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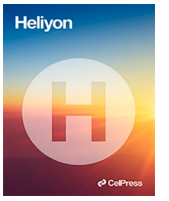

Exploring genotypic variability and interrelationships among growth, yield, and quality characteristics in diverse tomato genotypes

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ABSTRACT

Tomato is the most consumed vegetable crop worldwide, with excellent beneficial health properties and high content of vitamins, minerals, carotenoids, total antioxidants, and phenolic compounds. Hence, improving its genotypes is crucial to sustain its production and ensure food security, principally under the fast-growing worldwide population and abrupt global climate change. The present study aimed to explore the genotypic variability associated with specific characteristics in twenty-five diverse tomato genotypes. In addition, the relationships between growth, yield, and quality traits using both univariate (correlation coefficient, path analysis) and multivariate (principal component, principal coordinates, canonical variate) analysis methods were explored. The results indicated that the evaluated genotypes possessed highly significant variation. This is appropriate for future hybridization through tomato breeding programs. All evaluated genotypes demonstrated considerable potential to develop strong hybrid vigour for growth, yield, and quality characteristics. In particular, the genotypes LS009, LS011, and LS014 could be considered promising, high-yielding, and resistant to yellow leaf curl virus infestation (YLCV) disease parents for future breeding schemes. The number of fruits per plant, fruit diameter, and fruit weight proved strong positive relationships with fruit yield. Accordingly, these characteristics demonstrate their importance in improving fruit yield and could be exploited as indirect criteria for selecting high-yielding tomato genotypes through breeding programs.

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1. Introduction

Tomato (*Solanum lycopersicum*) is an essential commercial and dietary vegetable crop with powerfully nutritious and various uses [1]. It is a reliable source of vitamins C and A, fiber, carotenoids potassium, total antioxidants, and phenolic compounds [2]. Consumption of tomato diminishes triglyceride, and cholesterol levels in blood cells, which reduce the cardiovascular risk of breast cancer and risk associated with type 2 diabetes, as well as vigorously protect against neurodegenerative diseases [3,4]. The genetic variation of cultivated tomato presents a small percentage of the wild relatives [5–7]. Over the last centuries, plant breeders have developed various tomato cultivars through domestication and breeding, releasing modern tomato varieties and hybrids of different shapes, colors, and sizes [7,8].

Developing new and improved tomato genotypes is more vital than ever to maintaining tomato production and ensuring global food security, especially as the global population grows rapidly and the climate changes abruptly. The lack of genetic diversity and the unavailability of high-yielding cultivars are the main reasons for low yield [9–12]. Accordingly, assessing genetic variability is essential for developing new genotypes with the desired combination of traits [13–15]. Exploring genetic diversity becomes decisive before planning an appropriate breeding strategy for genetic improvement [16,17]. Assessment of genetic variability enables breeders to select superior germplasm, develop cultivars with desired trait combinations, and improve crop performance under various environmental conditions. Furthermore, studies of genetic variability can help breeders identify and exploit the existing variation within the gene pool, accelerating the selection of tomato genotypes with improved yield, disease resistance, and adaptability to climate change [18–20]. Hence, evaluating available germplasm is imperative to increasing genetic diversity to develop high-yielding tomato cultivars [21–23]. Statistic parameters such as genotypic (GCV) and phenotypic (PCV) coefficients of variation are valuable tools for detecting the variability in the available genotypes. Moreover, GCV, PCV, heritability, and genetic gain are needed to partition the genotypic variability into non-heritable and heritable components [24,25]. Thus, they allow for determining the environmental and genotypic effects and the extent to which improvement is feasible after selection [26,27].

