RESEARCH ARTICLE

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Morphological and agronomical characterization of beef type tomato hybrids

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Abstract

Tomato (*Solanum lycopersicum L.*) is one of the most important vegetable crops and agro-morphological characterization has a key role in the development of new varieties. In this study, 228 samples of the tomato hybrid type "Beef" (*Solanum lycopersicum L.*) were characterized by comparing with 11 standard varieties based on 24 quantitative traits and 2 qualitative traits to reveal the phenotypic diversity by using conventional descriptors proposed by IPGRI (1996) and UPOV (2011). A significant level of variability was found in most of the traits studied among the genotypes in two locations. A high level of broad-sense heritability (H^2) was detected for many traits such as the number of fruits, firmness, immature fruit color, stem length up to the first inflorescence, total height, and number of days to the first flowering in both locations. There was a highly significant positive correlation among the color values (L*, a*, b*, c*, h*) but no positive correlation between a* and h*. Number of locule had a positive correlation with fruit width and fruit weight, and a positive correlation was determined between fruit length and pericarp thickness in both locations. While fruit weight had a highly significant negative correlation with the number of fruits and number of flowers, there was a highly significant negative correlation between the number of locules and the fruit length-to-width ratio in both locations. Results of PCA showed that PC1 and PC2 accounted for around 15.6% and 13.7% of total variation and 13.8% and 11.8% of total variation for Location 1 and Location 2, respectively. The first five principal components accounted for around 54.2% of the total variation for Location 1 and 48.2% of the total variation for Location 2. Cluster analysis grouped the 239 genotypes under six cluster groups for Location 1 and seven cluster groups for Location 2. Results of the cluster analysis revealed that Cluster 3 for Location 1 and Cluster 2 for Location 2 had prominent genotypes for some of the agronomically important traits like yield. The results showed that present phenotypic diversity could be useful in the selection of best-performing genotypes, which would be important candidates for the beef red tomato market in the spring season.

Keywords: Agro-morphological characterization, beef type tomato, *Solanum lycopersicum*

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the most popular and consumed vegetable crops and belongs to the Solanaceae (nightshade) family, including many important agronomic crops such as eggplant, pepper, and potato (Jenkins, 1948; Peralta et al., 2008). Tomato is one of the most produced vegetable crops in the world and total production of tomatoes is around 180 million tons in a cultivation area of 5 million hectares (FAOSTAT, 2021). China, India, Turkey, USA,

and Italy are the top countries in tomato production in the world. Turkey is one of the countries that has an important share in total production of tomato in the world and its tomato production is around 13 million tons in a cultivation area of 180 thousand hectares (FAOSTAT, 2021). Tomato has a high nutritional value, is a great source for human nutrition, and is used for fresh and processed consumption like sauces, paste, ketchup, and juices (Gosselin and Trudel, 1984). Ripe tomato includes mainly 95% of water and 5% of other components (sugar, polyphenols, vitamins, etc.) and lycopene of 20-50 mg per 100 g ripe fruit (Davies and Hobson, 1981). Tomato variety "Beefsteak", also known as "Beef", can have determinate or indeterminate growth habits. Beef tomatoes have generally flattened or round shape, and more than three locules with green shoulder. There are some essential characteristics for a variety that is used for fresh consumption, these are mainly; high yield, external and internal fruit quality, earliness, long shelf-life and resistance to biotic and abiotic stresses (Prohens-Tomás, and Nuez, (Eds.), 2007). In a breeding program, it is crucial to measure and analyze important morphologic and agronomic traits properly and to comprehend and benefit more from phenotypic variation. Phenotypic characterization is generally implemented with conventional morphological and agronomical descriptors that are mainly seedling, plant, inflorescence, flower, fruit, and agronomic traits (IPGR, 1996). Phenotypic characterization also provides good estimation about parental lines that are used to make new hybrids.

MATERIALS AND METHODS

Plant Materials

11 samples of standard red tomato type "beef" as control and 228 samples of the red tomato hybrid type "beef" which were newly developed by tomato breeders at Enza Zaden were studied by using morphological and agronomical descriptors proposed by IPGRI (1996) and UPOV (2011). Control varieties were named as A, B, C, D, E, F, H, I, J, K, and M and newly developed hybrids were named as between G1 and G228.

Growth Conditions and Experimental Design

The trials were conducted in two locations and coded Location 1 (L1), namely Enza Zaden R&D Turkey station, and Location 2 (L2), namely Kurşunlu region, Antalya, Turkey between February and June 2021. The experimental plots were arranged as double rows: 1.4 m between each double row, 0.5 m between rows within a double row, and 0.4 m between plants. Transplantation of tomato seedlings was carried out at the end of January 2021 in Location 2 and around mid-February 2021 in Location 1. All the plants were tied up with rope to support them as they all had indeterminate growth habits. The apex of all the plants was cut when control varieties had a seventh inflorescence. General agronomic practices such as drip irrigation, weeding control, and fertilizing were carried out.

All the genotypes were transplanted in two different trials into non-heated greenhouses with an Augmented randomized complete block (ARCBD) experimental design due to the limited amount of seeds and limited space, and the number of blocks was determined according to the following formula: $b \geq [(10/r-1)]+1$

Where, r is the number of control varieties used in this study and b is the number of blocks (Federer and Raghavarao, 1975). As 11 standard variety samples were used as control varieties, two blocks were decided as sufficient according to the formula. Therefore, control varieties were used in two blocks and each block included newly tested genotypes.

Phenotypic Analysis

The descriptors were the number of days to the first flowering (FD), number of days to the first maturity (MD), plant height (TH), stem length between 1st and 2nd truss (L1.2), stem length up to the first inflorescence (L1trs), leaf attitude (LA), leaf length (LL), leaf width (LW), number of truss on main stem (NT), number of flowers (NF), number of fruit (NFr), the ratio of fruit set (FS), immature fruit color (IMC), fruit external color (L, a, b, c, h), fruit length (FL), fruit width (FW), the fruit length-to-width ratio (FL.FW), pericarp thickness (PT), number of locules (NL), fruit weight (Fwe), fruit firmness (F), and average yield (Y). A total of 26 morphological and agronomical traits were characterized as 2 qualitative traits and 24 quantitative traits.

Data Collection

All the data were collected from randomly selected 4 individual plants from 10 plants within each genotype. The number of days elapsed from the planting date to the first flowering was determined in 50% of all plants within hybrid when they had the first fully open flower. Similarly, the number of days elapsed until the first maturity was also determined in 50% of all plants within hybrid when they had the first mature fruit. Total plant height, stem length between 1st and 2nd trusses, and stem length up to first inflorescence were measured on 4 plants per hybrid by 2 meters, and leaf length and leaf width were measured on 4 plants per hybrid by using a 30-cm ruler, respectively. Leaf attitude and immature fruit color were scored for each genotype according to the morphological descriptors used in this study. Fruit weight was measured on collected 4 marketable representative fruits (1 fruit per plant) by using a

weighing scale and recorded for each plant within the genotype. The average yield per hybrid sample was calculated by multiplying an average number of fruits per hybrid sample with the mean weight of 4 marketable representative fruits per hybrid sample. Fruit external color was measured on 3 parts of a marketable, ripe representative fruit per plant within each hybrid by using a Colorimeter PCE CSM device and L*, a*, b*, c*, and h* values were obtained. These values indicate lightness, red or green coordinates, yellow or blue coordinates, color scale (red, yellow, blue, and green) and saturation, respectively. Fruit firmness was also measured on 3 parts of fruit per plant by using a Force Gauge device and firmness values were obtained as Newton (N) unit. Pericarp thickness and number of locules were recorded by cutting fruit cross-sectionally. Pericarp thicknesses were measured by using a slide gauge and number of locules was counted.

