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Multivariate Studies for Fruits Yield and Quality Components in Diverse Tomato (*Lycopersicon Esculentum* MILL) Genotypes

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Abstract **– The objective the study was to estimate genetic diversity among tomato genotypes. Thirty six tomato genotypes were evaluated at Melkassa and Kulumsa Agricultural Research Centers South Eastern Ethiopia, during 2017/2018 in 6*6 simple lattice design. Cluster analysis was made by Wards method. Mahalanobis distance (D2) was used to estimate the genetic distance between pair of clusters. Based on ward clustering method the 36 tomato genotypes were grouped into six distinct clusters. Cluster III was the largest cluster which consisted of 13 genotypes (36.11%) followed by Cluster VI comprised of 7 genotypes (19.44%) while Cluster V had the lowest number of genotypes that comprises only one genotype (2.77%). Based on D^2 analysis cluster III had minimum intra cluster distance (2.03714) followed by cluster VI (3.2752). The maximum intra cluster distances was found in cluster V (7.16704) followed by cluster II. Maximum inter cluster distance was between cluster V and III (1392) followed by cluster V and I (1390), cluster V and IV (1134). The cluster VI and III displayed the lowest degree of divergence (29.1). From the 18 principal components (equal number to the original variables) extracted, the first five PC's with an Eigen value >1 accounted for 78.1 % and the first and the second PC's accounted for 48.29.The study showed that there was sufficient genetic divergence between genotypes.**

Keywords **– Clusters, Genetic Diversity, Genetic Divergence, Multivariate Analysis, Principal Component Analysis.**

I. INTRODUCTION

Genetic diversity is very important factor for any hybridization program aiming at genetic improvement of yield especially in self-pollinated crops. To breed desired plant type, information about germplasm diversity and genetic relatedness among elite breeding material is a fundamental element in plant breeding. For creating variability, crossing among parental lines is the most potent and assured method. However, selection of divergent parent is most important, as greater the genetic divergence among the parents for the characters; better are the chances of releasing the variability (Singh 1991). Genetic study based on the multivariate analysis is a powerful tool for determining the degree of divergence between populations, the relative contribution of different components to the total divergence and the nature of forces operating at different levels (Ceolin *et al.,* 2007).

An insight into the magnitude of variability in a vegetable crop species is of prime importance as it forms the basis for any plant improvement program. Genetic divergences have together played an important role in evolution of vegetable crop plants (Mohanty, 2003). A measure of genetic divergence must reflect the difference in gene frequencies and in the absence of experimental technique to measure diversity with respect to genes affecting quantitative characters phenotypic diversity is usually considered to be an indicator of underlying genetic differences. Cluster analysis is a multivariate statistical procedure whose primary purpose is to group individuals or objects based on the characteristics they possess, so that individuals with similar descriptions are mathematically gathered into the same cluster". The resulting clusters of individuals should then exhibit internal

(within cluster) homogeneity and high external (between clusters) heterogeneity, thus, if the classification is successful, individuals within a cluster shall be closer when plotted geometrically and different clusters shall be farther apart (Akhilesh and Gulshan, 2005).

The principal component analysis (PCA) is one of the powerful statistical methods widely applied to classify phenotypic traits in crop germplasm into groups based on similarities. PCA guides the choice of parents for genetic improvement (Beheshtizadeh *et al*., 2013). PCA reduces the original variables into a new set of uncorrelated variables known as principal components (PCs). These PCs clarify the connections between traits and divide the total variance of the original traits into a small number of uncorrelated new variables (Wiley and Lieberman, 2011). The PCA allows visual differentiation among entries and identify possible associations (Mohammadi and Prasanna, 2003) by providing a two dimensional scatter plot consisting of individual entries.

Hence, the present study was undertaken to study the nature and magnitude of genetic divergence, to identify characters which contribute maximum to genetic diversity and to identify suitable genotypes for use in breeding programme for broadening the genetic base in tomato.

II. Materials and Methods

2.1. *Description of the Study Area*

The experiment was conducted at Kulumsa and Melkassa Agricultural Research Centers. Kulumsa Agricultural Research Center is found in Arsi, Zone Oromia Regional State, Ethiopia, is located 175km South East of Addis Ababa on the road from Adama to Asella. The geographical location of Kulumsa is 8^0 01' 10''N latitude and 39^0 09'13''E longitude and at an altitude of 2200 meter above sea level (m.a.s.l). The agro-ecology of the area is characterized by an average annual rain-fall of 850 mm, with short rain between March and April and long rain between June and September, and with annual mean minimum and maximum temperatures of 23.1° C and 7.9 ° C respectively. The soil types of the area is clay and silt loam with pH of 5.6 (Abayneh *et al*., 2003).