Tomato yellow leaf curl virus (TYLCV), is one of the most destructive diseases worldwide [28]. It is transmitted by the whitefly and its infection results in chlorosis, cupping of leaves, flower abscission, and prominent stunting of the growing point. Depending on the timing of the infection yield losses can reach 100% [29]. Therefore it is considered a limiting factor in tomato production in both open fields and protected cultivation systems. Accordingly, identifying resistant genotypes to TYLCV is valuable to be exploited in breeding programs to develop newly developed high-yielding and resistant genotypes. To obtain helpful information, it is required to understand the association among the studied traits [30–32]. As yield is the ultimate goal of breeders, it is required to understand the indirect and direct effects of both genotypic and phenotypic variations of associated characters on yield performance [33]. The extent of the associations of these characters can be measured by Pearson correlation, which would help breeders to develop an efficient breeding scheme based on relevant traits to ameliorate yield production [34]. Nevertheless, to understand the specific influence of the studied characters on yield performance, it is essential to use path analysis, which enables the breakdown of correlation coefficients into indirect and direct effects of numerous traits on yield characters [35]. Furthermore, it would also be possible to choose desirable parents for establishing a new breeding population and gather in-depth knowledge on genetic diversity that could enormously assist in maintaining selection gain in the long run [36]. Therefore, the pinpoint of the present study was to explore the genetic divergence in different tomato genotypes, identify potential parental genotypes for hybridization in future breeding programs, and study the association among growth, yield, and quality characteristics.

2. Materials and methods

2.1. Experimental site and plant materials

This study was performed at the Horticulture Research Centre (HRC) of Bangladesh, Gazipur, Bangladesh (23°74′N, 90°35′E). The experimental site soil was shallow red-brown terrace soil, the chemical and physical soil properties are exhibited in Table S1. Twenty-five tomato accessions were selected from the Plant Genetic Research Centre (PGRC) and Horticulture Research Centre (HRC), belonging to the Bangladesh Agricultural Research Institute (Table S2). This set of accessions was selected to represent the overall genetic variation of the tomato cultivars in Bangladesh. Seeds of these accessions were sown in the seedbed and afterward treated by Bavistin for 5 min to protect the seedlings from fungal diseases and soil-borne, for ensuring healthy germination and improved seedling vigour [37]. After 30 days, seedlings were transferred into a 2.4 × 2.0 m plot with a spacing of 60 × 40 cm between rows and plants. The experiment was conducted following a Randomized Complete Block Design (RCBD) with 25 genotypes and three replicates. The YLCV virus entered healthy plant cells and whiteflies transmit the virus from infected to healthy plants. All recommended agricultural practices were conducted to get maximum yields in this study.

2.2. Morphological traits measurement

To avoid the border effect, the following traits were measured on ten plants at random designated from the middle rows of each plot. Plant height was recorded at the last harvest from the ground surface to the longest stem tip (PH), days to 50% flowering (from the date of planting to 50% of plants flowered (DTF). On the other hand, days to the first harvest was recorded in the first harvest of fruits (DFH). Fruit length was determined using a meter scale from stalk end to blossom end of fruits (FL). Whereas, fruit diameter was determined at the middle portion of the fruit employing a digital calipers-515 (FD, cm). To avoid error fruit diameter was measured

three times and considered the mean of the estimation. A total number of fruits/plant was recorded for the full growth period (NFP). At the same time, a digital weighing machine was used to measure fruit weight (FW). Most importantly, the shelf life of fruit was determined by recording the number of days needed to reach the point of rotting (SL). To estimate Total Soluble Solids percentage (TSS) a portable refractometer (ERMA, Tokyo, Japan, Model No. 16110) was used at room temperature. Briefly, single fruit was blended, one drop of collected juice was placed over the prism of the refractometer, and the TSS % was measured as a percentage from a direct reading of the instrument. However, fruit yield/plant was recorded by weighing the whole fruit from each plant through a digital weight machine (FYP). The appearance of YLCV symptoms regularly was observed and recorded such as leaf curling, yellowing, stunted growth, and reduced fruit production, in each plot. The determined number of YLCV-infested plants in each plot was based on the presence of symptoms. The percentage of YLCV-infested plants for each plot was calculated by dividing the number of infested plants by the total number of plants in the plot and multiplying by 100. Analyzed the data to determine the extent of YLCV infestation across the field and its impact on tomato growth and yield. Finally, fruit yield/hectare was determined by converting the fruit yield of the plot into hectare (FYH).