Statistical Analysis

As there are too many genotypes to be characterized with a limited number of seeds and a limited experimental field area, an augmented randomized complete block design was used, and data were analyzed by using R statistical software (R 4.1.0 version). Analysis of variance (ANOVA) was run by using the 'augmented RCBD' package in R program (Aravind *et al*., 2019). Descriptive statistics, genetic variability and frequency distribution were also performed by using augmented RCBD package in R program. Phenotypic, genotypic, and environmental variances (σ^2p, σ^2g, σ^2e) were calculated by using a mean square from ANOVA result (Federer and Searle, 1976) according to the formula as:

σ^2p = Mean sum of squares of newly tested genotypes, σ^2e = Mean sum of squares of residual

$\sigma^2g = \sigma^2p - \sigma^2e$

Phenotypic and genotypic coefficients of variation (PCV and GCV) were also calculated according to Burton (1951, 1952). The broad-sense heritability was obtained based on Lush (1940) method as in the formula: $H^2 = \sigma^2g / \sigma^2p$

And estimation was categorized according to Johnson *et al*., (1955) as:

H^2	Category
x < 30	Low
30 ≤ x <60	Medium
≥ 60	High

Pearson's correlation analysis was performed by using the function 'cor()' and plots were obtained with the 'corrplot' and 'Performance Analytics' R packages. Principal component analysis (PCA) was performed by using 'corrplot', 'factoextra' and FactoMiner' R packages. Cluster analysis was applied as hierarchical two-way clustering through Ward method by using SAS JMP 16.0 version and was obtained for both locations.

RESULTS

Descriptive statistics was carried out to interpret 228 beef-type tomato hybrids in terms of 26 morphological and agronomical traits in two locations, (L1) and (L2) (Table 1). Analysis of variance (ANOVA) revealed significant differences between blocks for firmness, days to the first flowering, fruit length, fruit length-to-width ratio, fruit set, fruit weight, hue value, stem length up to the first inflorescence, leaf attitude, number of flowers, number of fruits, number of truss and yield in Location 1 (treatment adjusted) (Table 2). Block effects were also significant for most of the traits except for a*, fruit length, fruit set, fruit weight, hue value, stem length between 1st and 2nd trusses, stem length up to the first truss, leaf width, and pericarp thickness in Location 2 (treatment adjusted). Block effects were significant for stem length up to the first truss (17.28*) in Location 1 and there were significant differences between blocks for firmness, fruit length, number of days until the first maturity, and total height in Location 2 (block adjusted). All the genotypes including control varieties in Location 1 showed significant differences in firmness, days to the first flowering, fruit set, immature fruit color, stem length up to the first truss, leaf attitude, number of flowers, pericarp thickness and total height (treatment adjusted). Significant differences were also found among genotypes for days to the first flowering, fruit weight, immature fruit color, length between 1st and 2nd trusses, stem length up to the first truss, leaf length, number of fruits, number of truss and total height in Location 2 (treatment adjusted).

Genetic variability analysis was applied based on the ANOVA results. The broad-sense heritability was calculated as the highest for the number of fruit (92.09%), rate of fruit set (88.91 %), stem length up to the first truss (88.11%), and number of flowers (87.24%) and the lowest heritability was found for fruit width (4.15%), fruit weight (4.61%), and hue value (10.05%) in Location 1. The heritability was recorded as the highest for plant total height (94.77%), fruit weight (90.27%), and stem length between 1st and 2nd trusses (85.02%), and the lowest heritability was estimated for hue value (1.51%), fruit width (11.52%) and L* value (22.7%) in Location 2. The broad-sense heritability could not be calculated mostly for color values, as well as a fruit length-to-width ratio and pericarp thickness, because

environmental variance (EV) was higher than phenotypic variance (PV) (Table 3).

Correlation analysis for agro-morphologic traits was done separately for Location 1 and Location 2 (Figure 1). The Pearson correlation coefficient showed highly significant positive correlations between color values (L*, a*, b*, c*, and h*) in both locations. Fruit width had highly significant and positive correlations with fruit length, number of locule, and leaf length and fruit length had highly significant and positive correlations with pericarp thickness, leaf length and leaf width, number of days to the first flowering and stem length up to the first truss in both locations. Highly significant and negative correlations were also found between the number of days to the first flowering and number of flowers, number of fruits, total height; and between the number of days to the first maturity and number of fruits, number of fruit and fruit weight in both locations (Figure 1).

Table 1. Descriptive statistics of 239 beef-type genotypes for 26 agro-morphological traits

Location 1								Location 2						
Trait	**Mean**	**SE**	**SD**	**Min**	**Max**	**Skewness**	**Kurtosis**	**Mean**	**SE**	**SD**	**Min**	**Max**	**Skewness**	**Kurtosis**
L	35.77	0.08	1.3	32.71	39.99	0.35 *	3.2 ns	34.53	0.08	1.2	31.88	38.62	0.55 **	3.67 ns
a	32.94	0.12	1.82	26.97	37.92	-0.11 ns	3.42 ns	31.65	0.14	2.18	24.04	40.13	-0.08 ns	4.78 **
b	30.01	0.15	2.32	23.62	36.9	0.26 ns	2.94 ns	28.85	0.14	2.14	22.59	36.48	0.49 **	4.09 **
c	44.58	0.17	2.64	36.56	52.36	0.13 ns	3.37 ns	42.74	0.15	2.38	34.97	48.11	-0.42 **	3.56 ns
h	42.23	0.1	1.54	38.76	47.23	0.53 **	3.16 ns	42.3	0.13	2.04	38.01	50.3	0.64 **	3.71 *
NF	40.71	0.51	7.84	21.66	61.34	0.2 ns	2.77 ns	41.31	0.47	7.23	25.42	62.09	0.11 ns	2.53 ns
NFr	27.82	0.38	5.9	12.77	45.48	0.32 *	3.19 ns	32.75	0.37	5.79	19.89	49.44	0.27 ns	2.63 ns
FS	68.93	0.52	8.06	48.02	93.14	0.23 ns	3.03 ns	79.43	0.5	7.74	55.96	96.49	-0.45 **	3.19 ns
FL	57.2	0.23	3.6	48.2	66.05	0.16 ns	2.64 ns	63.24	0.27	4.13	53.16	77.79	0.29 ns	3.25 ns
FW	72.11	0.24	3.65	61.97	81.47	-0.11 ns	2.81 ns	79.03	0.31	4.85	64.94	91.77	-0.07 ns	3.08 ns
FL.FW	0.79	0.0033	0.05	0.67	0.97	0.48 **	3.53 ns	0.8	0.0033	0.05	0.66	0.94	0.19 ns	2.87 ns
NT	6.71	0.04	0.6	4.98	8.52	0.24 ns	3.28 ns	6.84	0.04	0.58	5.59	8.41	0.15 ns	2.47 *
F	27.79	0.16	2.43	21.41	33.26	-0.16 ns	2.52 ns	22.06	0.19	2.9	15.06	30.03	0.12 ns	2.69 ns
NL	4.63	0.06	0.99	2.62	7.63	0.48 **	2.83 ns	4.49	0.05	0.84	2.26	7.51	0.12 ns	3.52 ns
PT	6.3	0.05	0.76	4.46	8.31	0.06 ns	2.61 ns	9.41	0.06	0.87	4.9	11.98	-0.54 **	5.62 **
Fwe	186.39	1.52	23.47	125.48	252.48	0.12 ns	2.74 ns	220.31	1.85	28.67	150.59	296.29	0.34 *	2.91 ns
Y	5167.83	61.96	957.91	3108.76	7850.24	0.28 ns	2.78 ns	7133.84	72.39	1119.12	4483.75	9996.67	0.15 ns	2.7 ns
LL	40.28	0.22	3.34	34.14	50.36	0.51 **	2.91 ns	35.81	0.21	3.25	28.17	43.33	0.08 ns	2.51 ns
LW	46.84	0.31	4.72	35.14	57.64	0.22 ns	2.4 *	39.61	0.33	5.1	27.53	53.16	0.17 ns	2.77 ns
LA	7.46	0.11	1.77	1	9	-0.88 **	2.99 ns	6.89	0.09	1.37	3	9	-0.25 ns	2.94 ns
IMC	4.92	0.09	1.36	1	9	-0.25 ns	4.42 **	4.28	0.11	1.66	1	9	0.42 **	3.95 *
L1trs	27.67	0.32	4.89	18.11	43.39	0.43 **	3.03 ns	31.33	0.25	3.8	20.48	42.02	-0.01 ns	2.96 ns
L1.2	22.62	0.32	4.89	9.48	36.02	0.04 ns	2.94 ns	24.99	0.28	4.36	14.3	35.3	0.0033 ns	2.45 *
TH	165.6	0.96	14.88	133.68	203.32	0.42 **	2.69 ns	174.19	0.86	13.36	136.02	219.98	0.05 ns	3.92 *
FD	22.31	0.14	2.14	16.91	29.09	-0.1 ns	2.52 ns	33.26	0.14	2.16	28.55	40.55	0.65 **	3.85 *
MD	82.39	0.19	2.93	75.77	91.23	0.5 **	3.37 ns	100.54	0.28	4.28	94.59	113.41	0.91 **	3.62 ns

ns P > 0.05; * P <= 0.05; ** P <= 0.01 SE : Standard Error, SD : Standard deviation, Min : Minimum, Max : Maximum; L, a, b, c, h : Color values, NF : Number of Flower, NFr : Number of fruits, FS : Fruit set (%), FL : Fruit length, FW : Fruit width, FL.FW : Fruit length-to-width ratio, NT : Number of truss, F : Firmness, NL : Number of locule, PT : Pericarp thickness, Fwe : Fruit weight, Y : Yield, LL : Leaf length, LW : Leaf width, LA : Leaf attitude, IMC : Immature fruit color, L1trs : Stem length up to the first truss, L1.2 : Stem length between 1st and 2nd truss, TH : Total Height, FD : Days to the first flowering, MD : Days to the first maturity.

