11.979	25.331	8.337	17.803	**1.91**	
VI	8.616	21.891	4.924	14.367	3.977	**1.84**

Table 3: Cluster means for 17 morphological characters in tomato

Characters	Cluster					
	I	II	III	IV	V	VI
% of ash	0.8	0.5	0.7	0.5	0.6	0.6
% of protein	1.6	1.5	1.9	1.3	1.6	1.5
% of vit.-C	9.2	10.9	12.7	9.3	12.1	13.9
% Brix	4.8	4.4	4.8	3.6	5.5	4.4
% Chlorophyll	53.5	54.7	54.7	56.2	55.9	57.6
Flowers/cluster (no.)	6.3	5.6	7.6	7.0	6.4	7.2
Fruit/cluster (no.)	4.4	3.8	5.6	5.2	4.5	5.1
Length of fruit (mm)	14.6	25.9	34.0	37.7	37.6	36.5
No. of seed/fruit	114.6	61.8	87.2	60.5	70.0	69.4
pH of tomato juice	4.1	4.0	4.1	4.0	4.1	4.1
Plant height (cm)	133.9	116.6	109.8	77.7	101.9	87.5
Primary branches/plant (no.)	9.4	11.4	10.2	12.5	9.3	8.8
Secondary branches/plant (no.)	10,7	14.4	10.7	13.4	8.0	9.2
Shelf life of tomato (days)	7.0	8.8	10.9	9.5	10.5	9.7
Individual fruit weight(g)	29.3	13.6	27.9	42.8	33.1	33.3
Width of fruit (mm)	54.1	28.6	35.3	54.4	37.1	35.4
Yield/plant (g)	2755.8	4590.7	2335.3	3662.6	1289.6	1734.8

Table 4: Latent vectors for 17 morphological characters in tomato

Characters	Vector 1	Vector 2
% of ash	0.2538	0.2504
% of protein	0.3193	0.1539
% of vit.-C	0.0877	-0.0617
% Brix	0.2403	0.1947
% Chlorophyll	-0.2031	-0.1775
Flowers/cluster (no.)	0.2424	-0.4519
Fruit/cluster (no.)	0.2209	-0.4526
Length of fruit (mm)	-0.3796	0.1423

No. of seed/fruit	0.0880	0.3804
pH of tomato juice	0.0736	0.0145
Plant height (cm)	0.3523	0.2395
Primary branches/plant (no.)	-0.2660	-0.1075
Secondary branches/plant (no.)	-0.2645	-0.1120
Shelf life of tomato (days)	-0.0625	-0.2670
Individual fruit weight (g)	-0.3730	0.1551
Width of fruit (mm)	-0.2097	0.2989
Yield/plant (g)	-0.1012	-0.0019

Moreover, breeding progenies incorporate genes from varied sources particularly that crops which has a chance for cross pollination, thus losing the basic geographical identity of the genotype. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection are responsible for genetic diversity. It may also be possible that causes for clustering pattern were much influenced by environment and interaction (genotype×environment) resulting in differential gene expression during the time of experiment. Another possibility may be that estimates might not have been sufficient information for the variability caused some other traits such as physiological or biochemical which might have important contributors in respect of the total genetic diversity in the experimental populations.

The divergence within the cluster (intra-cluster distance) indicates the divergence among falling in the same cluster. On the other hand, inter cluster divergence suggest the distance (divergence) between the genotypes of different clusters. The intra and inter clusters D^2 values among 48 genotypes presented in Table 2. revealed that cluster II showed minimum intra cluster D^2 value (0.000) distance (contain only one genotype) followed by cluster I (1.737), whereas, maximum intra-cluster D^2 value (4.111) was shown by cluster IV followed by cluster V (1.91) indicated that genotypes included in this cluster are very diverse and was due to both natural and artificial selection forces among the genotypes.

Minimum inter-clusters D^2 value was observed between the clusters V and VI (3.977) indicated close relationship among the genotypes included in these clusters. Maximum inter-clusters D^2 value was observed between the clusters II and V (25.331) indicated that the genotypes belongings to these groups were genetically most divergent and the genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregating population in future [10]. 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 [1,3]. Average inter and intra-cluster distance revealed that, in general inter-cluster distance were much higher than those of intra-cluster distances, suggesting homogenous and heterogenous nature of the germplasm lines within and between the clusters respectively. These results are in accordance with the findings of [8,9] in tomato.