2.3. Statistical analysis

The obtained data of studied traits were analyzed using univariate and multivariate analyses using R (V 4.1.2), SPSS (V 23), and MiniTab V (21.2) statistical software. Tukey's HSD test was applied to determine the differences among evaluated genotypes at $p \leq 0.05$. Genetic parameters of measured traits were estimated according to Johnson, Robinson [38], Comstock and Robinson [39], and Singh and Chaudhary [40]. The correlation coefficients between fruit yield and yield contributing traits were breakdown into direct and indirect effects on fruit yield using path analysis following Dewey and Lu [41].

3. Results

3.1. Genotypic variation

The results displayed appreciable genetic diversity revealed by the significant difference among tomato genotypes for most assessed traits (Table 1). Phenotypic and genotypic variances were high for plant height, the number of fruits/plant, fruit weight, yellow leaf curl virus infestation, and fruit yield/plant, while were low for the remaining traits (Table 1). The genotypic variance (GCV) was lower versus the phenotypic variance (PCV) for all traits. The PCV and GCV were high for days to first harvest, plant height, number of fruits/plants, shelf life, yellow leaf curl virus infestation, and fruit yield/plant, while the low values were assigned for days to flowering and fruit yield/ha (Table 1). The broad-sense heritability varied from 50.93 (DTF) to 99.62 (TYCLV). The genetic advance ranged from low in days to first harvest to high in plant height (Table 1).

3.2. Genetic diversity study in tomato

The principal component analysis (PCA) results exhibited five different clusters of tomato genotypes on plans Z1-Z2 (Fig. 1, Table 2). Plant height, fruit diameter, fruit weight, and fruit yield per plant were the most contributing traits in the formation of PCA, while the PC2 was mostly loaded by days to 50% flowering and then fruit length and number of fruits per plant. Therefore, the PC1 was more related to fruit yield, while the PC2 was related to plant phenology. High heritability and genetic advance were observed for the measured traits, indicating the presence of additive gene action, which is crucial for selecting superior genotypes in breeding programs. Cluster analysis of tomato genotypes revealed that Clusters II, III, and V showed a higher association among them, while clusters

Table 1
Genetic parameters for studied traits of the evaluated twenty-five tomato genotypes.

Traits	SS	SSE	σ^2_g	σ^2_{ph}	σ^2_e	h^2_b	GCV	PCV	ECV	GA
DTF (day)	25.9**	6.30	6.54	12.84	6.30	50.93	4.34	6.08	4.26	3.76
DTH (day)	1.27	0.02	0.42	0.43	0.01	99.53	30.01	30.08	2.06	1.34
PH (cm)	2402**	71.75	776.7	848.5	71.75	91.54	26.73	27.94	8.13	54.93
FL (cm)	1.69	0.11	0.53	0.63	0.11	83.12	14.30	15.68	6.44	1.36
FD (cm)	1.88*	0.15	0.58	0.72	0.15	79.56	15.69	17.59	7.95	1.39
NFP	255.9**	17.25	79.56	96.80	17.25	82.18	24.60	27.13	11.45	16.66
FW (g)	477.1**	12.32	154.9	167.2	12.32	92.63	20.39	21.18	5.75	24.68
SL (day)	23.40**	0.14	7.75	7.89	0.14	98.23	28.02	28.27	3.77	5.69
TSS (%)	1.62	0.04	0.53	0.57	0.04	93.63	16.50	17.05	4.30	1.45
TYCLV	836.8	1.06	278.6	279.7	1.06	99.62	102.5	102.72	6.33	34.32
FYP (kg)	1269**	13.69	418.3	432.0	13.69	96.83	30.17	30.66	5.46	41.46
FYH (ton/ha)	93.49**	16.65	25.61	42.26	16.65	60.60	5.10	6.55	4.11	8.12