Table 2. Mean squares from the ANOVA made on the evaluated traits for 228 genotypes and 11 control varieties.

	Source	Df	a	b	c	F	FD	FL	FL.FW	FS	FW	Fwe	h	IMC
L1 (Treatment Adjusted)	Block (ignoring treatments)	1	0.34 ns	12.8 ns	0.16 ns	45.57 **	14.88 **	122.26 **	0.01 *	2814.97 **	35.14 ns	4008 *	15.25 *	0.14 ns
	Treatment (eliminating blocks)	238	3.17 ns	5.44 ns	6.88 ns	5.65 *	4.74 **	11.67 ns	0.0026 ns	60.45 **	13.73 ns	564.11 ns	2.39 ns	1.93 *
	Control	10	3.18 ns	7.53 ns	5.26 ns	3.42 ns	2 ns	15.3 ns	0.0034 ns	44.02 **	21.5 ns	706.31 ns	1.39 ns	3.71 **
	Test and Test vs. Control	228	3.17 ns	5.34 ns	6.95 *	5.75 *	4.86 **	11.51 ns	0.0026 ns	61.17 **	13.38 ns	557.87 ns	2.43 ns	1.85 *
	Residuals	10	2.48	6.28	2.71	1.58	0.78	7.33	0.0014	8.09	13.02	549.21	2.25	0.58
L1 (Block Adjusted)	Treatment (ignoring blocks)	238	3.16 ns	5.46 ns	6.86 ns	5.84 *	4.8 **	12.16 ns	0.0027 ns	72.18 **	13.87 ns	580.38 ns	2.45 ns	1.93 *
	Control	10	3.18 ns	7.53 ns	5.26 ns	3.42 ns	2 ns	15.3 ns	0.0034 ns	44.02 **	21.5 ns	706.31 ns	1.39 ns	3.71 **
	Test vs. Control	1	4.76 ns	10.15 ns	10.39 ns	8.96 *	63.31 **	7.8 ns	0.01 *	177.89 **	1.23 ns	367.9 ns	0.94 ns	6.84 **
	Test	227	3.15 ns	5.35 ns	6.92 ns	5.93 *	4.67 **	12.04 ns	0.0026 ns	72.96 **	13.59 ns	575.77 ns	2.5 ns	1.83 *
	Block (eliminating treatments)	1	3.78 ns	7.69 ns	4.61 ns	0.59 ns	0.18 ns	6.71 ns	0.00023 ns	22.77 ns	1.08 ns	135.01 ns	0.61 ns	0.18 ns
	Residuals	10	2.48	6.28	2.71	1.58	0.78	7.33	0.0014	8.09	13.02	549.21	2.25	0.58
L2 (Treatment Adjusted)	Block (ignoring treatments)	1	11.33 ns	37.78 *	74.42 *	528.09 **	8.84 *	2.4 ns	0.09 **	5.89 ns	562.71 **	19.49 ns	8.06 ns	10 **
	Treatment (eliminating blocks)	238	4.86 ns	4.71 ns	5.75 ns	8.55 ns	4.77 *	15.71 ns	0.0022 ns	55.59 ns	24.2 ns	831.82 **	4.3 ns	2.88 **
	Control	10	4.94 ns	5.11 ns	7.12 ns	10.73 ns	7.91 **	34.05 *	0.0038 ns	80.47 ns	36.04 ns	994.3 **	5.05 ns	5.24 **
	Test and Test vs. Control	228	4.86 ns	4.69 ns	5.69 ns	8.45 ns	4.63 *	14.91 ns	0.0022 ns	54.5 ns	23.69 ns	824.69 **	4.27 ns	2.77 **
	Residuals	10	6.36	6.77	10.7	4.03	1.35	7.6	0.0026	35.01	22.71	80.1	4.22	0.44
L2 (Block Adjusted)	Treatment (ignoring Blocks)	238	4.91 ns	4.86 ns	6.05 ns	10.49 *	4.79 *	15.55 ns	0.0026 ns	55.1 ns	26.48 ns	830.57 **	4.33 ns	2.91 **
	Control	10	4.94 ns	5.11 ns	7.12 ns	10.73 ns	7.91 **	34.05 *	0.0038 ns	80.47 ns	36.04 ns	994.3 **	5.05 ns	5.24 **
	Test vs. Control	1	0.39 ns	4.84 ns	2.8 ns	0.03 ns	3.13 ns	43.14 *	0.0015 ns	354.39 **	113.7 *	838.23 **	7.49 ns	4.32 *
	Test	227	4.93 ns	4.85 ns	6.02 ns	10.52 *	4.66 *	14.62 ns	0.0026 ns	52.66 ns	25.67 ns	823.32 **	4.29 ns	2.8 **
	Block (eliminating Treatments)	1	0.18 ns	2.45 ns	1.98 ns	66.16 **	4.55 ns	39.49 *	7.1e-05 ns	124.04 ns	22.35 ns	315.97 ns	0.75 ns	1.64 ns
	Residuals	10	6.36	6.77	10.7	4.03	1.35	7.6	0.0026	35.01	22.71	80.1	4.22	0.44

Table 2. Mean squares from the ANOVA made on the evaluated traits for 228 genotypes and 11 control varieties (continued).