Melkassa Agricultural Research Center (MARC) is found 117 km South East of Addis Ababa at a geographic co-ordinate of 8° 24'N and 39° 12'E. KARC is located at an altitude of 1550 m.a.s.l. The area receives mean annual rainfall of 763 mm, about 70% of which is received during the main rainy season from June to September. The mean annual maximum and minimum temperature of the site is about 28.6 ^{0}C and 13.8 ^{0}C, respectively. The agro-climatic condition of the area is classified as semi-arid. The soil texture is dominantly loam and clay loam (MARC, 1995). Available soil water lies between 34.04 % at field capacity and 16.74 % at the permanent wilting point on the dry weight basis. The average bulk density of the soil in depth of 0-90 cm is 1.13 g/cm^3. The soil is slightly alkaline with pH ranging from 7.4 to7.6 pH (Tewodros *et al*., 2005). A total of 36 tomato materials 3 released varieties and 33 genotypes.

2.2. *Experimental Material, Design and Management*

The genotypes were obtained from the Ethiopian Institute of Agricultural Research (EIAR), Melkassa Agricultural Research Center. Simple lattice design (6x6) was employed where each plot consisted of two rows with length of 4m and width 2m that makes a total area of 8m^2. The spacing was 100cm and 30 cm between rows and plants respectively. Fertilizer rate of 200kg per ha of NPS and 150kg per ha of Urea was applied. All other necessary cultural practices were applied to all plots uniformly.

The following data were collected: days to first flowering, days to 50% flowering, days to fruit set, plant height, number of branches per plant, number of flowers per cluster, number of fruits per cluster, number of clusters per plant, number of fruits per plant, fruit length, fruit diameter, average fruit weight, fruit yield per plant, pericarp thickness, fruit shape index, pH, total soluble solid and juice volume.

2.3. *Statistical Analysis*

Cluster analysis based on Ward's method (Ward, 1963) using squared Euclidean distance of the distance metric and standardized variables was performed using Minitab release 17 (Minitab, 1998) to cluster the genotypes based on their agronomic traits. A measure of a group distance based on multiple characters was given by generalized Mahalanobis D^2 statistics (Mahalanobis, 1936) for 18 quantitative characters and was analyzed using the procedure Proc discrim of SAS Software. Squared distance (D^2) for each pair of genotype combinations was computed using the following formula: $D^2ij = ((Xi - Xj)\ S^{-1}(Xi - Xj)$

Where, D^2ij = the square distance between any two groups i and j; Xi and Xj = the vectors for the values for genotype i^{th} and j^{th} genotypes; and S^{-1} = the inverse of pooled variance covariance matrix within groups.

The average intra and inter cluster distances were calculated by the formula given by Singh and Chaudhary (2005)

Square of intra-cluster distance = $\sum Di^2/n$.

Square of inter-cluster distance = $\sum Di^2/ninj$.

Where; ΣDi^2 = Sum of distance between all possible combinations.

ni = number of genotypes in cluster i and nj = number of genotypes in cluster j.

III. Result and Discussion

The analysis of variance revealed highly significant differences among the genotypes for all the characters under study. The Ward's clustering method using squared Euclidean distance classified the 36 tomato genotypes into six distinct clusters (Table 1). This indicated the presence of diversity among the tested genotypes. Cluster III was the largest cluster which consisted of 13 genotypes (36.11%) followed by Cluster VI comprised of 7 genotypes (19.44%) while Cluster V had the lowest number of genotypes that comprises only one genotype (2.77%). The clusters with single genotype indicated their independent identity and importance due to various unique characters. Different authors reported the presence of diversity among tomato genotypes classifying in different number of distinct clusters.

Reddy *et al*. (2013) reported that on the basis of D^2 values, 19 tomato genotypes were grouped in five clusters and cluster I had three genotypes, cluster II had seven genotypes, cluster III had four genotypes, cluster IV had four genotypes and cluster V is solitary consisting of only one genotype; Shushay *et al.* (2014) reported that on the basis of D^2 values, 36 tomato genotypes were grouped in six clusters; Ullah (2015) reported that on the basis of D^2 values, 20 tomato genotypes were grouped in five clusters; Bhattarai *et al.* (2016) reported that on the basis of D^2 values, 71 tomato genotypes were grouped in six clusters; Babu *et al.* (2018) reported that on the basis of D^2 values, 60 tomato genotypes were grouped in eight clusters.

