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Evaluation of Tomato (*Solanum lycopersicum* MILL.) Genotypes for Quantitative, Qualitative and Quality Traits at Mid-altitude and Central Rift Valley

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***Abstract* – Tomato (*Lycopersicon esculentum* MILL.) is one of the most known and widely grown vegetables in the world. It is a valuable component of human diet with high content of important nutrients like β-carotene, lycopene and vitamin C. In Ethiopia, tomato is one of the most popular vegetables produced by small farmers and commercial growers for both local uses as well as processing industries. In the present experimental study, we evaluated some tomato genotypes in field conditions in order to determine superior genotypes for yield and yield component traits. The experiment was conducted at two locations. The experimental lay out adopted was the simple lattice design which was replicated two (2) times. Each experimental plot contained incomplete block size of 4m x 4m in 4 rows. Plants in a row were separated by a space of 30cm while the spacing between the rows was 100 cm. Distance of 1.5m was maintained between blocks and 3m between replications. The combined analysis of variance showed significant ($p<0.01$ and $p<0.05$) variability among the genotypes, locations and genotype-location interactions (G × L) for almost all the traits. Shannon-Weaver diversity index was ranged from 1.1 for foliage density and leaf arrangement to 0.73 for plant size indicates that the genotypes are heterogeneous. Over all mean of Shanon-weaver diversity showed that the genotypes are heterogeneous. Among the genotypes evaluated genotypes SHA-2-6, ADA-2-6 and ADA-3-6 had significantly better performance in most of the components measured and displayed superior performance for fruit yield across locations. Hence inclusion of these genotypes in advanced trials of variety development might lead to success.**

***Keywords* – Diversity Index, Environment, Tomato Genotypes, Yield Traits, Quality Traits.**

I. INTRODUCTION

Tomato (*Lycopersicon esculentum* Mill.) belongs to the family *Solanaceae*, which includes more than 3000 species. *Solanum* section *Lycopersicon* includes the cultivated tomato, *Solanum lycopersicum*, the only domesticated species, and a dozen other wild relatives [1]. There are approximately twelve species within genus *Lycopersicon*. On the basis of fruit colour, all these species have been classified into sub genera, viz., *Eulycopersicon* (characterized by red fruits with carotenoid pigmentation and annual growth habit) and *Eriopersicon* (characterized by green fruits with anthocyanin pigmentation). The cultivated species of Tomato (*L. esculentum*) and one wild species (*L. pimpinellifolium*) belong to *Eulycopersicon* and these two species were classified into five botanical varieties. There are 16 wild species of tomato, including *S. habrochaites, S. pennellii, S. pimpinellifolium, S. cheesmaniae, S. galapagense, S. peruvianum, S. corneliomulleri, S. chilense, S. chmielewskii, S. arcanum, S. neorickii, S. huaylasense, S. lycopersicoides, S. ochranthum, S. jugandifolium, and S. sitiens* [2]. One of these varieties, namely, *L. esculentum* var. *ceraseform* (cherry tomato) is considered as the immediate ancestor of present day cultivated tomato. The Central and South America are believed to be the origin of the crop. It became distributed to Europe and Asia in the early and mid-1960s. The crop spread via traders to Egypt,

Sudan, South Africa, and West Africa and to the rest of the world [3]. Like other vegetable crops, tomato is vital sources of carbohydrates, minerals, sugars, amino acids, vitamins (especially vitamin B and C), Phosphorus and dietary fibers [4]. China is the world's leading producer of tomato with the annual production of more than 30 million tons and followed by United States, India, Turkey, Egypt, and Italy, respectively [5].

Ethiopia's wide range of agro-climatic conditions and soil types make it suitable for the production of diverse varieties of vegetables and fruits both under rain fed and irrigation condition [6]. Large scale production of tomato takes place in the upper Awash valley, under irrigated and rain-fed conditions whereas small scale production for fresh market is a common practice around Koka, Ziway, Wondo-Genet, Guder, Bako and many other areas [7]. In Ethiopia tomato can be consumed in raw, ingredient in many dishes, salads, sauces and drinks. It is an important ingredient of diet for the majority of people in almost every household. It is also among the most economically important vegetable crop [8]. The total production of tomato in the Ethiopia has shown a marked increase recently, indicating that it became the most profitable crop providing a higher income to small-scale farmers compared to other vegetable beside the low production and productivity [9]. In the year of 2018/2019 of Meher season the total production of tomato in Ethiopia was about 23,583.75 ton harvested from 4,322 hectare of land, with the productivity of about 5.46 t ha^{-1} [10].