	Source	Df	L	L1.2	L1trs	LA	LL	LW	MD	NF	NFr	NL	NT	PT	TH	Y
L1 (Treatment Adjusted)	Block (ignoring Treatments)	1	4.87 ns	53.82 ns	22.8 *	21.9 **	2.12 ns	0.84 ns	13 ns	522.73 **	1395.94 **	0.29 ns	1.59 **	0.05 ns	65.03 ns	20005273.6 **
	Treatment (eliminating Blocks)	238	1.7 ns	23.4 ns	23.23 **	3.01 **	11.52 ns	23.21 ns	8.76 ns	60.66 **	31.03 **	1.01 ns	0.35 ns	0.58 *	231.02 *	854123.15 ns
	Control	10	1.16 ns	25.98 ns	31.27 **	3.78 **	19.89 ns	48.03 ns	7.54 ns	85.14 **	30.17 **	1.83 ns	0.26 ns	0.33 ns	333.56 *	579008.68 ns
	Test and Test vs. Control	228	1.73 ns	23.29 ns	22.88 **	2.97 **	11.15 ns	22.12 ns	8.81 ns	59.59 **	31.07 **	0.97 ns	0.35 ns	0.6 **	226.52 *	866189.58 ns
	Residuals	10	1.16	16.89	2.68	0.73	8.36	16.21	5.34	7.7	2.93	0.69	0.16	0.15	72.7	685359.7
L1 (Block Adjusted)	Treatment (ignoring Blocks)	238	1.72 ns	23.6 ns	23.25 **	3.09 **	11.52 ns	23.2 ns	8.81 ns	62.85 **	36.89 **	1.01 ns	0.36 ns	0.59 *	231.23 *	938178.46 ns
	Control	10	1.16 ns	25.98 ns	31.27 **	3.78 **	19.89 ns	48.03 ns	7.54 ns	85.14 **	30.17 **	1.83 ns	0.26 ns	0.33 ns	333.56 *	579008.68 ns
	Test vs. Control	1	8.16 *	1.09 ns	95.34 **	8.77 **	0.07 ns	51.13 ns	15.41 ns	405.77 **	67.21 **	8.72 **	0.004 ns	1.47 *	1366.6 **	4871824.18 *
	Test	227	1.72 ns	23.6 ns	22.58 **	3.04 **	11.2 ns	21.99 ns	8.84 ns	60.36 **	37.05 **	0.93 ns	0.36 ns	0.59 *	221.72 *	936672.08 ns
	Block (eliminating Treatments)	1	0.03 ns	6.01 ns	17.28 *	0.73 ns	0.41 ns	2.91 ns	1.14 ns	2.56 ns	1.64 ns	0.34 ns	0.01 ns	0.0012 ns	14.73 ns	110.81 ns
	Residuals	10	1.16	16.89	2.68	0.73	8.36	16.21	5.34	7.7	2.93	0.69	0.16	0.15	72.7	685359.7
L2 (Treatment Adjusted)	Block (ignoring Treatments)	1	7.34 *	0.04 ns	0.13 ns	18.5 **	63.59 **	14.22 ns	52.9 *	224.06 *	200.41 **	12.21 **	3.36 **	3.96 ns	1557.5 **	7218137.88 **
	Treatment (eliminating Blocks)	238	1.45 ns	19.69 **	15.08 **	1.85 ns	11.07 **	27.21 ns	17.73 ns	53.05 ns	32.78 **	0.76 ns	0.31 *	0.79 ns	157.24 **	1271629.69 ns
	Control	10	2.19 ns	35.6 **	26.93 **	1.35 ns	20.3 **	52.99 *	16.55 ns	52.95 ns	52.37 **	2 **	0.46 **	1.64 ns	225.06 **	1606527.52 ns
	Test and Test vs. Control	228	1.41 ns	18.99 **	14.56 **	1.87 ns	10.66 **	26.08 ns	17.79 ns	53.05 ns	31.92 **	0.71 ns	0.3 *	0.75 ns	154.26 **	1256941.19 ns
	Residuals	10	1.1	2.85	2.84	1.2	2.68	16.34	8.18	23.13	7.29	0.37	0.09	0.82	8.41	685694.18
L2 (Block Adjusted)	Treatment (ignoring Blocks)	238	1.46 ns	19.68 **	15.08 **	1.93 ns	11.32 **	27.27 ns	17.77 ns	53.7 ns	33.6 **	0.81 ns	0.32 *	0.81 ns	163.21 **	1301918.85 ns
	Control	10	2.19 ns	35.6 **	26.93 **	1.35 ns	20.3 **	52.99 *	16.55 ns	52.95 ns	52.37 **	2 **	0.46 **	1.64 ns	225.06 **	1606527.52 ns
	Test vs. Control	1	4.37 ns	14.21 *	30.24 **	9.44 *	40.12 **	129.02 *	5.59 ns	178.02 *	21.58 ns	2.51 *	3.01 **	0.97 ns	51.77 *	4431593.2 *
	Test	227	1.42 ns	19 **	14.49 **	1.92 ns	10.8 **	25.69 ns	17.88 ns	53.19 ns	32.83 **	0.75 ns	0.31 *	0.77 ns	160.98 **	1274712.85 ns
	Block (eliminating Treatments)	1	3.38 ns	1.92 ns	0.01 ns	4.4e-31 ns	3.96 ns	0.56 ns	43.68 *	67.98 ns	4.25 ns	1.25 ns	0.13 ns	0.53 ns	135.01 **	9319.1 ns
	Residuals	10	1.1	2.85	2.84	1.2	2.68	16.34	8.18	23.13	7.29	0.37	0.09	0.82	8.41	685694.18

ns P > 0.05; * P <= 0.05; ** P <= 0.01, L1 : Location 1, L2 : Location 2, L, a, b, c, h : Color values, NF : Number of Flower, NFr : Number of fruit, FS : Fruit set (%), FL : Fruit length, FW = Fruit width, FL.FW : Fruit length-to-width ratio, NT : Number of trusses, F : Firmness, NL : Number of locule, PT : Pericarp thickness, Fwe : Fruit weight, Y : Yield, LL : Leaf length, LW : Leaf width, LA : Leaf attitude, IMC : Immature fruit color, L1trs : Stem length up to the first truss, L1.2 : Stem length between 1st and 2nd trusses, TH : Total Height, FD : Days to the first flowering, MD : Days to the first maturity.

Table 3. Genetic variability estimates from the ANOVA results.

	Location 1								Location 2							
Trait	**PV**	**GV**	**EV**	**GCV**	**PCV**	**ECV**	**HBS**	**Category**	**PV**	**GV**	**EV**	**GCV**	**PCV**	**ECV**	**HBS**	**Category**
L	1.72	0.56	1.16	2.09	3.67	3.01	32.57	Medium	1.42	0.32	1.1	1.64	3.45	3.03	22.7	Low
a	3.15	0.67	2.48	2.49	5.39	4.78	21.42	Low	4.93	-	6.36	-	7.01	7.97	-	-
b	5.35	-	6.28	-	7.7	8.35	-	-	4.85	-	6.77	-	7.63	9.02	-	-
c	6.92	4.2	2.71	4.6	5.9	3.69	60.8	High	6.02	-	10.7	-	5.74	7.65	-	-
h	2.5	0.25	2.25	1.19	3.74	3.55	10.05	Low	4.29	0.06	4.22	0.6	4.89	4.86	1.51	Low
NF	60.36	52.66	7.7	17.82	19.08	6.82	87.24	High	53.19	30.05	23.13	13.27	17.65	11.64	56.5	Medium
NFr	37.05	34.12	2.93	21	21.88	6.15	92.09	High	32.83	25.53	7.29	15.43	17.49	8.24	77.79	High
FS	72.96	64.86	8.09	11.68	12.39	4.13	88.91	High	52.66	17.65	35.01	5.29	9.14	7.45	33.51	Medium
FL	12.04	4.7	7.33	3.79	6.07	4.73	39.08	Medium	14.62	7.02	7.6	4.19	6.05	4.36	48	Medium
FW	13.59	0.56	13.02	1.04	5.11	5	4.15	Low	25.67	2.96	22.71	2.18	6.41	6.03	11.52	Low
FL.FW	0.0026	0.0012	0.0014	4.42	6.45	4.7	46.92	Medium	0.0026	-	0.0026	-	6.34	6.38	-	
NT	0.36	0.21	0.16	6.8	8.98	5.87	57.31	Medium	0.31	0.21	0.09	6.74	8.08	4.46	69.57	High
F	5.93	4.35	1.58	7.5	8.76	4.53	73.33	High	10.52	6.49	4.03	11.55	14.7	9.1	61.67	High
NL	0.93	0.25	0.69	10.73	20.87	17.9	26.45	Low	0.75	0.37	0.37	13.62	19.23	13.57	50.2	Medium
PT	0.59	0.44	0.15	10.56	12.22	6.15	74.7	High	0.77	-	0.82	-	9.31	9.64	-	
Fwe	575.77	26.56	549.21	2.76	12.87	12.57	4.61	Low	823.32	743.22	80.1	12.37	13.02	4.06	90.27	High
Y	936672.08	251312.38	685359.7	9.7	18.73	16.02	26.83	Low	1274712.85	589018.67	685694.18	10.76	15.83	11.61	46.21	Medium
LL	11.2	2.85	8.36	4.19	8.31	7.18	25.4	Low	10.8	8.11	2.68	7.96	9.18	4.57	75.16	High
LW	21.99	5.78	16.21	5.13	10.01	8.6	26.28	Low	25.69	9.35	16.34	7.72	12.8	10.21	36.38	Medium
LA	3.04	2.31	0.73	20.38	23.37	11.43	76.07	High	1.92	0.72	1.2	12.3	20.1	15.9	37.45	Medium
IMC	1.83	1.25	0.58	22.7	27.49	15.5	68.2	High	2.8	2.37	0.44	35.9	39.07	15.42	84.43	High
L1trs	22.58	19.9	2.68	16.12	17.17	5.92	88.11	High	14.49	11.66	2.84	10.9	12.15	5.38	80.43	High
L1.2	23.6	6.71	16.89	11.45	21.48	18.17	28.43	Low	19	16.16	2.85	16.08	17.44	6.75	85.02	High
TH	221.72	149.02	72.7	7.37	8.99	5.15	67.21	High	160.98	152.57	8.41	7.09	7.28	1.66	94.77	High
FD	4.67	3.89	0.78	8.84	9.69	3.96	83.25	High	4.66	3.31	1.35	5.47	6.49	3.49	71.13	High
MD	8.84	3.5	5.34	2.27	3.61	2.8	39.61	Medium	17.88	9.7	8.18	3.1	4.21	2.84	54.24	Medium

PV : Phenotypic Variance, GV : Genotypic Variance, EV : Environmental Variance, PCV : Phenotypic coefficient of variation, GCV : Genotypic coefficient of variation, ECV : Environmental coefficient of variation, HBS : Broad-sense Heritability, L1 : Location 1, L2 : Location 2, L, a, b, c, h : Color values, NF : Number of Flowers, NFr : Number of fruits, FS : Fruit set (%), FL : Fruit length, FW = Fruit width, FL.FW : Fruit length-to-width ratio, NT : Number of trusses, F : Firmness, NL : Number of locules, PT : Pericarp thickness, Fwe : Fruit weight, Y : Yield, LL : Leaf length, LW : Leaf width, LA : Leaf attitude, IMC : Immature fruit color, L1trs : Stem length up to the first truss, L1.2 : Stem length between 1st and 2nd trusses, TH : Total Height, FD : Days to the first flowering, MD : Days to the first maturity.