Table 1. Distribution of 36 tomato genotypes in to different cluster groups.

Cluster	No. of genotypes	Percentage	Name of genotypes
I	5	13.89	MAR-1, COR-1-6, ANN-2-6, CLN-3078-G and TYC-2-6
II	4	11.11	TYC-3-6, ADA-3-6, ADA-2-6 and SHA-3-6
III	13	36.11	COR-3-6, TYG-2-6, DSH-1-6, COR-2-6, XIC-2-6, XIC-1-6, OMN-1-6, AON-2-6, Gelilema, CLN-3125-L, CLN-3125-O, ANN-1-6 and SER-1-6
IV	6	16.66	TYG-1-6, TYC-1-6, TYG-3-6, ADA-4-6, SHA-2-6 and ADA-1-6
V	1	2.77	COR-4-6
VI	7	19.44	CLN-3078-C, Melka shola, ARP-tomato D2, AON-3-6, CLN-3078-A, SHA-1-6 and AON-1-6

3.1. *Cluster Mean Analysis*

The mean values of genotypes were computed in each cluster and registered as mean of the respective cluster and results are presented in Table 2. The cluster mean values revealed considerable differences among the clusters for different characters. Cluster I had five genotypes (13.89 %) having a property of moderate days to 50% flowering and first fruit set (25.85 and 39.70 days). It showed lowest fruit length (5.19 cm) and high plant height (59.88 cm) next cluster VI, number of flowers per cluster (5.58), number of fruits per cluster (4.66), number of clusters per plant (21.27) and number of fruits per plant (63.38). Majority of the genotypes in this cluster showed high performance in fruit yield as compared to clusters II. It had relatively low average fruit weight (77.84), moderate fruit diameter (4.80 cm), pericarp thickness (0.62 cm) and fruit shape index (1.07).

Cluster II consisted of 4 genotypes having the characteristic of moderate first flowering (25.75 days), 50% flowering (37.60 days) and first fruit set (39.06 days) than clusters IV. The genotypes had highest fruit diameter (6.04 cm), average fruit weight (155.71 g), fruit yield per plant (2716 g) and juice volume (818.8 ml). It showed the lowest number of fruits per cluster (3.51). Cluster III, contained the largest genotypes thirteen (36.11%) characterized by early days to first flowering and days to 50% flowering. Moreover, they had moderate number of branches per plant (5.33cm), fruit shape index (1.23), pH (4.30), total soluble solid (4.03) and juice volume (553.40).

Cluster IV comprised six (16.16%) genotypes having characteristics of relatively late days to first flowering (28.50 days), days to 50% flowering (39.89) and days to first flowering next to cluster VI. The genotypes in this cluster had the lowest plant height (45.31cm), number of flowers per cluster (4.32) number of fruits per plant (35.39) and fruit yield per plant (1931.04g). Cluster V which contained the lowest number of genotypes had a characteristic of relatively medium days to first flowering (24.50 days) as compared to clusters, I, II, IV and VI. The genotypes also had the low number of fruit length (3.63 cm), average fruit weight (74.37g), pericarp thickness (0.59 cm) and juice volume (390 ml) but the pH (4.51), fruit length (9.12) and total soluble solid (4.45).

Cluster VI which contained seven (19.44) genotypes had a characteristic of the latest days to first flowering (29.11 days), days to 50% flowering (40.72) and days to first fruit set (43.54 days) and highest number branches per plant (8.03) as compared to all clusters. It had the highest number of branches per plant (8.03) next to cluster I and moderate fruit yield per plant (2514.55g), number of clusters per plant (21.16) and number of fruits per plant (50.96).

Kumar *et al*.(2017) reported that minimum days taken to 50% flowering were recorded in cluster I (30.67), maximum number of fruits per cluster was recorded in cluster II (5.87), maximum number of fruits per plant was recorded in cluster IV (35.83) followed by cluster II (35.71), cluster I (16.09) and cluster III (13.51), maximum average fruit weight was recorded in cluster IV (64.34) followed by cluster III (62.41), cluster I (52.71), and cluster II (48.28) and maximum fruit shape index values for fruit shape index were recorded in cluster III (1.10) followed by cluster I (1.01), clusters II (0.93) and cluster IV (0.88). Kiran *et. al* (2017) reported that among the nine clusters, cluster VIII, the largest group included 9 genotypes followed by cluster I comprising of 8 genotypes, cluster III comprising of 7 genotypes, cluster IV having 6 genotypes, cluster IX with 5 genotypes and cluster II with 3 genotypes. Cluster V, VI and VII comprised of 2 genotypes each.