Table 5: Eigen values and percentage of variation in respect of 17 morphological characters in tomato

Principal component characters	Eigen values	% of total variation accounted for	Cumulative percent
% of ash	18.29	28.84	28.84
% of protein	15.97	23.88	52.72
% of vit.-C	13.26	14.60	67.32
% Brix	8.97	7.39	74.71
% Chlorophyll	8.10	6.41	81.12
Flowers/cluster (no.)	6.49	4.48	85.60
Fruit/cluster (no.)	5.54	3.35	88.95
Length of fruit (mm)	4.62	2.65	91.60
No. of seed/fruit	4.25	2.22	93.82
pH of tomato juice	3.66	2.14	95.96
Plant height (cm)	3.04	1.92	97.88
Primary branches/plant (no.)	2.99	1.01	98.89
Secondary branches/plant (no.)	1.95	0.57	99.46
Shelf life of tomato (Days)	1.55	0.34	99.80
Individual fruit weight (g)	1.20	0.13	99.93
Width of fruit (mm)	0.10	0.05	99.98
Yield/plant (g)	0.01	0.02	100.00

Table 6: Inter genotype distance (D^2) of 15 the highest and 15 the lowest genotype of different clusters of Tomato

Sl. No.	Between genotype (G)	Distance (Highest)	Sl. No.	Between genotype (G)	Distance (Lowest)
1	30-27	6.192	**1**	20-40	0.756
2	27-42	6.132	**2**	22-40	0.772
3	9-27	6.070	**3**	47-48	0.776
4	2733	5.957	**4**	12-19	0.795
5	27-43	5.761	**5**	19-38	0.805
6	27-48	5.705	**6**	7-39	0.811
7	20-27	5.689	**7**	7-37	0.813
8	27-29	5.688	**8**	12-38	0.830
9	27-47	5.634	**9**	1-2	0.848
10	27-41	5.632	**10**	25-39	0.877
11	27-44	5.582	**11**	28-45	0.885
12	11-27	5.552	**12**	5-6	0.886
13	1-27	5.520	**13**	3-28	0.892
14	18-27	5.372	**14**	12-28	0.899
15	17-27	5.366	**15**	37-39	0.903

The cluster mean of 48 genotypes Table 3. showed that the mean value of clusters varied in magnitude for all the seventeen characters. Genotypes in cluster I showed maximum performance for % of ash (0.8), plant height (133.9 cm), no. of seed per fruit and genotypes included in this cluster are useful in inducing high amount of minerals, plant height and no. of seed per fruit. Cluster II showed maximum mean value for yield per plant (4590.7g), primary branches (11.4) and secondary branches (14.4). It reveals that genotypes in this cluster are beneficial considering the higher yield. Cluster III registered maximum performance for % of protein (1.9) and flower per cluster (7.6). Genotypes in cluster IV showed maximum performance individual fruit weight (42.8), fruit length (37.7) and second highest amount of yield per plant (3662.6). Cluster V showed maximum mean value for% brix (5.5). It's revealed that the highest amount of TSS. Cluster VI showing the highest value of % of Vit.-C (13.9) and chlorophyll % (57.6) and the genotypes included in this cluster are useful in inducing highest amount of Vit.-C and healthy plant. Depending upon the aim of breeding, the potential lines to be selected from different cluster as parents in a hybridization programme should base on genetic distance. In accordance to the findings [2, 5] reported that the clustering pattern could be utilized in choosing parents for cross combinations likely to generate the highest possible variability for various economic characters.

In a plant breeding programme aimed at crop improvement, the choice of parents is quite important and only component character of yield should be taken into account for selecting genetically divergent parents. Contribution towards genetic divergence is presented in Table 5. and the highest contribution in manifestation of genetic divergence was exhibited by % of ash (28.84%) followed by % of protein (23.88%) and % of vit.-C (14.60%). The highest inter-cluster distance was observed between II and V and the lowest inter-cluster distance was observed between V and VI. The highest and the lowest intra-cluster distances were observed in cluster IV and II respectively. Genotypes included in cluster V were important for % of brix in tomato whereas secondary branches/plant and yield/plant were remarkable feature for cluster II. Cluster III was important for vit.-C, chlorophyll % of the leaf and shelf life of the fruit ambient temperature can be utilized as donor parent for selecting transgressive segregants followed by continued selection in advance generations which may lead to development of high yielding varieties with desired component characters. The genotypes of highly divergent clusters may also be utilized in a breeding programme for development of high yielding varieties with desirable attribute and can also be utilized in heterosis breeding programme for development of F_1 hybrids with superior yield and quality characters.

CONCLUSION

Both the D^2 analysis of the agro-morphological traits clearly showed the existence of wide variation among the germplasms. Moreover, these variations are well spread under the diverse agro-ecological situation. Otherwise, these would have vanished by the time. This more vivid from the fact that farmers still maintain these germplasms and they maintain these for risk management and optimization of production factors will matching with different water, soil regimes, other environmental and economic factors rotating of different uses. For each and every character, these variations could exploit in improvement programme. The study also suggests that cluster II and V may be better parent for considering yield, cluster IV and V for fruit weight and cluster III and cluster VI for % of vit.-C. Multi

variety clustering pattern could also suggest the breeders about the suitability of different germplasms of tomato for breeding programme.

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