According to [11] genotypes evaluation studies would help in the identification of genetic material for quality and yield traits in crop plants, effectively to generate noble variants having yielding potential far better than other genotypes. The production and productivity not only depends on cultural practices and area of cultivation but on high yielding genotypes, which have good adaptability to the growing area. Hence, evaluation of tomato genotypes is very essential to see the performance of genotypes for their adaptability and agronomic performance like growth and yield traits to identify the potential genotype. Keeping the above facts in mind, present investigations was carried out considering 33 genotypes and 3 released varieties with respect to quality and important traits so that feasibility of developing extra variety with high yield in tomato.

II. MATERIALS AND METHODS

2.1. *Description of the Study Areas*

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 [12]. 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°C and 13.8°C, respectively. The agro-climatic condition of the area is classified as semi-arid. The soil texture is dominantly loam and clay loam [13]. 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 [14].

2.2. *Experimental Materials*

A total of 36 tomato materials 3 released varieties and 33 genotypes (Table 1). The genotypes were obtained from the Ethiopian Institute of Agricultural Research (EIAR), Melkassa Agricultural Research Center.

2.3. *Experimental Procedures and Experimental Design*

The seeds of 36 genotypes including released materials were sown in plastic plug trays with size of 1m length by 0.5m width which has a total of 144 holes which can accommodate a total of 288 seeds and plastic plug trays containing mixture of soil, filter cake, compost and sand in the ratio of 2:2:1:1, respectively and seedlings were sown in polyhouse in October 2/2017. The seedlings were raised in polyhouse which constructed from plastic and has maximum temperature of 35°C and minimum temperature of 10°C. Agronomic practices such as watering and weeding recommended for the vegetable crop were performed after sowing the seeds. During the raising seedlings, since there was no significant pest infestation in the polyhouse, hence no control measure was undertaken. The seedlings were raised at Melkassa. The seedlings were transplanted into the main field in the late October 2017(October 26/2017 and October 30/2017 at Melkassa and Kulumsa respectively) and watering immediately after transplanting. Each experimental plot contained incomplete block size of 4m x 4m in 4 rows. Plants in a row were separated by a space of 30cm while the spacing between the rows was 100 cm. Distance of 1.5m was maintained between blocks and 3m between replications. The experiment was laid down by Simple Lattice Design with two replications in the field; each replications containing with six incomplete blocks each containing six genotypes.

2.4. *Crop Management*

When the seedlings were ready for transplanting the main field was well prepared. During transplanting seedlings to the main field the recommended fertilizer rate was applied (200kg per ha of NPS and 150kg per ha of Urea). When the plants were well established, staking was done using eucalypts sticks and string to keep the plants erect. Hand weeding was done to keep experimental field weed free as per requirement.

2.5. *Data Collected*

Five representative plants per plot were selected randomly and observations were recorded on these plants for different characters as described below. The selection of sample plants was done from the rows excluding the border row and all the variables were recorded from the average of five selected sample plants per plot. The following data were collected from the two rows, both per plot and plant basis. The data' were collected according to the procedures given by International Plant Genetic Resources Institute [15] descriptors list for Tomato. The following quantitative 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 and qualitative data such as; Plant growth habit (Dwarf (1), Determinate (2), Semi-determinate (3), Indeterminate (4)), Plant size (Small (3), Intermediate (5), Large (7)), Foliage density (Sparse (3), Intermediate (5), Dense) (7)) and Leaf arrangement (Erect

(3), Horizontal (5), Drooping (7)) were recorded.

2.6. *Statistical Analysis*

2.6.1. *Analysis of Variance (ANOVA)*

The collected quantitative data on different components were compiled and analyzed statistically using 9.2 [16]. Data were subjected to analysis of variance (ANOVA) using General linear model procedure of SAS. Means were separated using DMRT (Duncan's Multiple Range Test). The model lattice design for combined $yijk = \mu + lij + rlj + brlj + gj + gElj + \varepsilon_{ijk,}$ Where, Yijk = denotes the value of the observed trait for i^{th} treatment received in the k^{th} block within j^{th} replicate, μ = over all mean, gi = effect of the i^{th} genotype (i = 1, 2,…,t), r_j = effect of the j^{th} replicate (j = 1, 2,…,r); b_{jk} = effect of the k^{th} incomplete block within the j^{th} replicate (k = 1, 2, …s) and ε_{ijk} = an experimental error associated with the observation of the i^{th} treatment in the k^{th} incomplete block within the j^{th} complete replicate (Table 1). Homogeneity of variance was tested by F-max method and genotypes was considered as fixed and location random.

Table 1. Analysis of Variance (ANOVA) for simple lattice for across location.

Source of Variation	DF	MS	EMS
Location	l-1	MSl	
Replication(Location)	l(r-1)	MSrl	
Block(Replication Location)	lr(b-1)	MSbrl	
Genotype	g-1	MSg	$\sigma^2e+ r \sigma^2gl +rl\sigma^2g$
Genotype*Location	(g-1) (s-1)	MSgl	$\sigma^2e + r \sigma^2gl$
Error	Subtraction	Mse	σ^2e
Total	lrg-1		

'*' Means genotype by location.

