Global Science Research Journals

ISSN: 2437-1874 Vol. 7 (2), 1-8, August, 2020.

http://www.globalscienceresearchjournals.org/

Global Journal of Plant Breeding and Genetics

Full Length Research Paper

Genetic diversity among tomato *(Solanum lycopersicon L.)* genotypes in Northern Ethiopia

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The objective of the study was to estimate genetic diversity among tomato genotypes. Thirty-six genotypes introduced from different countries were evaluated at Humera Agricultural Research Center, Northern Ethiopia, during 2010/2011 in 6 × 6 simple lattice design with two replications. Cluster analysis was made by average linkage method. Mahalanobis distance (D^2) was used to estimate the genetic distance between pair of clusters. Estimates of cluster analysis revealed that the thirty-six genotypes were grouped in to six distinct clusters. Genetic distance between any pair of clusters showed very highly significant difference. The maximum and minimum distances were recorded between clusters IV and V (1805.00) and cluster II and III (81.94) respectively. This indicated the existence of a possibility to improve genotypes through hybridization from any pair of clusters and subsequent selection can be made from the segregant generations. Principal component analysis showed that the first six principal components explained about 83.03% of the total variation. Generally, the study confirmed presence of adequate genetic diversity between any pair of clusters which could be exploited through hybridization.

Key words: Cluster analysis, Mahalanobis distance, principal component analysis, eigenvalue, eigenvector.

INTRODUCTION

Tomato (*Solanum lycopersicon* L.) belongs to the large and diverse *Solanaceae* family also called Nightshades which includes more than three thousand species. Among them, major crops arose from old world (Eggplant from Asia) and new world (pepper, potato, tobacco, tomato from South America) (Guillaume and Mathilde, 2012). All related wild species of tomato are native to the Andean region that includes parts of Chile, Ecuador, Bolivia and Peru (Sims, 1980). The most likely ancestor is the wild *Lycopersicon esculentum* var. *cerasiforme* (cherry tomato), which is indigenous throughout the tropical America. Tomatoes were domesticated in America;

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however, the original site of domestication and the early events of domestication are largely obscure (Peralta and Spooner, 2007). Although definite proof for the time and place of domestication is lacking, Mexico is presumed to be the most probable region of domestication, with Peru as the center of diversity for wild relatives (Larry and Joanne, 2007). It is a diploid species with 2n = 2x = 24 chromosomes.

Tomato is an important vegetable crop in the world. In Ethiopia the crop is cultivated by small scale farmers under irrigation and rain fed condition and large scale commercial vegetable growers. In Tigray region, were the study is conducted, the crop is cultivated mainly by small scale farmers and some investors in southern and western part of the region. The western low land of Tigray has vast plain arable land suitable for production of vegetables fruits and field crops both under rain fed and irrigation condition.

Tomato is one of the commercial vegetable grown by many farmers in Western Tigray. The crop is produced by 655 small holder farmers in the zone (CSA, 2009). However, cultivation of the crop is constrained by many factors in the whole country and the region. According to Lemma (2002) the major production constraints are shortage of varieties, unknown sources of seeds, disease and insect pests and high post-harvest loses. This showed that developing or introducing high yielding genotypes with desirable fruit characteristics should be primary task.

Information on the extent of genetic diversity among genotypes is very important in crosses between groups with maximum genetic divergence that would be more responsive for improvement since they are likely to produce desirable recombination and segregation in their progenies after hybridization (Norden, 1980; Reddy, 1988). To have this type of knowledge, research on genetic diversity is very essential. So far a number of research activities have been conducted by different research institutions and researchers in Ethiopia. Since 1969, about 300 tomato lines/cultivars of both short and tall set open-pollinated genotypes and hybrids have been introduced by Melkassa Agricultural Research Centre (MARC) from international seed companies, and from Asian Vegetable Research and Development Center (AVRDC). The lines have been tested at different research centers to identify lines having high fruit yield and good quality, resistance/ tolerance to diseases as well as insect pests (Lemma, 2002). It is because of the efforts a number of varieties released for different agro ecologies. Regarding diversity studies a number of authors' from different countries viz., Sekhar et al. (2008), Agong (2001), Naz et al. (2013) and Cebolla-Cornejo et al. (2013) studied genetic diversity in tomato genotypes. However, little information is available with respect to diversity study on tomato genotypes preserved under Ethiopian condition. Therefore, a study was conducted to estimate the genetic diversity among different tomato genotypes.