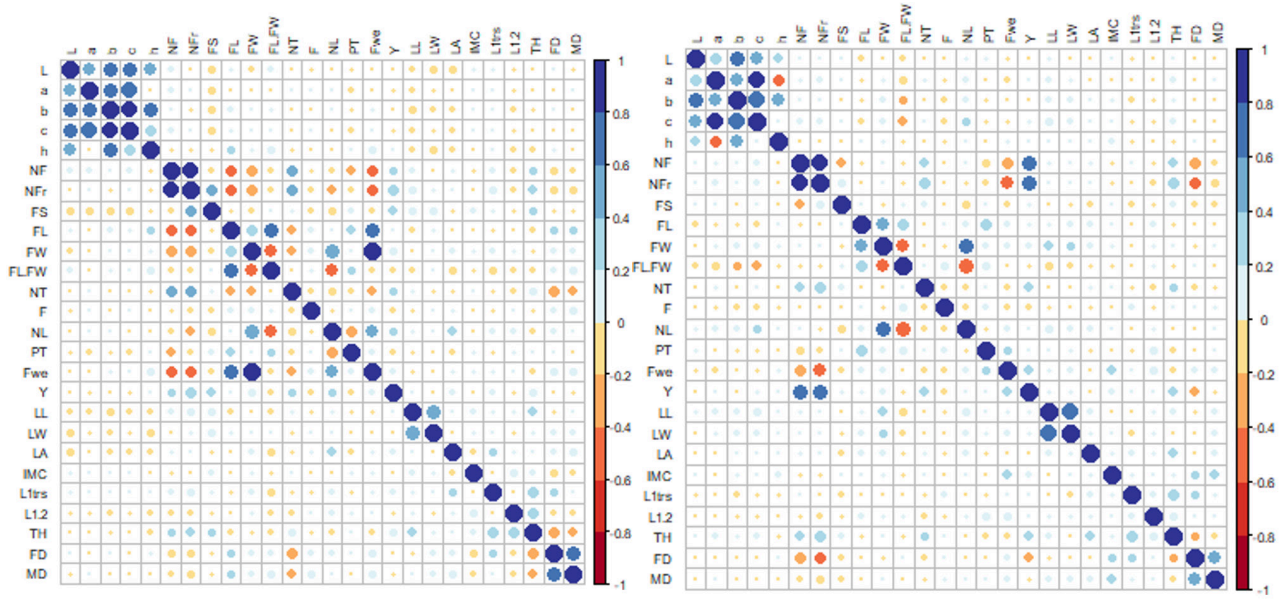


Figure 1. Correlation matrix for the traits in Location 1 (left) and Location 2 (right).

The first five principal components (PCs) accounted for 54.2343% of total variation for Location 1 and 48.1802% of total variation for Location 2 (Table 4). The first two components PC1 (15.5936%) and PC2 (13.7491%) for Location 1, and PC1 (13.7779%) and PC2 (11.8345%) for Location 2 made contribution to higher variation and they were used for biplots. Principal component analysis (PCA) indicated that PC1 for Location 1 accounted for 15.59 (%) of total variation by showing positive correlation with number of flowers, number of fruits, ratio of fruit set, number of trusses, yield, leaf length, leaf width, and total height; whereas, PC1 in Location 2 accounted for 13.7779 (%) of total variation and showed a positive correlation with fruit length, firmness, pericarp thickness, fruit weight, number of days to the first flowering and number of days to the first maturity. PC2 in Location 1 accounted for 13.7491 (%) of total variation by having positive correlation with number of flower, number of fruit, fruit length-to-width ratio, number of trusses, firmness, and total height; whereas, PC2 in Location 2 accounted for 11.8345 (%) of total variation and correlated positively with fruit length, fruit width, firmness, number of locule, pericarp thickness, fruit weight, leaf length, leaf width, leaf attitude, immature fruit color, stem length between 1st and 2nd truss, total height, days to the first flowering, and days to the first maturity. Biplots belonging to the both locations showed variability of genotypes studied for 26 agro-morphologic traits (Figure 2). Genotypes were scattered in four groups according to x and y axis. The genotypes present in positive axis were mostly correlated with pericarp thickness, number of locule, fruit width, fruit weight, days to the first flowering and maturity for Location 1 and with number of trusses, number of flowers and fruits, yield and total height for Location 2. The genotypes present in negative axis were correlated with these traits, negatively.

Table 4. Eigenvalue, variance (%), and cumulative variance (%) of the first five principal components

	Location 1					Location 2				
Traits	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
L	0.4342	-0.3227	0.4889	-0.1317	0.0503	0.1610	-0.7778	0.0844	-0.0431	0.1225
a	0.5724	-0.2877	0.3329	0.0543	0.3975	0.1302	-0.7041	0.2469	0.0461	-0.0497
b	0.5916	-0.4872	0.4167	-0.1783	-0.0064	0.3259	-0.8610	0.1809	-0.0092	0.1733
c	0.6972	-0.4202	0.4021	-0.0349	0.2079	0.2265	-0.8299	0.2112	0.0177	0.0780
h	0.0949	-0.2275	0.1004	-0.2447	-0.3512	0.3258	-0.5143	-0.0014	-0.0595	0.2658
NF	0.6205	0.5136	-0.2063	0.1492	-0.0465	-0.6507	-0.3056	0.2033	0.3280	-0.0516
NFr	0.6599	0.6368	-0.1296	0.0063	0.0199	-0.7834	-0.1587	0.1608	0.2543	0.2693
FS	0.0085	0.1794	0.1741	-0.2920	0.0859	-0.3464	0.2103	-0.0585	-0.0542	0.5480
FL	-0.1289	-0.0812	-0.4589	-0.4772	0.2016	0.6589	0.0607	-0.2789	-0.0899	0.4346
FW	0.2847	-0.4317	-0.6213	-0.0918	-0.2453	0.6282	0.3244	0.5683	-0.1496	0.0989
FL.FW	-0.4308	0.3878	0.1801	-0.3385	0.4743	0.1280	-0.1995	-0.7703	0.0505	0.3227
NT	0.28477	0.3803	-0.0440	-0.0394	0.0726	-0.5797	-0.1730	0.0202	-0.0328	-0.0010
F	-0.2050	0.1088	0.0820	0.0389	0.2214	0.2308	0.0621	-0.1580	0.0992	-0.1017
NL	0.3255	-0.5015	-0.4287	0.1176	-0.3842	0.3634	0.2299	0.7107	0.0859	-0.1640
PT	-0.2031	-0.1021	-0.1748	-0.5097	0.3200	0.1402	0.1294	-0.4211	-0.3612	0.2271
Fwe	-0.2591	-0.3917	-0.3426	-0.0879	0.0112	0.7400	0.2538	0.3436	-0.1453	0.2341
Y	0.4850	0.3899	-0.4034	-0.0451	0.0307	-0.1896	0.0879	0.3953	0.1342	0.3969
LL	0.3078	-0.3265	-0.3556	-0.1434	0.3613	-0.2677	0.2595	0.1594	0.0991	0.4104
LW	0.1981	-0.3112	-0.3687	-0.2381	0.3505	-0.0665	0.2821	-0.0073	0.2326	0.4769
LA	0.1244	-0.0706	-0.2878	0.2526	0.1543	0.0429	0.2685	0.2898	0.3745	-0.1368
IMC	-0.0272	-0.2084	-0.1217	0.2793	0.0823	-0.0456	0.0301	0.1260	-0.4387	0.1984
L1trs	-0.0558	0.0313	-0.1175	0.5602	0.2827	-0.0679	0.0126	0.3939	0.2421	0.3058
L1.2	-0.0724	-0.1188	-0.2698	0.0154	0.2983	-0.0126	0.1893	0.1613	-0.4674	-0.0757
TH	0.4217	0.2956	-0.1613	0.3127	0.3197	-0.4319	0.0596	0.2812	-0.3646	0.3695
FD	-0.3988	-0.4293	0.1312	0.4159	0.1777	0.4449	0.1131	-0.1235	0.6372	0.1335
MD	-0.2200	-0.3412	-0.0806	0.3903	0.2888	0.3881	0.1386	-0.2018	0.6335	0.0839
Eigen Value	4.0543	3.5747	2.6344	2.0186	1.8187	3.5822	3.0769	2.4140	1.8146	1.6388
Variance (%)	15.5936	13.7491	10.1325	7.7638	6.9951	13.7779	11.8345	9.2847	6.9795	6.3033
Cumulative Variance (%)	15.5936	29.3427	39.4753	47.2392	54.2343	13.7779	25.6125	34.8973	41.8768	48.1802