2.6.2. *Estimation of Shannon-weaver Diversity Index for Qualitative Traits*

Shannon-Weaver diversity index (H") which has been widely used in measuring the diversity of germplasm collections was used [17] and expressed as follows: $H' = -\sum piln(pi)$; Where, pi is the proportion of the total number of individuals (genotypes) in the ^{i}th class and and n is the number of phenotypic class for a given character.

III. Results and Discussion

3.1. *Mean and Range Values for Morphological Traits*

Across location the range of days to flowering was 17 for genotype "DSH-1-6" to 34 "ADA-1- 6" with the overall mean 25.78. Significant differences ($P < 0.05$) were recorded among the genotypes with respect to days to 50 percent flowering across location the value ranged from 33.75 to 44.25 days, for the genotypes "ANN-2-6" and "SHA-1-6" respectively and with overall mean value of 38.10 days. Regarding days to first fruit set significant differences ($P < 0.05$) were recorded among the genotypes across locations and the value ranged from 33.25 to 47.5 days with a mean value of 40.43 days the genotype "ANN-2-6" was the earliest to set fruit

while “Melka shola” was the latest to set a fruit (Table 2). Significant differences ($P < 0.05$) were recorded among the genotypes with respect to plant height across location and the value ranged from 40.25 to 77.35 cm with the genotypes “ARP-tomato d2” and “COR-2-6” respectively and the mean value was 51.92 cm. The number of branches per plant significant differences was recorded among the genotypes. The value ranged from 5.55 to 9.4 in the genotypes “TYG-1-6” and “Melka shola” respectively with a mean value of 7.20. The maximum 6.4 flowers number per cluster were observed in the genotype, “MAR-1”while the minimum 3.7 in the genotype “TYG-3-6” with the mean value of 4.85 (Table 2). Regarding the number of fruits per cluster the value ranged from 3.04 to 4.97 with a mean of 3.92. The maximum number fruits per cluster were recorded in the genotype “TYC-2-6” while the minimum in the genotype “TYC-3-6” across location. The number of clusters per plant significantly differed ($P < 0.05$) among the genotypes. The value ranged from 12.45 to 24.45 in the genotype “COR-3-6” and “CLN-30778-A” respectively with a mean value of 18.37 clusters. The mean number of number of fruits per plant was 48.39. It had a range of 27.06 to 76.02. The genotype “CLN-3078-G” had the maximum value of 76.02 while “TYG-1-6” had the minimum value of 27.06. Across location the mean values of number of fruit length and diameter were 6.85 and 5.19 cm respectively. Fruit length ranged from 4.72 to 9.1 cm. The genotype “COR-4-6” had the maximum value of fruit length 9.1 cm while “ANN-2-6” had the, minimum 4.72 cm. Fruit diameter had a range of 3.63 to 6.44 cm. The genotype “ADA-2- 6” had the maximum while “COR-4-6” had the minimum.

Fruit yield per plant showed significant difference among genotypes across locations and it ranged from 1,722.2 to 3,906.2g with the mean value of 2,388.73g. The maximum fruit yield per plant was recorded from genotype “TYC-2-6” while the minimum from genotype “AON-2- 6”. Across location the average fruit weight of tomato varied significantly among genotypes at both locations and it ranged from 69.54 to 164.02g with a mean of 106.88g. The minimum fruit weight was recorded by the genotype “COR-1-6” and the maximum by “ADA-3- 6”. Across location the fruit yield per plant of tomato varied significantly among genotypes it ranged from 1722.2 to 3906.2g with a mean of 2388.72g. The minimum fruit yield per plant was recorded by the genotype “AON-2-6” and the maximum by “TYC-2-6” (Table 2).

3.2. *Mean and Range Values for Physical and Chemical Quality Traits*

Across location the range of pericarp thickness was from 0.58 to 0.82cm with the mean value of 0.68 cm. The minimum value was recorded from genotype “AON-1-6” and the maximum from the genotype “TYG-1-6”. Across location significant variation was found among the genotypes for the fruit shape index and it varied from 0.85 to 2.52 with the mean value of 1.22. The genotype “COR-2-6” showed the lowest fruit shape index while the genotype “COR-4-6” showed the highest. Across location concerning pH the minimum was recorded from genotype “ANN-1-6” and the maximum from the genotype “TYG-3-6”, with the values 4.2 and 4.94 respectively with a mean value of 4.45. TSS of fruit ranged from 2.93 to 4.7 °Bx with a mean of 4.1°Bx. The highest TSS content of fruit was recorded with the genotype e “AON-2-6” while the lowest with genotype e “XIC-1-6”. Regarding the Juice volume significant differences were recorded among the genotypes at both locations. Across location the value ranged from 320 to 890 ml with a mean value of 553.23ml. The genotype “MAR-1” had the lowest juice volume while the genotype “ADA-3-6” had the highest (Table 2). Generally the present investigations regarding mean and range of genotypes were in line with findings reported by [18-20]. Reported that wide range and mean variation were observed for all the characters in tomato [21, 22].