Table 1. Mean values of six clusters for 18 characters of 36 tomato genotypes.

		Clusters				
Traits	**C-I**	**C-II**	**C-III**	**C-IV**	**C-V**	**C-VI**
DFF(days)	25.85	25.75	22.83^{L}	28.50	24.50	29.11^{H}
D50%F(days)	37.81	37.60	36.13^{L}	39.89	37.20	40.72^{H}
DFFS(days)	39.70	39.06	38.33^{L}	42.79	41.00	43.54^{H}
PLH(cm)	59.88^{H}	50.69	53.91	45.31^{L}	55.65	46.33
NBPL(no)	7.70	6.75	6.68^{L}	7.14	7.04	8.03^{H}
NFLC(no)	5.58^{H}	4.45	5.06	4.32^{L}	4.85	4.60
NFC(no)	4.66^{H}	3.51^{L}	3.97	3.60	3.80	3.85
NCPL(no)	21.27^{H}	15.27^{L}	17.20	17.26	18.65	21.16
NFPLT(no)	63.38^{H}	38.74	45.68	35.39^{L}	58.63	50.96
FL(cm)	5.19L	6.00	6.46	7.01	9.12^{H}	5.70
FD(cm)	4.80	6.04^{H}	5.33	4.91	3.63^{L}	5.21
AFW(g)	77.84	155.71^{H}	105.85	118.12	74.37^{L}	96.62
FYPLT(g)	2692.00	2716.00^{H}	2324.00	1931.04^{L}	2230.95	2514.55
PTH(cm)	0.62	0.73	0.69	0.77^{H}	0.59^{L}	0.65
FSI	1.07	0.98^{L}	1.23	1.43	2.52^{H}	1.10
pH(pH meter)	4.28^{L}	4.28^{L}	4.30	4.36	4.51^{H}	4.28^{L}
TSS(Brix)	4.16	4.01^{L}	4.03	4.16	4.45^{H}	4.14
JV(mm)	391.50	818.80^{H}	553.40	624.5833	390.00^{L}	478.93

Where L = represent the lowest value, H = Represent the highest value, DFF = Days to first follower, D50%F = Days to 50% flowering date, DFS = Days to fruit set, PLH = Plant height, NBPL = Number of branches per plant, NFLC = Number flowers/cluster, NFC = Number fruit/cluster, NCPL = Number of clusters/plant, NFPLT = Number of fruits/plant, FL = Fruit length, FD = Fruit diameter, AFW = Average fruit weight, FYPLT = Fruit yield/plant, PTH = Pericarp thickness, FSI = Fruit shape index, pH = Power of hydrogen, TSS = Total soluble solid, JV = Juice volume.

3.2. *Estimation of Inter and Intra Cluster Distance*

The results of intra and inter clusters distance are in Table 3. Cluster III had minimum intra cluster distance (2.03714) followed by cluster VI (3.2752). The maximum intra cluster distances was found in cluster V (7.16704) followed by cluster II. Maximum inter cluster distance was between cluster V and III (1392) followed by cluster V and I (1390), cluster V and IV (1134). Clusters VI and III displayed the lowest degree of divergence (29.1). The smallest inter-cluster distances between clusters suggest that the genotypes were relatively close to each other, in comparison to genotypes grouped in other clusters. It is well recognized that the greater the distance between clusters, the wider the genetic diversity would be between the genotypes. The present results are in line with the findings of other workers; for example: Ullah (2015) reported that cluster I had maximum intra cluster distance (0.979) followed by cluster III (0.244). The intra cluster distances for cluster V was 00.00. Maximum inter cluster distance was between cluster III and I (13.546) followed by cluster V and III (11.218), cluster III and II (6.978).

Kumar *et al*. (2017) reported that the intra cluster distance was maximum in cluster III (3.103) and minimum in cluster IV (2.435), whereas, highest inter cluster distance (4.774) was recorded between I and IV and lowest (2.767) was observed between cluster II and IV; Babu *et al*. (2018) reported that the intra cluster distance varied from 0 to 382.80 and cluster VIII recorded maximum D^2 value (382.80) followed by cluster V (271.17), cluster VII (215.88), cluster II (154.35) and cluster I (98.04). The inter cluster D^2 values revealed that highest inter cluster distance (1296.49) was between cluster V and VIII, while the lowest (130.38) was between cluster I and VI. The inter cluster distance was minimum between cluster I and VI indicating narrow genetic diversity, whereas the inter cluster distance was maximum between V and VIII followed by II and VIII (852.84) indicating wider genetic diversity between these groups.