SS: sum of the square of genotype, SSE: sum of the square of error, σ^2g: genotypic variance, σ^2p: phenotypic variance, σ^2e: environmental variance, h^2b: heritability, GCV: genotypic coefficient of variation, PCV: phenotypic coefficient of variation and ECV: environmental coefficient of variation, and GA: genetic advance. DTF: days to 50% flowering, DTF: days to 50% flowering, DTH: days to the first harvest, PH: plant height, FL: fruit length, FD: fruit diameter, NFP: number of fruits/plants, FW: fruit weight, SL: shelf life, TSS: total soluble solids, TYLCV: tomato yellow leaf curl virus infestation, FYP: fruit yield/plant, FYH: fruit yield/hectare, * reveal significant (*P*-value <0.05) and ** reveal highly significant (*P*-value <0.01).

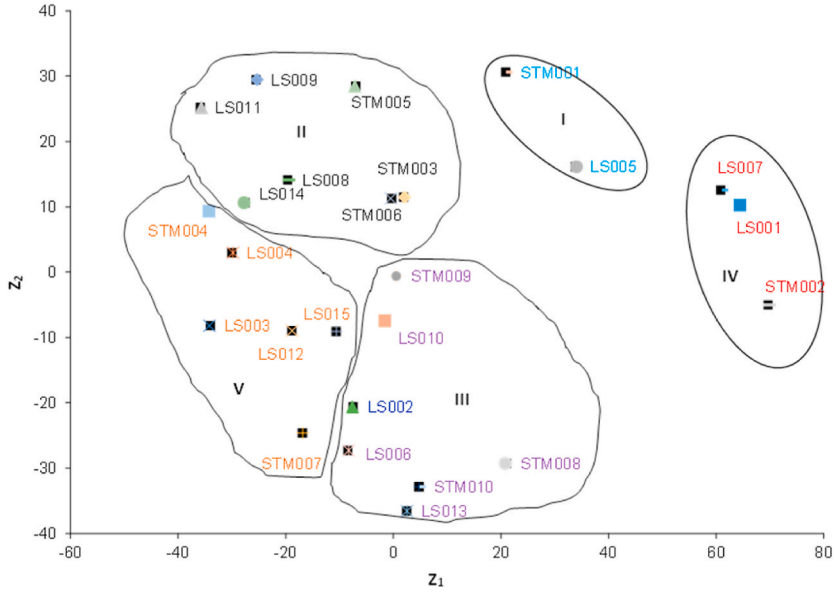

Fig. 1. Scattered diagram illustrates the principal component analysis (PCA) derived clusters of selected tomato genotypes.

Table 2
Tomato genotypes for each cluster and the cluster mean values for measured traits.

Trait	I	II	III	IV	V	Percentage contribution (%)
DTF (day)	58.75	57.91	60.81	59.48	57.86	12.28
DTH (day)	97.85	100.69	97.98	98.80	99.66	20.63
PH (cm)	136.65	99.01	94.32	165.03	80.75	23.99
FL (cm)	5.60	5.48	5.00	4.60	4.76	1.06
FD (cm)	6.05	5.07	4.45	4.33	4.87	1.03
NFP	28.98	45.81	31.62	27.88	37.16	7.14
FW (g)	81.42	65.16	54.85	52.66	60.93	13.13
SL (day)	8.84	11.03	11.01	8.17	8.66	1.99
TSS (%)	4.28	4.53	4.60	4.54	4.02	0.92
TYCLV	23.12	8.90	5.17	17.37	34.99	3.73
FYP (kg)	2.25	2.91	1.64	1.46	2.24	0.44
FYH (ton/ha)	69.27	91.23	51.19	45.99	70.20	13.66
Accession distribution (%)	8	28	28	12	24	

DTF: days to 50% flowering, DTH: days to the first harvest, PH: plant height, FL: fruit length, FD: fruit diameter, NFP: number of fruits/plants, FW: fruit weight, SL: shelf life, TSS: total soluble solids, TYLCV: tomato yellow leaf curl virus infestation, FYP: fruit yield/plant, FYH: fruit yield/hectare.