3.3. *Analysis of Variance and Mean Performance of Yield and Quality Traits*

Analysis of variance results for the genotypes showed that there were significant differences both at ($P < 0.05$) and ($P < 0.01$) among the genotypes involved in the study in yield and yield components and quality components. The results from the analysis of variance (Table 3) across location for 18 quantitative traits revealed significant differences among genotypes. The combined analysis of variance (Table 3) over two locations with respect to all the traits showed significant difference among genotypes. The genotype X environment interaction was significant for all characters. Generally, the mean squares of genotypes for most traits were much larger than the mean squares of genotype X environment interaction and error mean square. The mean performance among the genotypes at across location showed SHA-2-6, ADA-2-6 and ADA-3-6 had significantly better performance in most of the components measured. Hence inclusion of these genotypes in advanced trials of variety development might lead to success (Table 4). Revealed that highly significant differences among the genotypes for all the characters indicating sufficient variability existed in the present material selected for the study and indicating the scope for selection of suitable initial breeding material for crop improvement [23]; reported that significant differences among germplasm for all the traits studies indicating the presence of significant variability in the materials which can be exploited through selection [24]; a significant variations were observed among different genotypes for morphological traits [25].

Similar results obtained for; fruit number per plant, single fruit weight, plant height to the findings of [26]. However [23] reported very wide range of variations in mean performance of genotypes for all the characters under study and mean performance of genotypes for their traits using critical differences revealed the existence of very high level of variability among the genotypes; reported that the mean performance of different genotypes for different characters showed significant differences [27].

3.4. *Estimation of Shannon-Weaver Diversity Index for Qualitative Traits*

The proportion and estimates of Shannon-Weaver diversity index for qualitative traits of 36 tomato genotypes were presented in Table 5. Regarding plant growth habit, 41.7% of genotypes were determinant, 13.9% semi determinant and 44.4% indeterminate. The studied genotypes were grouped into three on their plant size. Accordingly 2.8% of genotypes were small, 66.7% of intermediate and 30.5% large. The genotypes were characterized by foliage density of genotypes as sparse, intermediate and dense. Accordingly 30.6% of genotypes had sparse foliage density, 33.3% intermediate and 36.1% dense. The genotypes were characterized according to their leaf arrangement as erect, semi erect and dropping. Accordingly 41.7% of genotypes were erect, 27.8% semi erect and 30.5% dropping (Table 5). Shannon-Weaver diversity index was ranged from 1.1 for foliage density and leaf arrangement to 0.73 for plant size indicates that the genotypes are heterogeneous. Over all mean of Shanon-weaver diversity showed that the genotypes are heterogeneous. Reported that tomato genotypes showed genetic diversity in all the studied characters such as plant growth habit, plant size and foliage density [28].

Table 2. Mean and Range values for 18 quantitative traits of tomato genotypes tested at across locations in 2017/2018.

Genotype		**Traits**	**Range**		**Mean ± SE**
			Minimum-Maximum		
DSH-1-6	ADA-1-6	DFF	17	34	25.78 ± 1.21

Genotype		Traits	Range		Mean ± SE
			Minimum-Maximum		
ANN-2-6	SHA-1-6	D50%F	33.75	44.25	38.1 ± 0.87
ANN-2-6	Melka shola	DFFS	33.25	47.5	40.43 ± 0.89
ARP-tomato d2	COR-2-6	PLH	40.25	77.35	51.92 ± 1.84
TYG-1-6	Melka shola	NBPL	5.55	9.4	7.2 ± 0.38
TYG-3-6	MAR-1	NFLC	3.7	6.4	4.85 ± 0.18
TYC-3-6	TYC-2-6	NFC	3.04	4.97	3.92 ± 0.12
COR-3-6	CLN-30778-A	NCPL	12.45	24.45	18.37 ± 1.05
TYG-1-6	CLN-3078-G	NFPLT	27.06	76.02	48.39 ± 2.88
ANN-2-6	COR-4-6	FL	4.72	9.1	6.85 ± 1.7
COR-4-6	ADA-2-6	FD	3.63	6.44	5.19 ± 0.16
COR-1-6	ADA-3-6	AFW	69.54	164.02	106.88 ± 5.72
AON-2-6	TYC-2-6	FYPLT	1722.2	3906.2	2388.73 ± 163
AON-1-6	TYG-1-6	PTH	0.58	0.82	0.68 ± 0.01
COR-2-6	COR-4-6	FSI	0.85	2.52	1.22 ± 0.035
ANN-1-6	TYG-3-6	pH	4.2	4.94	4.45 ± 0.01
XIC-1-6	AON-2-6	TSS	2.93	4.7	4.1 ± 0.13
MAR-1	ADA-3-6	JV	320	890	553.23 ± 38.5

Where, Std = Standard deviation, DFF = Days to first flowering, D50%F = Days to 50% flowering, DFS = Days to fruit set, PLH = Plant height, NBPL = Number of branches per plant, NFLC = Number flowers/cluster, NFC = Number fruits/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.