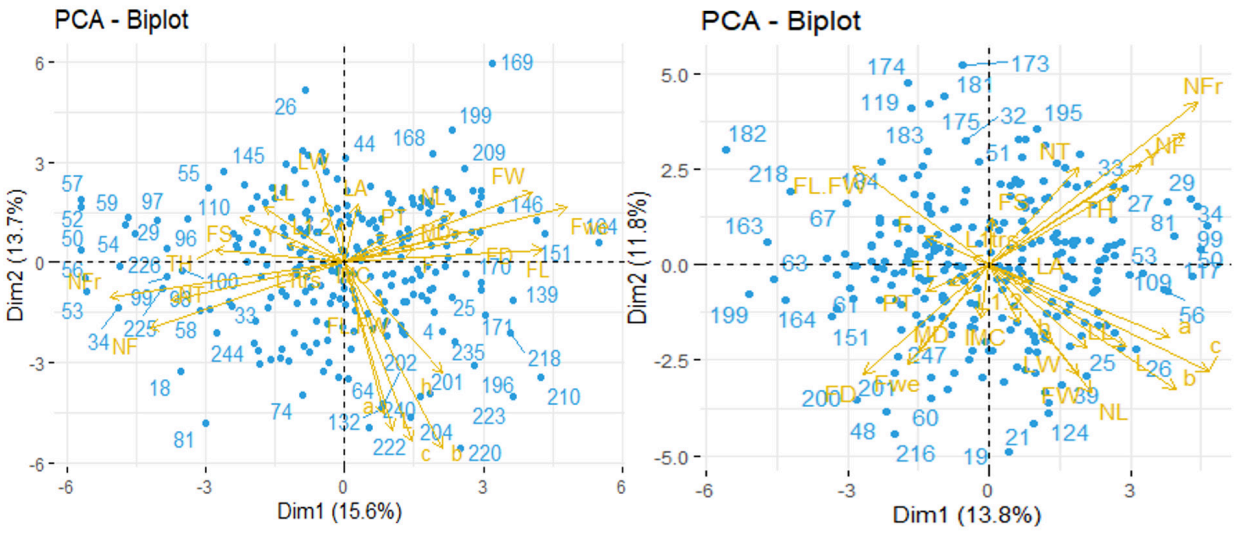
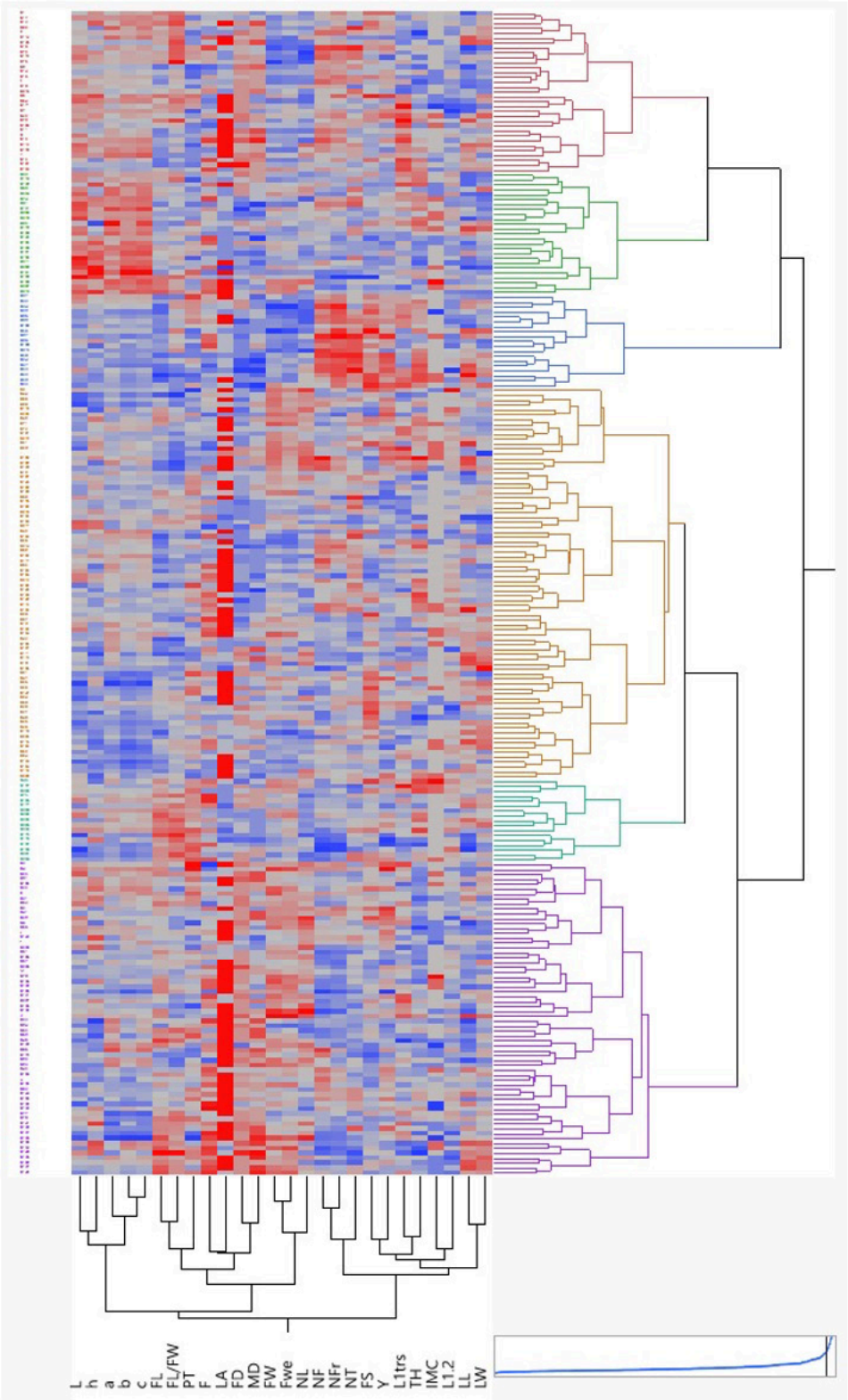


Figure 2. Biplots showing the correlation of 26 agro-morphological traits with 239 genotypes for Location 1 (left) and Location 2 (right).

The cluster analysis grouped the 239 genotypes into six cluster groups for Location 1 (Figure 3) and seven cluster groups in Location 2 (Figure 4). The number of genotypes was the highest in Cluster 4 (80), followed by Cluster 6 (64), Cluster 1 (33), Cluster 2 (25), Cluster 3 (19) and Cluster 5 (18) for Location 1 as shown in Figure 3 and Table 5. Genotypes belonging to Cluster 2 had higher color values (L*, a*, b*, c*, h*) in other word they are highly light and saturated, and lesser in ratio of fruit set, yield, leaf length and leaf width for Location 1. The genotypes were agglomerated mostly into Cluster 6 (60) and Cluster 3 (50), followed by Cluster 1 (38), Cluster 7 (31), Cluster 2 (29), Cluster 4 (20) and Cluster 5 (11) for Location 2. Cluster 5 for Location 2 was characterized by high lightness and saturation, high firmness, high pericarp thickness, moderate yielding, high stem length between 1st and 2nd trusses and low total height and late flowering and maturity. Cluster 1 for Location 2 was characterized by more flowers, moderate fruit set, the lowest fruit length, the widest fruit, low firmness, high yielding, mostly drooping leaf attitude, the tallest plant height, and moderately early mature (Table 6).