I and IV displayed higher variation than the other clusters (Fig. 1). The maximum distance was detected between clusters IV and V, suggests that these clusters are genetically different (Fig. 1). The result of the Principal Coordinates Analysis (PCoA) indicated that the longest distance was found between clusters IV and V (Fig. 2), which reinforced the results of PCA (Fig. 1). Furthermore, clusters II, III, and V observed the lowest inter-cluster distance, but their intra-cluster distance was considerably lower than the inter-cluster distance (Fig. 2). Thus, different tomato genotype clusters exhibit more genetic diversity. Clusters II, III, and V have the most tomato genotypes (Table 2). Furthermore, the mean performance of measured traits was estimated for each cluster. Cluster I displayed the highest fruit weight (81.42 g), length (5.60 cm), and fruit diameter (6.05 cm). At the same time, cluster II had the highest days to the first harvest (100.69), number of fruits/plant (45.81), fruit yield/plant (2.91 ton/ha), and fruit yield/ha (91.23) compared to other clusters (Table 2). Likewise, days to 50% of flowering (60.81 days) and TSS (4.60%) were found to be higher in cluster III, whereas cluster IV was characterized by higher plant height (165.03 cm). Finally, cluster V showed moderate values for all measured traits and higher yellow leaf curl virus infestation (34.99). The percentage contribution for genetic divergence demonstrated the most increase in plant height (23.99%) followed by days to first harvest (20.63%).

3.3. Genotypic performance

The highest value of days to 50% of flowering was exhibited by the tomato genotype LS013 (65 days), while the lowest one was assigned for STM-001 (53.50 days) (Table 3). The most extended period to harvest (110.50 days) and the shortest one (92.07 days) were observed by LS011 and STM010 genotypes, respectively. Plant height was highest in LS-001 (165.60 cm) and STM-002 (165.20)

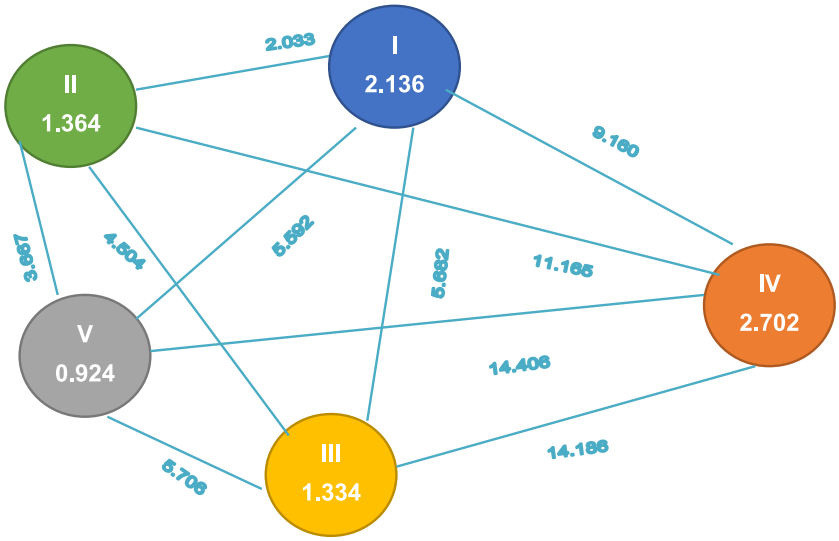

Fig. 2. Intra and inter-cluster distance (D^2) among different clusters through PCoA analysis.