Table 3. Analysis of variance for the 18 characters across location.

		Mean Square									
Source of variation	**DF**	**DFF**	**D50%F**	**DFFS**	**PLH**	**NBPL**	**NFLC**	**NFC**	**NCPL**	**NFPT**	**FL**
Location	1	79.51*	580**	283.36**	246.36*	60.262**	20.33**	0.13	436.81**	511*	0.36
Genotypes	35	46.8**	23.95**	28.25**	213.44**	2.695**	1.39**	0.77**	28.66**	537.15**	25.85*
Loc. x genotype	35	38.88**	1521*	16.53*	32.25**	2.765*	0.386**	0.26*	25.63*	169.32*	22.84*
Error	50	11.76	6.11	6.35	27.20	1.36	0.245	0.13	8.86	66.39	23.18
CV%		13.30	6.49	6.23	10.12	16.23	10.22	9.24	16.21	16.84	70.3

Continued from table 3.

		Mean Square							
Source of variation	**DF**	**FD**	**AFW**	**FYPLT**	**PTH**	**FSI**	**PH**	**TSS**	**JV**
Location	1	6.63**	14412.78*	23022786.13**	0.063**	0.71*	1.9**	7.2**	616879.34**

		Mean Square							
Source of variation	**DF**	**FD**	**AFW**	**FYPLT**	**PTH**	**FSI**	**PH**	**TSS**	**JV**
Genotypes	35	1.51**	1948.3**	790856.82**	0.015**	0.4**	0.064**	0.621**	66641.245**
Location x genotype	35	0.40*	413.65*	671549.79**	0.0097*	0.0407**	0.0693**	0.434**	12466.324**
Error	50	0.22	261.63	212765.25	0.00344	0.0105	0.0040	0.138	11858.785
CV%		9	15.13	19.31	8.571	8.41	1.42	9.065	19.68

Where, CV = Coefficient of variation, ** = highly significant at 1%, * = significant at 5%, DF = Degree of freedom, DFF = Days to first flowering, D50% F = Days to 50% flowering, DFS = Days to fruit set, PLH = Plant height, NBPL = Number of branches per plant, NFLC = number flowers/cluster, NFC = Number of fruits/cluster, NCPL = Number of clusters/plant, NFPLT = Number of fruits/plant, FL = Fruit length, FD = Fruit diameter, AF = Average fruit weight, FYPLT = Fruit yield/ plant, PTH = Pericarp thickness, FSI = Fruit shape index, p^H = power of hydrogen, TSS = Total soluble solid, JV = Juice volume.

Table 4. The Mean performance of 36 tomato genotypes tested at across location in 2017/2018.