MATERIALS AND METHODS

Experimental site

The experiment was conducted at Humera Agricultural Research Center experimental site, Northern Ethioipia from July 2010 to February 2011 cropping season under irrigation condition. Humera is located 14° 06' N latitudes and 38° 31' E longitudes at an altitude of 604 m above sea level. It has chromic vertisol black in color characterized with very deep (>150 cm) clay textured. Agro-ecologically it is described as hot to warm semiarid plain sub agro-ecology (SA1-1). The maximum temperature varies from 42°C in April to 33°C in May while minimum temperature varies from 22.2°C in July to 17.5°C in August. The area receives an average rainfall of 400 to 650 mm per year (EARO, 2002).

Experimental material

The experimental materials comprise 36 tomato genotypes introduced from Asian Vegetable Research and Development (AVRDC), Israel, Italy, United States of America (USA), and France (Table 1). Seedlings of each genotype were raised in nursery in August and transplanted in the main field in September.

Experimental design and management

The trial was laid out in 6 x 6 simple lattice design in two replication. Seedlings of each genotype were raised in nursery in August 2010 and transplanted to the main field in September 2010. Each genotypes were planted in the main field in a plot size of 20.4 m^2 (4 rows, 5.1 m row length, 100 cm meter between rows and 30 cm between plants spacing). 200 kg ha^{-1} Di-ammonium Phosphate DAP and 100 kg ha^{-1} Urea were applied at time of planting and two weeks after transplanting as of recommended for the crop (Lemma, 2002). All agronomic practices were applied as per recommendation for the crop. The middle two rows were used for data collection leaving the two rows as borders.

Data collected

Ten plants were randomly sampled from the central two rows of each plot to measure growth parameters, fruit yield components and fruit characteristics data. At plant height (cm), primary and secondary branches, number of flowers per plant, average number of fruit clusters per plant, average number of fruits per cluster, average number of fruits per plant, fruit set percentage, weight of fruit per plant (kg $plant^{-1}$), single fruit weight (g), fruit polar diameter (mm), equatorial diameter (mm), fruit shape index, number of locules per fruit, pericarp thickness (mm), number of seeds per fruit and total soluble solids (TSS) (°Brix) were recorded from 10 plants selected. Measurements such as days to 50% flowering, days to 50% fruiting, days to maturity, number of pickings, marketable and unmarketable fruit yield (t ha^{-1}), average total yield per hectare (t ha^{-1}) were taken on plot basis.

Data analysis

Analysis of variance (ANOVA) was made using SAS version 9.2 (SAS Institute, 2008) after testing the ANOVA assumptions. Clustering of genotypes into different groups was carried out by

Table 1. List of experimental materials.

S/No.	Genotypes	Source	Growth habit
1	Fetan	Italy	Determinate
2	CLN-5915-206-D4-2-2-0	AVRDC	Indeterminate
3	Beaf steak	NA	Determinate
4	CLN-2037 H	AVRDC	Indeterminate
5	CLN-2366 C	AVRDC	Indeterminate
6	Chali	Italy	Determinate
7	CLN-2498 A	AVRDC	Determinate
8	CLN-2037 C	AVRDC	Indeterminate
9	Miya	Italy	Semi-determinate
10	Roma VF	France	Determinate
11	CLN-2037 A	AVRDC	Indeterminate
12	PT-4719 B	AVRDC	Determinate
13	Fire ball	Italy	Determinate
14	Supper Roma VF	NA	Determinate
15	CLN-2037 E	AVRDC	Indeterminate
16	Bishola	France	Determinate
17	CLN-2037 I	AVRDC	Indeterminate
18	Tomato1358/95	Hazera Seed Company	Indeterminate
19	CLN-1621 F	AVRDC	Determinate
20	Eshet	Italy	Determinate
21	Marglobe	USA	Determinate
22	CLN-5915-93-D4	AVRDC	Determinate
23	CLN-5915-206-D4-2-5-0	AVRDC	Indeterminate
24	Metadel	Guadaloupe	Semi-determinate
25	ARP-Tomato No.367-2	AVRDC	Determinate
26	Cathrine	Hazera Seed Company	Indeterminate
27	Tomato1365/95	Hazera Seed Company	Determinate
28	Electra	Hazera Seed Company	Indeterminate
29	CLN-1314 G	AVRDC	Determinate
30	H-1350	NA	Determinate
31	Cochoro	NA	Determinate
32	CLN-2366 A	AVRDC	Indeterminate
33	Melka-Salsa	Italy	Determinate
34	CLN-2366 B	AVRDC	Indeterminate
35	CLN-2070 A	AVRDC	Indeterminate
36	Melka-Shola	Italy	Semi-determinate