while lowest in LS-003 (70.79 cm). The smallest size of tomato fruit length (3.30 cm) and fruit diameter (3.10 cm) was found in STM-002, whereas the highest fruit length (6.36 cm) was obtained in STM-005. The most increased fruit diameter (6.20 cm) was observed in LS010 (Table 3). LS014 behaved as the top fruit-bearing plant (56.9 fruits/plant) followed by LS-009 (55.67), while LS010 possessed the fewest fruit number per plant (22.10) (Table 3). The uppermost value of fruit weight was assigned for LS-005 (82.51 g), while the lowest value was recorded by STM-008 (33.72 g). The shelf life of tomato fruits was highest in LS-006, LS-007, and LS011 (13.50 days) and the lowest in LS-001 (4.0 days). The total soluble solids (TSS) from tomato pulp were highest in STM-006 (5.46%), and lowest in LS015 and STM-003 (3.20%) (Table 3). The top-yielding tomato was the LS011 (105.7 ton/ha), followed by LS-009 (102.8 ton/ha) and LS014 (92.8 ton/ha), while the lowest yielding was assigned for STM-002 (37.5 ton/ha) and STM-008 (39.60). In terms of disease occurrence, infestation by yellow leaf curl virus (YLCV) was highest in the STM-004 (54.5%), while there was no disease occurred in LS-009, LS011, and LS014 (Table 3, Fig. 3). Less than one-third of the genotypes were infected by YLCV disease, including some high-yielding genotypes. This indicates the variability of selected tomato genotypes in disease occurrence.

3.4. *Relationships among measured traits*

Although there is a relationship observed among different traits, only fruit length, fruit diameter, number of fruits/plant, and fruit weight demonstrated highly significant positive correlations with fruit yield/plant as well as fruit yield/hectare (Table 4). Additionally, days to flowering indicated a significant positive correlation with days to first harvest and fruit length, while there was a negative correlation with total soluble solids. Furthermore, days to first harvest illustrated significant positive correlations with fruit length and fruit diameter while negative correlations with total soluble solids. Likewise, fruit length showed a substantial relationship between the fruit diameter and fruit weight, as well as fruit weight, revealing a significant positive correlation with the fruit diameter (Table 4).

Moreover, the path coefficient analysis in Table 5 displayed that number of fruits/plant, fruit weight and fruit diameter strongly affect fruit yield/hectare. However, a small direct effect is illustrated by the days to first harvest, fruit length, and fruit diameter with fruit yield. Furthermore, the number of fruits/plant and fruit weight have a strong indirect effect on fruit yield (Table 5). Contrastingly, days to first harvest and fruit diameter showed a small indirect positive effect on fruit yield. Besides, days to first harvest demonstrated a positive small indirect effect through number of fruits/plant and fruit weight. Otherwise, plant height indicated a small negative indirect effect on fruit yield through number of fruits/plant and fruit weight (Table 5).

The multivariate analysis of principal component (PCA) indicated that the first principal component (PC1) explained a higher variation (53.31%) compared to the second principal component (PC2) with a lower magnitude (15.98%) of the total variation (Fig. 4). The PC1 seemed to correspond with the performance of tomato genotypes. The genotypes with lower performance were situated on the negative side of the PC1, while the others with the highest performance were on the opposite positive side. Indeed, the genotypes LS011, LS-009, LS014, and STM-005 were associated with fruit yield and its attributes on the PC1 positive side. Otherwise, the genotypes STM-002, STM-008, STM010, and STM-007 proved a negative relationship with fruit yield characters on the PC1 negative side. The number of fruits/plant, fruit diameter, fruit weight, fruit length, and shelf life strongly correlated with fruit yield donating adjacent vectors.

On the contrary, total soluble solids, yellow leaf curl virus infestation, and plant height were negatively associated with fruit yield traits presenting opposite vectors with angles more than 90°. Similarly, the heatmap and hierarchical clustering based on the studied characters displayed the evaluated genotypes into four clusters (Fig. 5). The genotypes LS011, LS-009, and LS014 were clustered as the

Table 3
Mean performance for the measured characters of the tested twenty-five tomato genotypes.

