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QUANTIFICATION OF GENETIC DIVERSITY ANALYSIS FOR THE IMPROVEMENT OF CULTIVATED TOMATO GENOTYPES

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Abstract

Fourteen commercial cultivars of tomato were investigated to understand the extent genetic diversity through 17 yield attributes. Based on D^2 statistics 14 genotypes were grouped into four clusters. The highest inter-cluster distance was observed between clusters I and III (38.17) and lowest in between the clusters I and II (6.23). The result revealed that yield/plant (46.2%) contributed maximum to the total divergence followed by fruit weight (28.7%) and thickness of pericarp (17.5%). Cluster III showed highest mean for primary branches/plant, number of fruits/plant, fruit length, fruit width, fruit weight, pedicel length, harvesting period and yield/plant. Cluster IV showed highest mean for leaflet length and width, number of leaflets/leaf, flowers/cluster, number of fruits/cluster and thickness of pericarp. Clusters I and III produced maximum lowest mean for almost all characters. Therefore, genotypes belonging to the clusters III and IV may be used as potential parents for future hybridization to produce new high yielding tomato lines with desired traits.

Introduction

Tomato (*Solanum lycopersicum* L.) belongs to Solanaceae is one of the most important and popular vegetables in the world. It is now the most widely grown vegetable crop in Bangladesh for consumption either fresh or processed. It is considered the "queen'' of garden crops and second important vegetable after potato because of its wider adaptability, high nutritional value, high yielding potential, multipurpose uses and commercial importance (Sekhar *et al.* 2008).

Tomato contains high nutritive value and rich source of vitamin A, C and minerals like Ca, P and Fe (Dhaliwal *et al*. 2003). Tomatoes are major contributors of antioxidants especially lycopene and β-carotene, phenolics, ascorbic acid (Vitamin C) and small amounts of vitamin E in daily diets (Rai *et al*. 2012). Lycopene is treasured for its anticancer attribute and acts as an antioxidant which protects cells and cellular components against oxidative damage.

The success of any breeding program for evolving superior genotypes depends upon the nature and magnitude of genetic diversity and extent to which the desirable characters are heritable (Dudley and Moll 1969). Better knowledge on genetic diversity could help to sustain long term selection gain in plants (Chowdhury *et al*. 2002). The present investigation was therefore, undertaken to evaluate the potentiality of existing commercial cultivars of tomato in Bangladesh through the genetic diversity.

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Materials and Method

The investigation was conducted during Rabi season (November, 2013 to April, 2014) at the Botanical Garden of Jahangirnagar University, Savar, Dhaka. Fourteen genotypes of tomato namely Ratan, Holland tomato, Roma VF, Ankhi, P.K.M-1 (Debgiri), Patharkuchi, BARI tomato, 2, BARI tomato-8, BARI tomato-14, BARI tomato-15, Delta, Minto, Soushan-8323 and Sorna were collected from different local seed market, certified seed companies and national research institution of Bangladesh. The experiment was laid out in RCBD with three replications. The unit plot size was 3 × 3 feet maintaining a plant spacing of 1 × 1 feet. The genotypes were randomly assigned in different blocks. The fertilizer and manure were applied as per recommended dose and the cultural practices were followed.

Data were recorded randomly for 17 quantitative traits such as plant height (cm), primary branches/plant, inter node length (cm), leaflet length (cm), leaflet width (cm), number of leaflet/leaf, number of leaflet/leaf, days to 1st flowering, flowers/cluster, number of fruits/plant, fruit length (cm), fruit width (cm), fruit weight (gm), flowers/cluster, thickness of pericarp (mm), pedicel length (cm), harvesting period and yield/plant (gm). For each character, except days to first flowering ten randomly selected plants of each genotype from each replication were considered for data collection. Analysis of variance was performed with the help of a MSTAT-C program (Freed 1986). To test the differences between genotypes, DMRT was performed according to the method of Steel and Torrie (1960).

The genetic diversity among the germplasms was assessed following Mahalanobis D^2 statistics (Mahalanobis 1936). D^2 values were calculated from transformed uncorrelated means of characters according to Singh and Chaudhary (1979). Mean data for each character was subjected to multivariate principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis (CLSA) and canonical variate analysis (CVA) using GENSTAT 5.5. Three dimensional scattered diagram for different principal component axis was done by R software.