AVRDC: Asian Vegetable Research and Development, USA: United States of America, NA: information not available.

average linkage method and the appropriate numbers of clusters were determined from the values of pseudo F and pseudo t^2 statistics using the procedures of SAS (SAS Institute, 2008) computer software facilities so as to group sets of genotypes into homogeneous clusters. The distance between clusters were assessed by the so called Mahalanobis distance (D^2) such that the values calculated between pairs of clusters were considered as Chi-square values and tested for significance using P-1 degrees of freedom, where 'P' is the number of characters used in the study (Singh and Chaudhary, 1985).

Principal components analysis was performed using correlation matrix by employing PAST software of version 2.02 (Hammer et al., 2001) in order to evaluate the relationships among characters that are correlated among each other by converting into uncorrelated characters called principal components. The contribution of each character in Principal Component Analysis (PCA) is determined by eigenvector that is greater than half divided by the square root of the standard deviation of the eigenvalue of the respective PCA as suggested by Johnson and Wichern (1988). Principal components (PCs) with eigenvalue > 1.0 were used as criteria to determine the number of PCs (Kaiser, 1960).

RESULTS AND DISCUSSION

Mean square values of ANOVA of 24 quantitative characters for the thirty-six tomato genotypes showed

Table 2. Analysis of variance for 24 characters of tomato genotypes.

Source of variation	Mean square		R^2
	Treatments unadjusted	Treatments adjusted	
Degree of freedom	35	35	
Days to 50% flowering	79.95	74.63**	92.19
Days to 50% fruiting	702.73	647.23**	97.42
Days to maturity	1465.06	1402.28**	98.10
Plant height	961.75	823.84**	95.27
No of primary branches	3.29	3.19**	80.82
No of secondary branches	2.63	2.42**	97.04
No of flowers per plant	2343.49	1980.03**	95.59
No of fruit clusters per plant	44.30	43.59**	96.07
Number of fruits per fruit cluster	0.86	0.78**	92.75
No of matured fruits per plant	957.71	903.04**	99.28
Fruit set percentage (%)	835.02	787.75**	98.41
Weight of fruits per plant (kg)	0.46	0.42**	95.71
Single fruit weight per plant (g)	1248.07	1112.25**	96.14
No of pickings	2.02	1.97**	92.37
Fruit polar diameter (mm)	135.61	132.33**	96.65
Fruit equatorial diameter (mm)	89.69	86.23**	94.29
Shape index	0.14	0.14**	95.86
Number of seeds per fruit	1221.45	1032.03**	99.12
Number of locules per fruit	2.04	1.69**	97.87
Perricarp thickness (mm)	3.00	2.63**	91.70
Total soluble solids (^{0} Brix)	0.85	0.74**	98.56
Marketable yield (t ha^{-1})	243.17	223.08**	97.97
Un-marketable yield (t ha^{-1})	2.35	2.215**	99.43
Total yield (t ha^{-1})	281.38	258.55**	98.23

**, Significance at 1% probability level, R^2: coefficient of determination.

highly significant difference (*P< 0.01*) for all the characters studied (Table 2). This is in agreement with the findings of Mohanty (2003) who reported significant differences for all characters studied (plant height, number of branches per plant, days to first harvest, fruits per plant, average fruit weight and yield per hectare). Similarly Pradeepkumar et al. (2001) and Golani et al. (2007) obtained highly significant difference for all characters studied among the test tomato genotypes. All the traits had more than 80% estimate of coefficient of determination (R^2), showed adequacy of the model in explaining the variation.