Genotypes	**DFF**	**D50%F**	**DFF**	**PLH**	**NBPL**	**NFLC**	**NFC**	**NCPL**	**NFPLT**	**FL**
MAR-1	23.25g-k	37.75c-k	40.75c-l	57.55c-g	8a-f	6.4a	4.465ac	21.05a-f	62.113b-d	5.992c
TYC-3-6	23.75f-k	37e-k	38.75h-n	52.898e-k	7.599a-h	3.85k-m	3.0498j	16.05f-l	44.483g-k	5.827c
COR-3-6	23.75f-k	37.75c-k	37.5j-n	62b-d	6.25e-i	5.05c-h	3.5995f-j	12.45l	37.6i-m	5.939c
COR-1-6	26d-j	38.75b-h	39.75f-n	67.5b	7.75a-g	6.0875ab	4.7335ab	17.65c-j	75.35a	4.833c
TYG-2-6	23.5g-k	35.75g-k	40.25e-m	44.4k-n	5.7ih	4.65e-k	3.766e-i	14.25h-l	44.775f-k	6.899bc
ANN-2-6	23h-k	33.5k	33.25o	64.9bc	6.55 c-i	5.15c-g	4.7325ab	21a-f	68.75ab	4.723c
DSH-1-6	17 l	36e-k	38j-n	53.4e-i	5.75g-i	4.65e-k	3.7495e-i	14.05i-l	47.775e-j	6.049c
COR-2-6	22.25h-k	37d-k	36.75k-o	77.35a	6.25e-i	5.45b-e	3.917c-h	13.7j-l	48.275e-j	5.043c
XIC-2-6	25.5e-j	35.5h-k	39.75f-n	48.95f-n	7.05c-i	5.85a-c	4.123b-f	18.2c-k	53.458c-h	7.716bc
TYG-1-6	24.75e-j	39.25b-h	39.75f-n	43.9mn	5.55i	3.775lm	3.349h-j	13.4kl	27.065m	7.97bc
TYC-1-6	31.5a-d	40.25a-e	43b-g	45.4j-n	6.4c-i	4.4g-m	4.014c-f	15.4g-l	42.025h-k	7.458bc
XIC-1-6	24f-k	35.75f-k	40.5d-m	49.065f-m	6.9c-i	5.4975b-e	4.3325b-e	17.7c-k	58.6c-f	6.954bc
COR-4-6	24.5e-k	37.25d-k	41b-j	55.65d-h	7.25b-i	4.85d-i	3.8015d-i	18.65b-j	57.525b-g	9.121bc
ADA-3-6	19.25 l	35h-k	39h-n	49.45f-m	6.85c-i	4.2825h-m	3.233ij	13.45kl	27.575lm	5.725c
TYG-3-6	24.5e-k	39.75b-g	42.5b-i	48.35h-n	9.175ab	3.7m	3.333h-j	20a-g	31.95k-m	6.552c
OMN-1-6	19l	33.75k	38.25i-n	56.1d-h	7c-i	5.6b-d	4.1505b-f	21.35a-e	53.725c-h	6.527c
ADA-2-6	30a-e	40b-f	38j-n	51.45f-l	6.05f-i	5d-i	3.8835c-h	15.6g-l	47.725e-j	6.55c
AON-2-6	21.75j-l	38b-j	36.25m-o	48.4h-n	6.55c-i	4.8375d-i	3.8835c-h	16.3e-l	40.625h-l	5.559c
ADA-4-6	26.75b-j	40b-f	44.25a-e	41.283nm	6.15e-i	4.72e-j	3.6f-j	19.25b-h	42.7h-k	8.161bc
Gelilema	21.75j-l	34.25i-k	35.75no	47.883h-n	9.3625a	4.7975d-j	4.0555c-f	19.1b-i	52.625c-h	6.816bc
CLN-3078-C	26.75a-j	38.5b-i	41b-j	53.1e-j	7.45a-i	5.2c-g	4.0335c-f	22a-c	58.5b-f	6.092c

Genotypes	DFF	D50%F	DFF	PLH	NBPL	NFLC	NFC	NCPL	NFPLT	FL
CLN-3125-L	22.75h-k	34jk	36.5l-o	57.8c-f	6.4d-i	5.3b-f	3.7995d-i	20.2a-g	40.975h-k	6.351c
CLN-3125-O	23.25g-k	37.5d-k	39.25g-n	57.45c-g	6.05f-i	4.7e-j	4.012c-f	16.5d-l	42h-k	6.377c

Continued from table 4.

Genotypes	DFF	D50%F	DFF	PLH	NBPL	NFLC	NFC	NCPL	NFPLT	FL
SHA-3-6	30a-e	39b-h	40.5d-m	48.95f-n	7.085c-i	4.65e-k	3.902c-h	15.95f-l	43.29h-j	5.916c
ANN-1-6	26.25c-j	39.75b-g	41.25b-i	45.533i-n	6.2625e-i	4.515f-m	3.5895f-j	16.1f-l	36.793i-m	6.816bc
SHA-2-6	29.5a-f	40a-f	43.5a-g	49.6f-l	8.1a-e	4.55e-l	3.3825h-j	18.85b-i	35.688j-m	5.349c
Melka shola	29a-g	41.25a-d	47.5a	48.398h-n	9.3625a	4.765d-j	3.9265c-h	21.6a-d	50.583d-i	6.323c
ARP-tomato D2	26.5b-j	35.5g-k	40.25e-l	40.248n	8.23a-d	4.17i-m	3.5458f-j	19.45a-g	41.308h-k	5.591c
AON-3-6	28.75a-g	39.75b-g	44.75a-d	46i-n	7.65a-h	4.95d-i	4.1095c-f	18.85b-i	43.725gijk	5.566c
CLN-30778-A	28.5a-j	42.25a	45.25ab	46.25i-n	8.3675 a-c	4.4375f-m	4.139b-f	24.45a	64.95a-c	19.106a
SER-1-6	26d-j	36f-k	38.25i-n	52.438e-k	8.2a-d	4.9125d-i	4.4465a-c	22.55a-c	54.4c-h	6.977bc
CLN-3078-G	25.5e-j	37.75c-k	40.75c-l	48.7g-n	7.6a-h	5.05c-h	4.3975a-d	23.5ab	76.025a	5.347c
TYC-2-6	31.5a-d	41.25a-d	44a-f	60.748c-e	8.25 a-d	5.1975c-g	4.9743a	22.45a-c	61.024b-e	5.033c
SHA-1-6	32.25a	44.25a	45a-c	44.233l-n	7.15c-i	3.9825j-m	3.3251-j	22.1a-c	45.95fg-j	5.129c
AON-1-6	32a-c	42a-c	41b-j	46.065i-n	8.265a-d	4.6975e-j	3.9803c-g	22.1a-c	50.3d-i	5.303c
ADA-1-6	34 a	40.5a-d	43.75a-f	43.3n	7.3a-i	4.75d-j	3.8835c-h	16.05f-l	31.875k-m	14.884ab
Mean	25.78	38.1	40.43	51.92	7.2	4.85	3.92	18.37	48.39	6.85
CV	13.3	6.49	6.23	10.12	16.23	10.22	9.24	16.21	16.84	7.29
LSD	4.87	3.51	3.58	7.41	1.65	0.7	0.52	4.23	11.57	6.84