Results and Discussion

Analysis of variances for yield and yield contributing traits showed that the genotypes differed significantly for the traits (Table 1). This indicates that the materials were genotypically divergent. The principal component analysis yielded Eigen values and per cent contribution of each principal component axis where variation among the genotypes accounted through the per cent contribution of these axes. Based on PCA score I, II and III obtaining from the principal component analysis which cumulatively accounted for 68.6% of the total variation among the genotypes, a three dimensional scattered diagram was developed. The positions of 14 genotypes in the generated 3-D scattered diagram were apparently distributed into four groups indicating a considerable genetic diversity (Fig. 1). Similar grouping of the genotypes has also been observed (Table 2) by Tocher's Method (Rao 1952).

The clustering pattern of different genotypes did not follow their geographical distribution and was fairly at random. This suggests that falling of materials of same origin into different clusters was an indication of broad genetic base of the genotypes belonging to the origin. Therefore, geographical diversity could not be related to genetic diversity in the material investigated. This is an agreement with results of Reddy *et al*. (2013) and Basavaraj *et al.* (2010). So selection of genotypes for hybridization to generate diverse new gene combinations should be based on genetic diversity rather than geographic diversity (Pawar *et al.* 2013).

Table 1. Analysis of variance for 17 quantitative traits in tomato.

Characters	Genotypes (DF =13)	CV (%)
Plant height (cm)	1285.111**	14.38
Primary branches/plant	3.014	24.95
Inter node length (cm)	3.690**	9.40
Leaflet length (cm)	8.537**	4.52
Leaflet width (cm)	1.310	11.82
Number of leaflets/leaf	12.991**	6.99
Days to first flowering	32.879**	2.67
Flowers/cluster	2.570**	11.41
Number of fruits/plant	581.750**	25.48
Fruit length (cm)	2.954**	3.72
Fruit width (cm)	19.000**	8.38
Fruit weight (g)	2807.359**	10.89
Number of fruits/cluster	2.056**	7.72
Thickness of pericarp (mm)	2.980**	5.63
Pedicel length (cm)	0.390**	4.79
Harvesting period	51.132**	9.26
Yield/plant (g)	7410921.258**	36.04

** = Significant at 1% level of probability, DF = degrees of freedom.

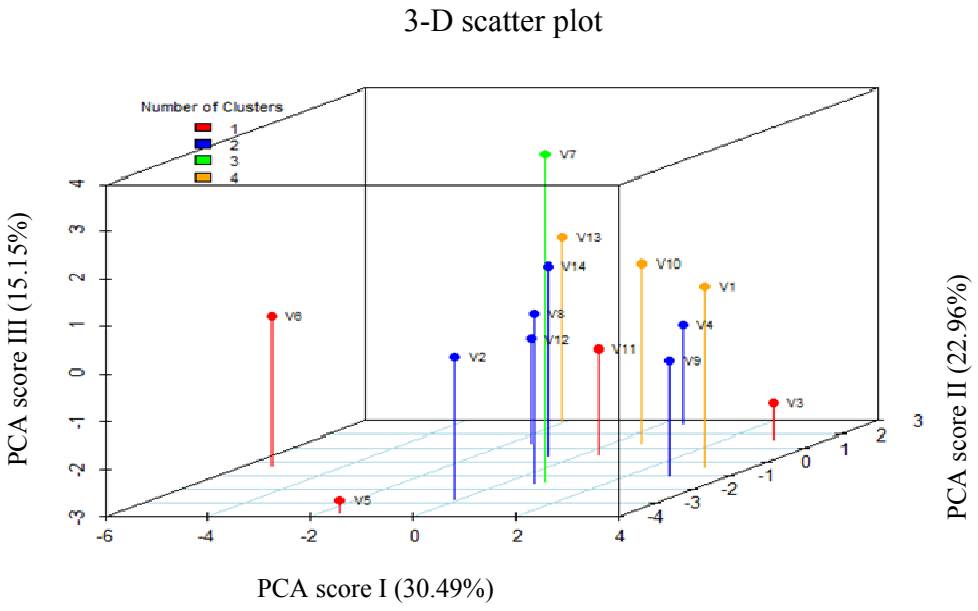

Fig. 1. Three dimensional scattered diagram based on three PCA scores showing the distribution of different tomato genotypes.