Cluster analysis

The dendrogram obtained from the cluster analysis grouped the thirty-six tomato genotypes into six clusters (Figure 1) based on the value of pseudo F and pseudo t-square results obtained from SAS. Clusters II was the largest cluster (55.56%) containing 20 genotypes together followed by Cluster I (19.44%) containing seven genotypes, Cluster III (11.11%) comprises four genotypes, clusters IV and V (5.56%) each containing two genotypes and Cluster VI (2.78%) containing one genotype (Table 3). Genotypes in cluster III had the highest fruit yield per hectare than any other clusters. In line with this, Yashavantakumar et al. (2009) grouped 70 tomato genotypes in to seven clusters. Similarly, Shashikanth et al. (2010) clustered 30 tomato genotypes in to 10 clusters using Mahalanobis distance. Ghosh et al. (2009) also reported that 40 segregating hybrids of tomato were grouped in to 6 distant clusters. Nala et al. (2014) also employed Mahalanobis distance (D^2) to classify 27 tomato genotypes in to 9 clusters.

Cluster mean analysis

The mean value of the quantitative characters in each cluster is presented in Table 4. Cluster I consisted of seven genotypes having the characteristic of late flowering (46 days), fruiting (101 days) and maturity (151 days) than remaining clusters. It had relatively moderate