Where, DFF = Days to first flowering, D50% F = Days to 50% flowering, DFS = Days to fruit set, PLH = Plant height, NBPL = Number of branches per plant, NFLC = Number flowers/cluster, NFC = Number fruits/cluster, NCPL = Number of clusters/plant, NFPLT = Number of fruits/plant, FL = Fruit length, CV = Coefficient of variation, LSD = Least significance difference **Means having common letter do not differ significantly at 5% level as per DMR.

Continued from table 4.

Genotypes	FD	AFW	FYPLT	PTH	FSI	Ph	TSS	JV
MAR-1	4.9051e-k	80.69i-k	2380.9bc-h	0.58743hi	1.22158gh-j	4.171k	4.475a-e	320 l
TYC-3-6	5.7124a-e	156.73a	2542.3b-g	0.7931ba	0.99981-r	4.25075jk	3.85e-k	827.5ab
COR-3-6	6.1323ab	111.39c-h	1834.4gh	0.71553b-f	0.96717o-r	4.34375f-j	4c-j	557.5c-j
COR-1-6	4.2792k-m	69.54k	1865.4f-h	0.5953hi	1.11575i-o	4.3925fg	4.1625a-i	357.5kl
TYG-2-6	4.7016h-k	93.29f-k	2068.8c-h	0.6635d-i	1.47417 b-d	4.36863f-h	4.375a-g	457.5g-l
ANN-2-6	5.0348e-k	77.74i-k	2551.3b-f	0.63363 e-i	0.9379qr	4.42425f	4c-j	402.5j-l
DSH-1-6	5.3998b-i	93.84f-k	2599.3b-f	0.6605de-i	1.12048i-o	4.52038de	4.5125a-d	521.25d-k

Genotypes	FD	AFW	FYPLT	PTH	FSI	Ph	TSS	JV
COR-2-6	5.9611a-d	111.6c-h	2863.2bc	0.67233 c-i	0.84641r	4.617c	4.4a-e	500f-l
XIC-2-6	5.0068e-k	112.67c-g	2003.8e-h	0.73428a-e	1.54237bc	4.617c	4.35a-g	565c-j
TYG-1-6	5.4276b-h	127.05b-d	2083.2c-h	0.81883a	1.46697b-e	4.61825c	3.775f-k	692.5b-d
TYC-1-6	5.1916d-j	122.92c-e	2046.3d-h	0.80328ba	1.44006b-f	4.70188bc	3.7625f-k	612.5c-h
XIC-1-6	5.3322b-i	114.24c-g	2405.7b-h	0.6528d-i	1.30567d-g	4.6585c	2.925l	630c-g
COR-4-6	3.6289m	74.37jk	2286.7b-h	0.58223i	2.52154a	4.91613a	4.45a-e	390jkl
ADA-3-6	6.0544a-c	164.02a	2885.2b	0.74688a-d	0.91743r	4.76275b	3.75h-k	890a
TYG-3-6	5.4179b-h	101.4de-j	1968.2e-h	0.79885ba	1.20854h-j	4.93738a	4.675ab	562.5c-j
OMN-1-6	5.5215b-g	110.16c-h	2948.7 b	0.70575b-g	1.18142h-k	4.78675b	3.675h-k	690b-e
ADA-2-6	6.4364a	151.9ba	2926.5b	0.68615c-h	1.01546k-r	4.89613a	4.25a-h	717.5bc
AON-2-6	5.6148b-f	96.29 e-k	1722.2h	0.59023hi	0.99021-r	4.91575a	4.7a	462.5f-l
ADA-4-6	5.1204e-k	129.99bc	2005.1e-h	0.77273a-c	1.6002b	4.39225f-h	3.5375j-k	612.5c-h
Gelilema	5.3318b-i	105.18c-i	2708.5b-e	0.7514a-d	1.28158f-i	4.36075f-i	3.65h-k	577.5 c-j
CLN-3078-C	5.1907d-j	89.25g-k	2085.8c-h	0.64355e-h	1.17421h-l	4.30975g-j	3.925d-k	515d-k
CLN-3125-L	4.7534h-k	110.78c-h	2233.2b-h	0.6715d-i	1.29983e-g	4.28425g-j	4.125a-h	502.5e-l
CLN-3125-O	5.571b-f	104.71c-i	1895f-h	0.68783c-h	1.14571h-m	4.30725g-j	3.45j-l	592.5c-i

Continued from table 4.