L, a, b, c, h : Color values, NF : Number of Flowers, NFr : Number of fruits, FS : Fruit set (%), FL : Fruit length, FW = Fruit width, FL.FW : Fruit length-to-width ratio, NT : Number of trusses, F : Firmness, NL : Number of locules, PT : Pericarp thickness, Fwe : Fruit weight, Y : Yield, LL : Leaf length, LW : Leaf width, LA : Leaf attitude, IMC : Immature fruit color, L1trs : Stem length up to the first truss, L1.2 : Stem length between 1st and 2nd truss, TH : Total Height, FD : Days to the first flowering, MD : Days to the first maturity.

Figure 3. Two-way hierarchical clustering analysis for Location 1.

Table 5. Mean values of agro-morphological traits in different clusters of genotypes of beef tomato type in Location 1.

Cluster	1	2	3	4	5	6
L	36.5	37.7	35.3	35.3	35.4	35.5
a	33.7	35.4	32.0	32.5	32.7	32.6
b	31.3	34.2	28.5	29.0	29.5	29.7
c	46.1	49.3	42.9	43.6	44.1	44.2
h	42.8	43.9	41.6	41.7	41.9	42.3
NF	46.2	39.2	50.9	40.5	33.1	38.1
NFr	32.2	24.5	39.8	27.7	23.2	25.1
FS	70.3	62.6	79.0	69.4	70.5	66.6
FL	57.3	57.5	53.1	55.6	61.2	59.4
FW	68.9	71.9	68.3	72.6	71.7	74.7
FL/FW	0.8	0.8	0.8	0.8	0.9	0.8
NT	6.8	6.6	7.4	6.7	6.6	6.5
F	27.3	28.0	27.2	27.3	28.5	28.5
NL	4.1	4.5	4.0	4.8	4.0	5.3
PT	5.9	6.1	6.2	6.3	7.2	6.5
Fwe	171.7	185.8	157.1	183.8	195.0	205.0
Y	5304.0	4716.5	6118.4	4926.7	4791.2	5314.2
LL	39.9	38.6	42.0	41.0	39.8	39.8
LW	47.4	44.0	47.5	47.1	47.6	47.0
LA	7.6	6.2	7.0	7.7	5.2	8.4
IMC	4.5	5.2	5.1	5.2	5.6	4.4
L1trs	29.8	27.9	29.2	26.7	26.9	27.3
L1.2	20.3	22.9	19.3	25.2	26.3	21.6
TH	162.5	169.1	180.3	167.4	174.4	157.7
FD	23.9	21.3	20.0	21.3	21.9	24.0
MD	84.1	80.9	79.6	81.5	81.4	84.3
Count	33.0	25.0	19.0	80.0	18.0	64.0

L, a, b, c, h : Color values, NF : Number of Flower, NFr : Number of fruit, FS : Fruits set (%), FL : Fruit length, FW = Fruit width, FL.FW : Fruit length-to-width ratio, NT : Number of truss, F : Firmness, NL : Number of locule, PT : Pericarp thickness, Fwe : Fruit weight, Y : Yield, LL : Leaf length, LW : Leaf width, LA : Leaf attitude, IMC : Immature fruit color, L1trs : Stem length up to the first truss, L1.2 : Stem length between 1st and 2nd trusses, TH : Total Height, FD : Days to the first flowering, MD : Days to the first maturity.

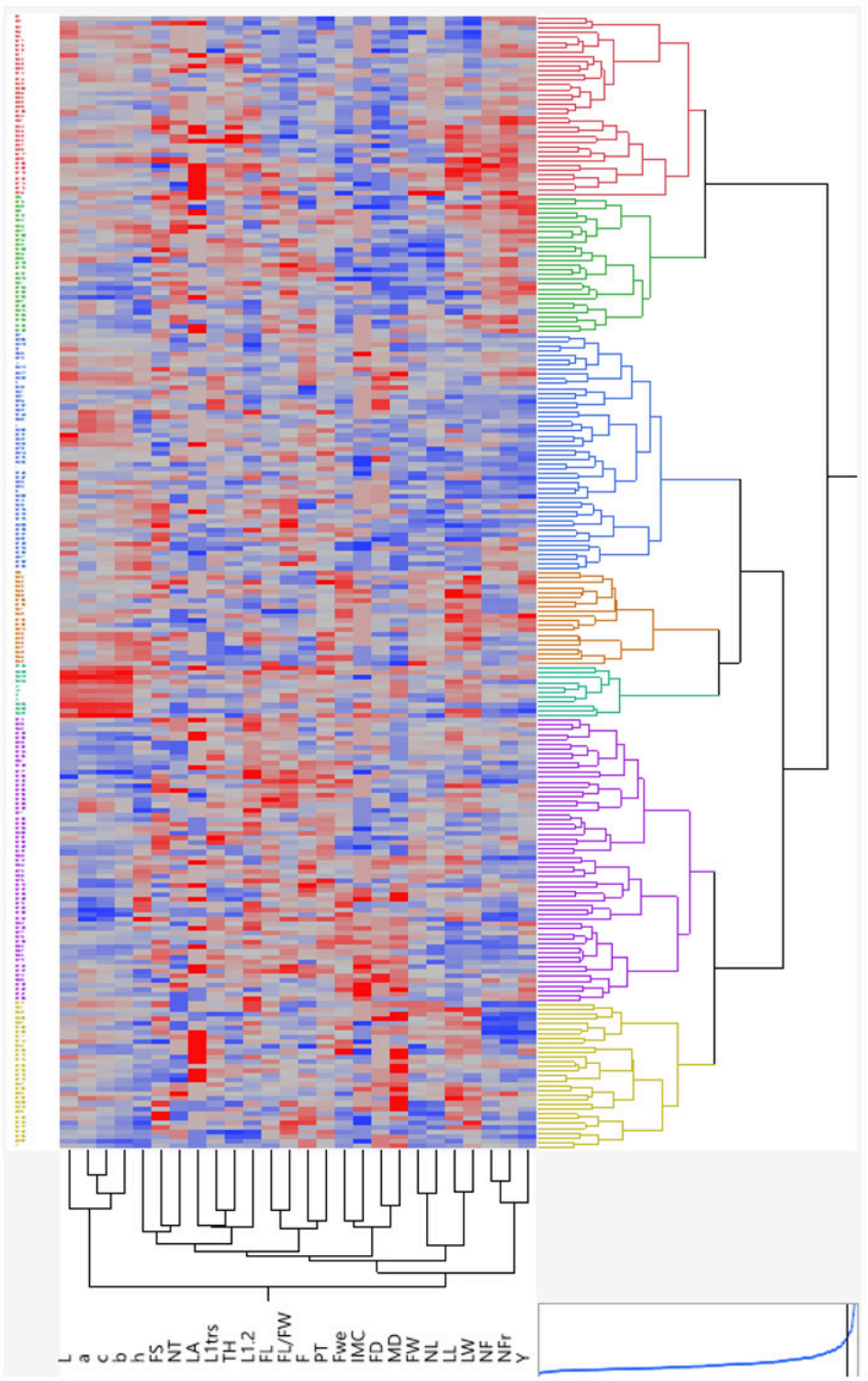


Figure 4. Two-way hierarchical clustering analysis for Location 2.