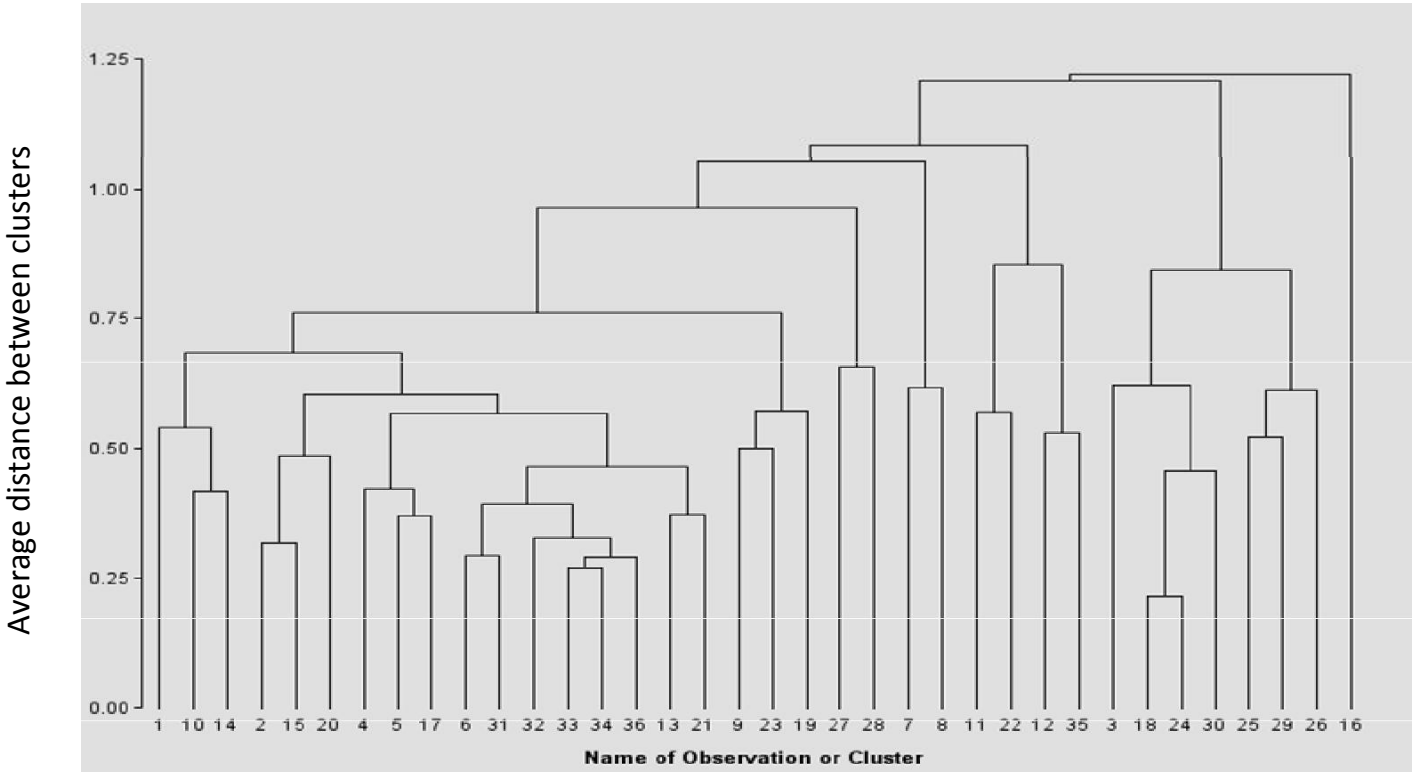

Figure 1. Dendrogram of 36 genotypes of tomato based on evaluation for 24 quantitative traits.

Table 3. Distribution of 36 tomato genotypes in to different cluster groups.

Cluster	No. of genotypes	Name of genotypes
Cluster I	7	Tomato 1358/95, Metadel, H-1350, ARP Tomato No 367-2, CLN-13114-G, Cathrine and Beaf steak
Cluster II	20	Melka-Salsa, CLN-2366-B, Melka-Shola, Chali, Cochora, 5915-206-d4-2-2-0, CLN-2037-E, CLN-2366-A, CLN-2366-C, CLN-2037-I, Fire ball, Marglobe, Roma-VF, Supper Roma-VF, CLN-2037-H, Eshet, Miya, 5915-206-d4-2-5-0, Fetan and CLN-1621-F
Cluster III	4	PT-4719B, CLN-2070-A, CLN-2037-A and CLN 5915-93-D4
Cluster IV	2	CLN-2498 and CLN-2037-C
Cluster V	2	Tomato 1365/95 and Electra
Cluster VI	1	Bishola

height (90.94 cm), number of primary and secondary branches per plant (6.3 and 3.4) and average single fruit weight (57.05 g). On the contrary cluster I had the least number of flowers per plant (61 flowers), number of fruit clusters per plant (2.4), number of matured fruits per plant (6.1), number of pickings (2.6) and average weight of fruits per plant (0.390 kg) as compared to the rest of clusters. As a result of less score from the yield contributing characters it had less total fruit yield per hectare (4.38 t ha^{-1}). Fruit characteristics data of cluster I showed moderate fruit length and width (40.8 and 38.9 mm) with shape index of (1.07) implies almost round shape. It had also thinner pericarp thickness (3.73 mm) than other clusters.

Cluster II consist majority of the test genotypes (55.65%) having the characteristic of moderate maturity period (94 days) as compared to cluster I and IV. Majority of the genotypes in this cluster showed moderate performance in most of the fruit yield and yield related traits as compared to Clusters I, IV and VI that is, moderate number of flowers per plant (108) with relatively moderate number of matured fruits per plant (28.1). It had relatively medium single fruit weight (50.58 g), moderate fruit weight per plant (0.920 kg), relatively many times of pickings (4.50) next to Cluster III, moderate total fruit yield per hectare (19.51 t ha^{-1}) as compared to Clusters I, IV and VI. It also showed relatively highest value of shape index (1.22) next to Cluster IV (1.27) implied the fruit was

Table 4. Cluster-wise mean values of characters in the studied tomato genotypes.