By the application of non-hierarchical clustering using co-variance matrix 14 genotypes of tomato were grouped into four clusters indicating the presence of diversity among the genotypes under study. The maximum numbers of genotypes (six) were grouped into cluster II and lowest in cluster III having only one genotype. Cluster I and cluster IV having two and three genotypes, respectively (Fig. 1 and Table 2).

Table 2. Distribution of different tomato genotypes by Tocher's clustering method.

Cluster	No. of genotypes	Genotypes
I	4	Roma VF, P.K.M-1(Debgiri), Patharkuchi, Delta
II	6	Holland tomato, Ankhi, BARI tomato-8, BARI tomato-14, Minto, Sorna
III	1	BARI tomato-2
IV	3	Ratan, BARI tomato-15, Soushan-8323

The average intra- and inter-cluster distances are presented in Table 3. The inter-cluster distances were larger than the intra-cluster distances that indicated wider genetic diversity among the genotypes of different groups. The intra-cluster distance was highest in cluster I (1.39) and lowest in cluster II (0.84). The cluster IV had intra-cluster distance (0.88). Cluster III showed no intra-cluster distance because of having solitary genotype. The inter-cluster distances were calculated by averaging all possible D^2 values among all genotypes belonging to different clusters concerned. The maximum inter-cluster distance was observed between cluster I and cluster III (38.17) followed by cluster II and cluster III (32.22), and cluster I and cluster IV (16.36) (Table 3). Therefore, the genotypes falling in these clusters were genetically more divergent. Hybridization between the genotypes from these clusters should generate greater number of useful segregants, maximum hybrid vigour and is expected to create high yielding varieties (Mehta and Asati 2008). The minimum inter-cluster D^2 value (6.23) was observed between cluster I and II indicating genetic relationship between genotypes of these two clusters (Table 3). Several authors also reported profound diversity in the germplasm of tomato by assessing genetic divergence on the basis of quantitative traits following D^2 statistics (Basavaraj *et al.* 2010 and Evgenidis *et al.* 2011).

Table 3. Average intra- (bold) and inter-cluster distance (D^2) for tomato genotypes.

Cluster	I	II	III	IV
I	**1.39**			
II	6.23	**0.84**		
III	38.17	32.22	**0**	
IV	16.36	10.44	22.11	**0.88**

The percentage contribution of different traits towards genetic divergence is presented in Fig. 2 and Table 4. The highest contribution towards divergence was found for yield/plant (46.2%) among the 17 characters studied. Similar findings were obtained by Nalla *et al*. (2014). Moderate contribution was found for fruit weight (28.7%) and thickness of pericarp (17.5%). Similar results were obtained by Mohanty and Prusti (2001), Singh *et al*. (2008), Reddy *et al*. (2013), Nalla *et al*. (2014) and Meena and Bahadur (2015). Remaining characters had very less contribution toward genetic diversity. De *et al*. (1988) opined that traits contributing maximum towards the D^2 values needed to be given more emphasis for deciding the clusters to be taken for the purpose of selection of parents for hybridization.

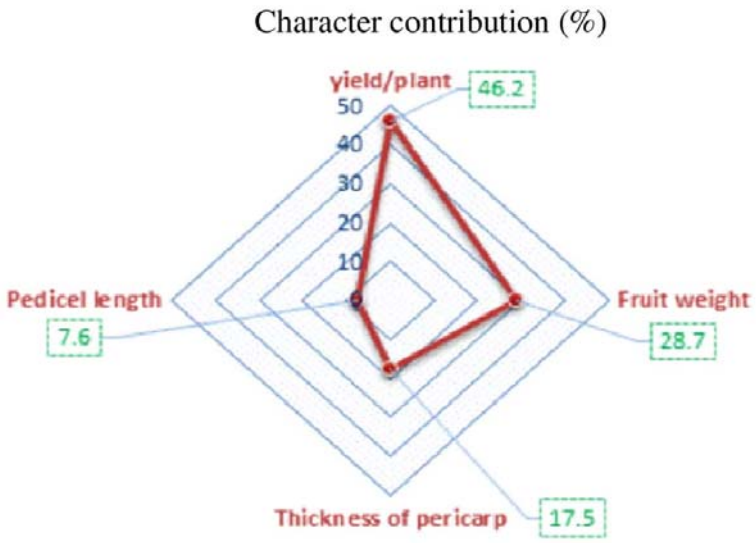

Fig. 2. Contribution of individual characters towards genetic divergence.