Genotypes	FD	AFW	FYPLT	PTH	FSI	pH	TSS	JV
SHA-3-6	5.9587a-d	150.2ba	2617b-f	0.68503c-h	0.98338n-r	4.30575g-j	4.2a-h	840ba
ANN-1-6	4.9124e-k	114.73c-g	1841.3f-h	0.7123b-f	1.38653c-g	4.15675k	4.125a-h	627.5c-g
SHA-2-6	3.8148lm	115.03c-g	1750.2gh	0.7328 a-e	1.38781c-g	4.297g-j	4.5a-d	647.5c-f
Melka shola	4.5942i-k	95.22e-k	2037.3d-h	0.6523d-i	1.38018c-g	4.3145 g-j	4.45a-e	402.5j-l
ARP-tomato D2	5.428b-h	119.52c-f	2801.9b-d	0.6501d-i	1.00793l-r	4.27525h-j	4.075a-i	627.5c-g
AON-3-6	4.982e-k	84.03i-k	2603.9b-f	0.71638 b-f	1.09945j-q	4.36425f-h	3.325kl	507.5d-k
CLN-30778-A	4.8083f-k	79.12i-k	2594.2b-f	0.61498e-i	1.22261-j	4.2715h-j	4.5a-d	412.5i-l
SER-1-6	4.9987e-k	97.21e-j	2777.1b-d	0.70695b-g	1.39389c-f	4.44275 ef	4.05b-j	510d-k
CLN-3078-G	4.469k-m	79.48i-k	2725.9b-e	0.65068d-i	1.15649h-m	4.25425i-k	3.6875h-k	425h-l
TYC-2-6	5.3244c-i	81.76i-k	3906.2a	0.6101g-i	0.94426p-r	4.34025f-j	4.625a-c	452.5g-l
SHA-1-6	6.0618 a-c	110.12c-h	2921.7b	0.66973d-i	0.91743r	4.159k	4.5625 a-d	360kl
AON-1-6	5.4342b-h	99.09e-j	2620bc-f	0.57685i	0.97656nopqr	4.35475f-j	4.1125a-i	527.5de-k
ADA-1-6	4.5038j-l	112.34c-g	1888e-h	0.71395b-f	1.45392bcde	4.3145g-j	4.6875ab	620c-g
Mean	5.19	106.88	2388.73	0.68	1.22	4.45	4.1	553.23

Genotypes	FD	AFW	FYPLT	PTH	FSI	pH	TSS	JV
CV	9.01	15.13	19.31	8.57	8.41	1.42	9.07	19.68
LSD	0.66	22.97	655.12	0.08	0.15	0.09	0.53	154.66

Where, 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, CV = Coefficient of variation, LSD = Least significance difference, **Means having common letter do not differ significantly at 5% level as per DMR.

Table 5. Estimates of frequency and Shannon-Weaver diversity index for qualitative traits.

Character	Code and Descriptor	Frequency	Percent	H''
Plant Growth Habit	2. Determinant	30	41.7	
	3. Semi-deteminat	10	13.9	
	4. Intermidiate	32	44.4	0.99
Plant Size	3. Small	2	2.8	
	5. Intemidiate	48	66.7	
	7. Large	22	30.5	0.73
Foliage Density	3. Sparse	22	30.6	
	5. Intemidiate	24	33.3	
	7. Dense	26	36.1	1.1
Leaf Arrangement	3. Erect	30	41.7	
	5. Semi-erect	20	27.8	
	7. Dropping	22	30.5	1.1

IV. Summary and Conclusion

Tomato is one of the most popular, important edible and nutritious vegetable crops in the world. Like in most parts of the world it is produced and consumed in Ethiopia .The study was conducted to evaluate some tomato genotypes in field conditions in order to determine superior genotypes for yield and yield component traits. The study was conducted at Kulumsa and Melkassa Federal Research Centers in 2017/2018 from late October to mid-February by using 6*6 simple lattice design. Across location all studied traits were significant; indicating the presence of sufficient genetic variability in the genotypes and considerable scope for their improvement. The mean performance among the genotypes SHA-2-6, ADA-2-6 and ADA-3-6 had significantly better performance in most of the components measured. Hence inclusion of these genotypes in advanced trials of variety development might lead to success. The Shannon-Weaver diversity index indicated high variability for plant growth habit, foliage density, and plant size and leaf arrangement.

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