Character	Cluster					
	I	II	III	IV	V	VI
Days to 50 % flowering	46**	38	31*	38	36	42
Days to 50 % fruiting	101**	71	46*	84	65	93
Days to maturity	151**	94	76*	106	87	112
Plant height (cm)	90.94	87.66*	91.71	120.5**	89.44	101.82
Number of primary branches	6.33	6.21*	6.53	8.03**	6.42	6.70
Number of secondary branches	3.37*	3.53	4.22	4.23	3.47	6.30**
Number of flowers per plant	61*	108	116	185**	83	119
Number of fruit clusters per plant	2.44*	8.25	14.31**	3.72	13.92	4.86
Number of fruits per fruit cluster	1.34	1.62	2.80**	1.07*	1.26	1.89
Number of matured fruits per plant	6*	28	76**	19	20	10
Fruit set percentage (%)	11.33	28.33	65.66**	10.12	24.73	8.54*
Weight of fruits per plant (kg)	0.39*	0.92	1.52**	0.68	1.36	0.59
Single fruit weight per plant (g)	57.05	50.58	33.41*	51.65	90.98	146.5**
No of pickings	2.64*	4.50	5.25**	4.25	4.25	3.00
Fruit polar diameter (mm)	40.8	48.2	37.3*	49.7	51.1**	41.1
Fruit equatorial diameter (mm)	38.9	40.4	37.8*	40.4	53.2**	50.7
Shape index	1.07	1.22	0.99	1.27**	1.02	0.81*
Number of seeds per fruit	44.1	38.5*	74.5	48.6	102.0**	44.0
Number of locules per fruit	3.31	3.17	3.60	2.80*	5.65**	2.90
Perricarp thickness (mm)	3.73**	5.05	4.10	4.99	5.45**	4.81
Total soluble solids (^{0} Brix)	5.10	5.06	5.83**	5.08	5.55	4.93*
Marketable fruit yield (t ha^{-1})	3.89*	17.64	34.35**	10.93	20.25	5.58
Un-marketable fruit yield (t ha^{-1})	0.50*	1.86	2.01	1.22	3.07**	0.60
Total fruit yield (t ha^{-1})	4.38*	19.51	36.36**	12.14	23.32	6.19

* , ** indicate the smallest and highest mean value of the character.

cylinder or pear shaped. It also had relatively thick pericarp thickness (5.05 mm) next to Cluster V (5.45) and less TSS content (5.05 °Brix) next to Cluster VI (4.93 °Brix). This cluster consists of the third high yielding genotype, Miya.

Cluster III, which comprised the highest yield bearing genotypes, contained four genotypes characterized by the earliest genotypes in days to 50% flowering, 50% fruiting and maturity (31, 46 and 76 days respectively). Moreover, they had the highest number of fruit clusters per plant (14.3), number of fruits per fruit cluster (2.8), number of matured fruits per plant (76), fruit set percentage (65.66 %), average weight of fruits per plant (1.520 kg), number of pickings (5.3), total fruit yield per hectare (36.36 t ha^{-1}) and TSS (5.83 °Brix). On the contrary it had the least average single fruit weight per plant (33.41 g), fruit length and width (37.3 and 37.8 mm) with shape index of (0.99), plant height (87.96 cm). It had also high number of primary and secondary branches (6.5 and 4.2) next to cluster IV (8.0 and 4.2) and number of flowers per plant (116) next to Cluster IV (185).

Cluster IV comprises four genotypes having characteristics of moderate maturity period (106 days) as compared to cluster I (151 days). The genotypes in this cluster had the highest number of flowers per plant (185 days), longest plant height (120.5 cm), relatively few matured fruits per plant (19) as compared to Cluster III (76), least fruit set percentage (10.12%) next to Cluster (VI), low fruit yield per hectare (12.14 t ha^{-1}) next to Cluster IV and I, relatively long fruit length and moderate width (49.7 and 40.4 mm) with the highest fruit shape index (1.27) indicated the fruit had cylinder or pear shape. It also had least number of locules (2.90) among other clusters. Cluster V contained two genotypes having a property of early flowering, fruiting and maturity period (38, 64 and 87 days respectively) next to Cluster III. It showed high fruit yield per plant (1.26 kg) next to Cluster III, high average single fruit weight (90.98 g) next to Cluster VI, relatively moderate fruit yield per hectare (23.32 t ha^{-1}) as compared to Cluster II, IV,VI and I. Similarly it had the longest fruit length and width (51.1 and 53.2 mm) with shape index of (1.02) that is, almost round shape, highest seed per fruit (102) and relatively high TSS (5.55 °Brix) as compared to cluster III (5.83 °Brix).