Table 4. Cluster mean for various characters of tomato genotypes.

Characters	I	II	III	IV	Contribution towards divergence (%)
Plant height (cm)	128.4*	117.5	86.3	98.2	0
Primary branches/plant	8	8	9*	8.2	0
Inter node length (cm)	8.8	9.1*	8.1	8	0
Leaflet length (cm)	13.3	13.8	13.1	14.3*	0
Leaflet width (cm)	6.2	6.2	5.7	6.3*	0
Number of leaflets/leaf	15.4	14.8	16	16.3*	0
Days to first flowering	62.9	65.7*	65.5	64.5	0
Flowers/cluster	6.7	7.6	5.8	8*	0
Number of fruits/plant	47.5	40.9	58.2*	56.1	0
Fruit length (cm)	8	9.2	10.2*	9.4	0
Fruit width (cm)	16.2	19.7	23*	18.3	0
Fruit weight (g)	80.5	115.6	173.1*	118.2	28.7
Number of fruits/cluster	5.7	5.9	4.8	6.7*	0
Thickness of pericarp (mm)	6.2	6.9	5.3	7.8*	17.5
Pedicel length (cm)	1.3	1	1.31*	1.2	7.6
Harvesting period	26.5	25.3	27*	25.2	0
Yield/plant (g)	3285.2	4345.9	10133.2*	6434.5	46.2
Contribution (%)	5.9	11.76	47.06	35.29	100

*Indicates highest mean value.

Further, for crop improvement, intercrossing among genotypes with outstanding mean performance was suggested by Roy and Sharma (1996), Kumar *et al*. (2013) and the reliable conformity for this can be known on the basis of cluster means. Character wise mean was

calculated for all the genotypes spread over four clusters (Table 4). The cluster means of genotypes revealed considerable genetic differences between the groups. Cluster I showed highest mean only for plant height (128.4). Cluster II showed highest mean for inter node length (9.1) and days to first flowering (65.7).

Table 5. A few important traits of selected tomato genotypes.

Sl. No.	Selection traits	Genotypes	Cluster	Mean value
1	Flowers/cluster	Ratan, BARI tomato-15, Soushan-8323	IV	8
2	Number of fruits/plant	BARI tomato-2	III	58.2
3	Fruit length (cm)	BARI tomato-2	III	10.2
4	Fruit width (cm)	BARI tomato-2	III	23
5	Fruit weight (g)	BARI tomato-2	III	173.1
6	Number of fruits/cluster	Ratan, BARI tomato-15, Soushan-8323	IV	6.7
7	Thickness of pericarp (mm)	Ratan, BARI tomato-15, Soushan-8323	IV	7.8
8	Yield/plant (g)	BARI tomato-2	III	10133.2

Cluster III showed maximum mean for primary branches/plant (9), number of fruits/plant (58.2), fruit length (10.2), fruit width (23), fruit weight (173.1), pedicel length (1.31), harvesting period (27) and yield/plant (10133.2) but lowest for plant height (86.3), leaflet width (5.7), flowers/cluster (5.8), number of fruits/cluster (4.8) and thickness of pericarp. Cluster IV showed highest mean for leaflet length (14.3), leaflet width (6.3), number of leaflets/leaf (16.3), flowers/cluster (8), number of fruits/cluster (6.7) and thickness of pericarp (7.8). Cluster I and II had the genotypes that showed lowest mean value for almost all the characters studied excluding some characters indicating selection of parental lines from this cluster for future hybrid tomato breeding programme will be ineffective. Cluster III and IV together contributed almost about 82.35% towards divergence that means possession of all characters in respect of yield indicating presence of most promising genotypes in them can be extensively used for further breeding programmes to generate new high yielding tomato lines.

Plant breeding programme aimed at crop improvement, the selection of parents is quite important and only component character of yield should be taken into account for selecting genetically divergent parents. From the cluster mean value it was observed that maximum variability found for plant height, number of fruits/plant, fruit length, fruit width, fruit weight, thickness of pericarp and yield/plant. Taking into consideration from cluster mean value, group distance and other agronomic performances, the genotypes BARI tomato-2 of cluster III, Ratan and BARI tomato-15 of cluster IV can be recommended as better parents for future breeding programme (Table 5).

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