Table 3. Intra (bold) and inter clusters distance between 36 tomato genotypes tested across locations in 2017/18.

Cluster	I	II	III	IV	V	VI
I	**3.95**	128.70	48.13	110.84	1390	47.53
II		**4.39**	59.76	51.81	1392	99.34
III			**2.04**	29.06	1103	29.36
IV				**3.58**	1134	52.56
V					**0.00**	1177
VI						**3.27**

3.3. *Principal Component Analysis for Quantitative Traits*

Principal component analysis (PCA) was used to examine the variability among the 36 tomato genotypes. To validate the clustering (grouping) observed by the cluster analysis (Table 4), principal components analysis (PCA) was executed using the 18 quantitative characters. From the 18 principal components extracted, the first five PC's with an Eigen value >1 accounted for 78.1% and the first and the second PC's accounted for 48.29. The PC-I showed positive factor loadings for most of the traits except fruit length, fruit diameter, average fruit weight, pericarp thickness and juice volume while PC-II indicated positive factor loading for plant height, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, fruit diameter, fruit yield per plant and

juice volume. Traits which contributed positive factor loadings towards PC-III were plant height, number of flowers per cluster, number of fruits per cluster, fruit length, pericarp thickness, fruit shape index and pH. PC-IV indicated highest positive factor loading for fruit yield per plant followed by number of clusters per plant and number of fruits per plant. PC-V indicated highest positive factor loading for pH followed by fruit yield per plant and number of branches per plant. Kumar *et al*. (2017) reported that the contribution of PC-I towards variability was highest (33.31%) followed by PC-II, PC-III and PC-IV which contributed 17.49%, 11.24% and 10.93% variability respectively; Kumar *et al*. (2017) reported that the PC-I showed positive factor loadings for most of the traits except fruit shape index, pericarp thickness and harvest duration while PC-II indicated positive factor loading for days to 50% flowering, average fruit weight, fruit shape index, pericarp thickness, plant height, total soluble solids, and fruit yield per plant.

Table 4. Eigenvectors, Eigenvalues, proportion and cumulative percentage of variation explained by five principal components (PCs) for morphological and fruit characters of 36 tomato genotypes tested in 2017/2018.

Traits	Eigen vectors				
	PC 1	PC 2	PC 3	PC 4	PC 5
DFF	0.066	0.377	0.221	0.023	-0.113
D50%F	0.050	0.408	0.263	-0.169	-0.103
DFFS	0.061	0.458	0.114	0.109	-0.107
PLH	0.163	-0.333	-0.037	-0.348	0.209
NBPL	0.216	0.233	0.153	0.056	0.343
NFLC	0.267	-0.251	-0.135	0.031	-0.242
NFC	0.343	-0.162	-0.038	0.146	-0.044
NCPL	0.316	0.140	0.130	0.321	0.186
NFPT	0.383	-0.084	0.013	0.271	0.085
FL	-0.145	0.151	-0.458	0.244	0.055
FD	-0.218	-0.219	0.355	-0.033	0.101
AFW	-0.379	-0.032	0.150	0.109	0.059
FYPT	0.096	-0.157	0.312	0.332	0.409
PTH	-0.339	0.083	-0.065	0.141	0.217
FSI	0.019	0.222	-0.524	0.135	0.041
pH	0.024	0.119	-0.249	-0.267	0.669
TSS	0.103	0.173	0.056	-0.552	0.091
JV	-0.365	-0.058	0.090	0.199	0.110
Eigen value	5.168	3.524	2.658	1.552	1.152
Proportion	28.712	19.578	14.768	8.620	6.402
Cumulative	28.712	48.290	63.058	71.678	78.1

IV. CONCLUSION

It can be concluded that tomato genotypes significantly differed for all traits studied showing presence of sufficient usable variation. Genetically distant parents could be used in hybridization to get high yielding recombinants. Thus, based on ward clustering method the 36 tomato genotypes were grouped into six distinct clusters. Cluster III was the largest cluster followed by Cluster VI while Cluster V had the lowest number of genotypes. Based on D^2 analysis cluster III had minimum intra cluster distance followed by cluster VI. The maximum intra cluster distances was found in cluster V followed by cluster II. Maximum inter cluster distance was between cluster V and III followed by cluster V and I, cluster V and IV. The cluster VI and III displayed the lowest degree of divergence. From the first five PC's with an Eigen value >1 accounted for 78.1 % and the first and the second PC's accounted for 48.29.

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