Cluster VI which contained single genotypes had a characteristics of relatively late matured (112 days) as compared to Clusters II, III, IV and V. This genotype also

Table 5. Mahalanobis distance between groups of tomato genotypes.

Cluster	I	II	III	IV	V	VI
I	___	132.44***	269.91***	480.45***	1102.00***	806.10***
II		___	81.94***	323.76***	756.56***	505.87***
III			___	403.10***	808.72***	525.17***
IV				___	1805.00***	787.94***
V					___	684.56***
VI						___

χ^2=48.27 at 0.1% probability level; ***, indicate very highly significant at 0.1% probability level.

had highest single fruit weight (146.5 g), least number of harvesting (3 times) next to Cluster I, less total yield per hectare (6.19 t ha^{-1}) next to Cluster I, moderate fruit length and larger fruit width (41.1 and 50.6 mm) with the least fruit shape index (0.81) implied the fruit had flattened shape. It also had the least TSS content (4.93 °Brix) as compared to the rest of clusters.

Estimation of inter cluster square distances (D^2)

The Chi-square (χ^2- test) for the six clusters indicated that there was a very highly significant difference among the clusters (Table 5). The highest inter-cluster distance were exhibited between cluster IV and V (D^2 = 1805.00), followed by Cluster I and V (D^2 = 1102), Cluster III and V (D^2 = 808.72) and Cluster I and IV (D^2 = 806.10) which implied these clusters were genetically more divergent from each other than any other pairs of cluster. Cluster II and III showed the least inter cluster distance (81.94) compared to other pair of clusters.

Increasing parental distance implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors (Ghaderi et al., 1984). Generally, divergence analysis showed presence of high genetic divergence among the tested tomato genotypes evaluated at Humera. Hence, hybridization of these genetically divergent parents could lead to the development of desirable recombinants and transgressive segregants, that in turn, may lead to the development of better performing varieties. Therefore, maximum recombination and segregation of the progenies is expected from crosses involving parents selected from Cluster IV, I or III with parents selected from genotypes in Cluster V as compared to others, however the breeder must specify his/her objectives in order to make best use of the characters where the traits are divergent.

Principal component analysis

The principal component analysis (Table 6) revealed that six principal components PC_1, PC_2, PC_3, PC_4, PC_5 and PC_6 with eigenvalues 8.915, 3.309, 3.104, 2.012, 1.430 and 1.330 respectively, have accounted for 83.03% of the total variation. The first two principal components PC_1 and PC_2 with a proportion of 37.14 and 13.79%, respectively, contributed more to the total variation. According to Chahal and Gosal (2002), characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in this study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather than the contribution of specific few characters. Characters having relatively higher value in the first principal component (PC_1) were total fruit yield ha^{-1}, marketable yield ha^{-1}, days to 50% fruiting, average weight of fruit per plant, number of matured fruits per plant, number of picking, days to maturity, number of fruit clusters per plant and fruit set percentage had more contribution to the total diversity and they were responsible for the differentiation of the six clusters. The second principal component, which accounted 13.79% of the total variation contributed from pericarp thickness, fruit polar diameter, number of primary branches per plant, number of secondary branches per plant, fruit equatorial diameter and single fruit weight per plant. Characters like fruit shape index, number of locules per fruit, fruit equatorial diameter and average single fruit weight were the characters which contributed to the third principal component (PC_3). Similarly number of seeds per fruit, number of flowers per plant, plant height, TSS and number of primary branches were the characters contributed to the fourth cluster (PC_4). Fifth Principal component (PC_5) contributed from characters number of seeds per fruit, number of flowers per plant and number of matured fruits per plant. The sixth principal component (PC_6) contributed from plant height, number of secondary branches, number of fruits per fruit cluster, number of locules per fruit and unmarketable yield per hectare. In line with the present finding, Agong (2001) employed PCA for detecting variation in 35 tomato germplasm in which the first three PCs were adequate in determining more than 70% of total variation. Similarly Ghosh et al. (2009) reported that the first two principal components accounted for 60% of the total variation among 22

Table 6. Eigenvectors and eigenvalues of the first six principal components (PCs).