Table 6. Mean values of agro-morphological traits in different clusters of genotypes of beef tomato type in Location 2

Cluster	1	2	3	4	5	6	7
L	35.0	34.3	35.3	34.9	36.9	33.6	34.3
a	32.2	31.3	32.2	32.2	37.2	30.3	32.1
b	29.5	27.9	29.9	30.6	35.1	27.5	27.7
c	43.7	42.0	44.0	44.5	51.2	41.0	42.4
h	42.4	41.7	42.8	43.4	43.3	42.2	40.8
NF	48.9	47.3	39.5	39.0	39.6	38.6	36.5
NFr	38.2	38.7	31.2	31.3	31.3	30.2	28.6
FS	78.6	82.0	79.4	80.8	78.9	79.0	79.1
FL	61.1	64.1	61.7	62.2	63.1	65.2	61.9
FW	81.4	77.3	76.0	83.2	77.5	80.2	77.9
FL/FW	0.8	0.8	0.8	0.7	0.8	0.8	0.8
NT	7.1	7.2	6.7	6.7	6.6	6.8	6.7
F	20.5	22.5	22.6	20.3	23.6	23.3	22.2
NL	5.2	3.9	4.1	5.1	4.0	4.4	4.7
PT	8.5	9.4	9.3	9.8	10.0	9.7	9.3
Fwe	203.1	208.4	210.9	252.5	214.7	234.5	218.6
Y	7696.3	8044.7	6554.3	7914.6	6713.5	7033.1	6176.4
LL	36.8	35.4	33.6	38.4	37.3	35.0	37.2
LW	39.0	39.9	36.4	45.0	42.3	38.4	42.2
LA	7.6	7.0	6.3	6.3	6.4	6.8	7.1
IMC	3.9	4.0	4.0	4.7	4.6	4.9	3.6
L1trs	31.4	31.0	31.5	29.4	30.5	32.9	30.7
L1.2	25.0	23.0	23.3	24.1	26.5	27.4	24.1
TH	184.8	179.4	171.5	168.8	166.1	174.2	166.1
FD	31.8	31.2	34.0	32.7	33.8	33.9	34.7
MD	99.0	98.0	99.4	99.0	102.6	101.3	105.7
Count	38.0	29.0	50.0	20.0	11.0	60.0	31.0

L, a, b, c, h : Color values, NF : Number of Flowers, NFr : Number of fruits, FS : Fruit set (%), FL : Fruit length, FW = Fruit width, FL.FW : Fruit length-to-width ratio, NT : Number of trusses, F : Firmness, NL : Number of locules, PT : Pericarp thickness, Fwe : Fruit weight, Y : Yield, LL : Leaf length, LW : Leaf width, LA : Leaf attitude, IMC : Immature fruit color, L1trs : Stem length up to the first truss, L1.2 : Stem length between 1st and 2nd trusses, TH : Total Height, FD : Days to the first flowering, MD : Days to the first maturity.

DISCUSSION

The desired genotypes should be compact, open plant, early, firm, and fast ripening, have a low light tolerance, a good fruit quality, deep red color, and a long shelf-life and fruit weight should be at least around 200-220 grams. The analysis of agro-morphological traits enables to describe the variability between different genotypes (Figas et al., 2015). The results of descriptive statistics showed that there was an important level of diversity among genotypes evaluated. Variability was high especially for number of flowers, ratio of fruit set, fruit weight, yield and height in both locations. Even though number of flowers was similar in both locations, the ratio of fruit set was higher in Location 2, so yield was higher in this location compared to Location 1. The lower yield in Location 1 may be associated with the fact that there were water and/or nutrient deficiencies such as phosphorus, zinc and boron during fruit set as also revealed by Wang et al., (2017). As well as the fruit set in the upper trusses was less in both locations; this was probably

because of high daily mean temperature (Sato et al., 2006). Optimum temperature for fruit set is between 20-24 °C, (Charles and Harris, 1972; De Koning, 1994), a temperature higher than 35 °C was observed in both locations. The highest number of fruits was found in G34 genotype for both locations and this genotype had the lowest fruit weight in both locations. Genotypes like G34 may be more stable for yield across two regions of Antalya. Transplantation of tomato seedlings was done one month earlier in Location 2 than Location 1. As climatic conditions were better during the time of transplantation in Location 1 than Location 2, number of days to the first flowering and maturity occurred in a shorter time in Location 1 even though transplantation was done almost a month ago in Location 2. The colder climatic condition below 10 °C in Location 2 may affect also fruit set (Picken, 1984) and cause slightly damages like catface on a few fruits belonging to trusses in the middle part of the plants and these fruits remain smaller. Although the cold affected fruit set in Location 2 at a particular time, it had still a higher ratio of fruit set in this location than Location 1. The use of augmented randomized complete block design (ARCBD) in this study enabled to make comparisons between newly tested genotypes and control varieties. The result of ANOVA showed the genotypic variability and a high level of heritability for many traits for both locations (Table 2) indicated that this diversity could be maintained in different environmental conditions. This is useful in the selection of the well-adapted and best performing genotypes. However, the broad-sense heritability for yield for each location was not high because of environmental effect. Avdikos et al., (2011) and El-Gabry et al., (2014) also reported the same result showing that yield was influenced more by environment as it is a very complex trait and therefore it did not have a high heritability. Combinations of high temperature with other factors like high humidity due to climate change can also affect the fruit set (Hanson et al., 2002) and increase the need of irrigation and clearly affects the yield changes. While fruit weight showed a high heritability in Location 2, it showed a low heritability in Location 1. This indicated that Location 2 had more stable greenhouse conditions in terms of fruit weight, and this may be due to differences in application of fertilizer and excessive application of fertilizer in case of sufficient nutrients and due to the fact that it caused the reduction in production as also indicated by Sainju et al., (2003). A low level of heritability was found for fruit width and hue value in both locations, thus demonstrating that these traits were not useful for the selection. Ortiz and Izquierdo (1994) also found stability changes in different traits. The small changes in agronomic practices may also differ the estimation of environmental effect. Principal component analysis (PCA) demonstrated that PC1 and PC2 accounted for around 15.6% and 13.7% of total variation and 13.8% and 11.8% of total variation in Locations 1 and 2, respectively. According to the PCA, the variability for Location 1 was obtained by number of flowers, number of fruits, yield and total height; and fruit length, fruit width, number of locule, fruit weight accounted for the variability in Location 2. Number of fruits, and b* and c* values made the highest contribution to help the variation for both locations. The first five principal components for all traits accounted for 54.23% and 48.18% of total variation. This result was lower in comparison with similar studies (Cortés-Olmos et al., 2015; Renna et al., 2019). Cortés-Olmos et al., (2015) found that the first two principal components accounted for 71% of the total variation in the characterization of 166 traditional tomato varieties and Renna et al., (2019) also determined that the first three principal components accounted for 79% of the total variation in the evaluation of three local tomato varieties. As all the tomato genotypes were the same variety, namely beef and specific to spring growing season and market, variability shown by multivariate principal component analysis was lower in contrast to the other studies done with core collections, landraces, or local varieties probably due to locations used, different genotypes, and number of genotypes. Cluster analysis revealed that all studied traits enabled to divide clusters into groups and traits' mean values in different clusters showed what genotypes became prominent with which traits. Yield has always been considered as an important trait and one of the main interests for growers and breeders, too. Two main traits determining average yield per plant are number of fruits and fruit weight which were grouped in Cluster 3 and Cluster 6 as a superior trait for these clusters for Location 1, respectively. As yield is one of the important selection criteria, common genotypes present in these clusters for both locations would probably be the potential genotypes for further evaluations. Fruit size and fruit quality traits were the more effective discrimination criteria as they affect the marketability of variety.

CONCLUSION

The present study showed that commonly used conventional agro-morphological descriptors provided detailed information of the tomato hybrid type "Beef" in two locations. This feature of the descriptors proved their importance for the characterization and evaluation of diversity. Even though there was no clear separation for some of the traits between the genotypes, some of the agronomically important traits like number of fruits, fruit weight, yield and fruit quality provided variability between genotypes. Phenotypic and statistical evaluation of genotypes revealed that some of the genotypes showing high adaptability demonstrated acceptable performances in terms of yield and fruit quality in both locations. The selected genotypes could be evaluated in multi-environmental conditions to figure out whether they are a good candidate to be released as a new variety. The two main concerns of today are climate change and population increase. Tomato (*Solanum lycopersicum*) is one of the most consumed vegetable crops in the world; therefore, grower needs high-yielding varieties with a good adaptation to different environmental

conditions for the compensation of global market needs. The present study also provided an estimation to plan for future breeding strategies by showing the positive and negative sides of developed hybrids, and gave opportunity to make better combinations of parents.

Compliance with Ethical Standards

Peer-review

Externally peer-reviewed.

Conflict of interest

The authors declare that they have no competing, actual, potential or perceived conflict of interest.

Author contribution

This article is derived from Ali ÜNAL's Master thesis. All the authors read and approved the final manuscript. All the authors verify that the text, figures, and tables are original and that they have not been published before.

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