Characters	Eigenvectors					
	PC_1	PC_2	PC_3	PC_4	PC_5	PC_6
Days to 50% flowering	-0.244	-0.084	0.123	-0.118	0.191	0.219
Days to 50% fruiting	-0.310	0.021	0.080	-0.046	0.134	0.052
Days to maturity	-0.285	-0.037	0.092	-0.074	0.129	-0.107
Plant height (cm)	-0.035	-0.049	0.166	0.385	0.093	0.507
Number of primary branches	-0.028	0.358	0.107	0.354	0.196	-0.128
Number of secondary branches	0.003	0.316	0.135	0.146	0.353	-0.422
Number of flowers per plant	0.090	0.249	-0.150	0.401	0.270	0.176
Number of fruit clusters per plant	0.281	0.008	0.003	0.005	-0.172	-0.104
Number of fruits per fruit cluster	0.219	-0.106	-0.030	0.016	0.065	-0.319
Number of matured fruits per plant	0.298	-0.128	-0.020	0.044	0.215	-0.105
Fruit set percentage (%)	0.277	-0.181	0.021	-0.112	0.124	-0.064
Weight of fruits per plant (Kg)	0.299	0.022	0.120	-0.062	0.057	0.083
Single fruit weight per plant (g)	-0.053	0.315	0.322	-0.191	-0.083	-0.090
Number of pickings	0.294	0.038	-0.097	0.009	-0.057	0.175
Fruit polar diameter (mm)	0.011	0.405	-0.284	-0.011	-0.177	0.196
Fruit equatorial diameter (mm)	0.063	0.295	0.398	-0.159	-0.168	0.029
Shape index	-0.034	0.141	-0.485	0.095	-0.056	0.142
Number of seeds per fruit	0.071	0.058	0.219	0.403	-0.277	-0.129
Number of locules per fruit	0.065	0.006	0.437	0.004	-0.113	0.284
Perricarp thickness (mm)	0.083	0.436	-0.134	-0.192	-0.069	-0.067
Total soluble solids (^{0} Brix)	0.074	-0.216	0.139	0.373	0.001	-0.053
Marketable fruit yield (t ha^{-1})	0.314	-0.019	0.021	-0.069	0.159	0.051
Un-marketable fruit yield (t ha^{-1})	0.241	0.138	0.088	-0.166	-0.049	0.281
Total fruit yield (t ha^{-1})	0.314	-0.005	0.028	-0.079	0.143	0.073
Eigenvalue	8.915	3.309	3.104	2.012	1.430	1.133
Proportion	37.143	13.786	12.932	8.385	5.959	4.721
Cumulative	37.143	50.929	63.961	72.346	78.305	83.026

characters describing 40 segregating populations of tomato hybrids. Merk et al. (2012) also found that the first three principal component explained 57.1% of the total variation for 143 processing tomato lines evaluated in North America.

Conclusion

The dendrogram obtained from the cluster analysis grouped the thirty-six tomato genotypes into six clusters. Chi-square (χ^2- test) demonstrated a very highly significant difference among the six clusters. This showed the possibility to improve genotypes through hybridization from any pair of clusters. Maximum recombination and segregation of progenies is expected from crosses involving parents selected from Cluster IV, I or III with parents selected from genotypes in Cluster V as compared to others, however the breeder must specify his/her objectives in order to make best use of the characters where the traits are divergent.

Conflict of Interest

The authors have not declared any conflict of interest.

ACKNOWLEDGEMENTS

The first author acknowledges Melkassa Agricultural Research Center (MARC) for providing the test genotypes. Staff members of Humera Agricultural Research Center (HuARC) are also acknowledged for their invaluable support in field trial implementation and data collection. The authors are also grateful to Rural Capacity Building Project (RCBP) for offering financial support.

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