Genotype	DTF (day)	DTH (day)	PH (cm)	FL (cm)	FD (cm)	NFP	FW (g)	SL (day)	TSS (%)	TYLCV	FYP (kg)	FYH (ton/ha)
LS-001	63.00 ^{abc}	101.50 ^{abcdf}	165.60 ^{a}	5.50 ^{abcde}	5.10 ^{cdef}	25.80 ^{hi}	55.60 ^{fg}	4.00 ^{i}	4.10 ^{cd}	41.80 ^{bc}	1.48 ^{klm}	47.36 ^{i}
LS-002	62.00 ^{abcd}	101.50^{abcdef}	86.43^{fghij}	5.40 ^{bcde}	5.20 ^{cde}	27.73 ^{gh}	62.51 ^{e}	12.40 ^{abc}	4.40 ^{bc}	5.20 ^{j}	1.68 ^{hijk}	54.72 ^{h}
LS-003	58.00 ^{bcdef}	101.50^{abcdef}	70.79 ^{k}	5.20 ^{cdef}	5.10 ^{cdef}	39.60 ^{cde}	60.60 ^{ef}	8.50 ^{fg}	4.30 ^{c}	15.50 ^{e}	2.39 ^{cd}	76.48 ^{de}
LS-004	60.00 ^{abcde}	100.50 ^{cdef}	77.71 ^{jk}	5.50^{abcde}	5.60 ^{abc}	39.80 cd	64.22 cd^{e}	8.90 ^{efg}	4.10 ^{cd}	41.17 ^{bc}	2.56 ^{c}	81.28 ^{d}
LS-005	64.00 ^{ab}	103.20 ^{abcde}	138.80 ^{b}	6.10 ^{ab}	6.00 ^{ab}	24.07 ^{hi}	82.51 ^{a}	5.00 ^{i}	3.40 ^{de}	5.43 ^{j}	1.92 ^{fgh}	61.44 ^{g}
LS-006	63.00 ^{abc}	100.50 ^{cdef}	77.50 ^{jk}	5.10 ^{def}	4.30 ^{fgh}	29.80 ^{g}	58.93 ^{ef}	13.50 ^{a}	4.20 ^{c}	8.50 ^{h}	1.75 ^{ghij}	56.00 ^{h}
LS-007	60.00 ^{abcde}	101.50^{abcdef}	164.30 ^{a}	5.00 ^{defg}	4.80 ^{cdefg}	28.00 ^{gh}	60.24 ^{ef}	13.50 ^{a}	4.30 ^{c}	2.50 ^{k}	1.65 ^{ijk}	53.12 ^{h}
LS-008	58.00 ^{bcdef}	100.50 ^{bcdef}	96.80 ^{de}	5.00 ^{defg}	4.60 ^{efg}	40.87 ^{cd}	52.01 ^{g}	10.50 ^{cde}	3.30 ^{e}	5.73 ^{ij}	2.89 ^{b}	92.48 ^{b}
LS-009	60.00 ^{abcde}	100.50 ^{cdef}	94.80 ^{efg}	5.60^{abcde}	5.50 ^{abcd}	55.67 ^{a}	78.22 ^{ab}	12.50 ^{abc}	5.36 ^{a}	0.72 ^{l}	3.23 ^{a}	102.80 ^{a}
LS-010	60.00 ^{abcde}	94.50 ^{def}	95.80 ^{def}	5.80 ^{abcd}	6.20 ^{a}	22.10 ^{i}	80.41 ^{a}	10.50 ^{cde}	4.20 ^{c}	2.70 ^{k}	1.82 ^{ghi}	57.92g ^{h}
LS-011	60.01 ^{abcde}	110.50 ^{a}	85.60 ^{ghij}	6.00 ^{abc}	6.10 ^{ab}	48.50 ^{b}	68.40 ^{cd}	13.50 ^{a}	5.10 ^{ab}	0.69 ^{l}	3.27 ^{a}	105.70 ^{a}
LS-012	58.00 ^{cdef}	109.50 ^{abc}	83.27 ^{hij}	4.30 ^{fgh}	4.70 ^{defg}	35.73 ^{ef}	60.51 ^{ef}	11.50 ^{abcd}	3.30 ^{e}	15.60 ^{e}	2.14 ^{ef}	68.48 ^{f}
LS-013	65.00 ^{a}	110.40 ^{ab}	90.17^{efghi}	5.10 ^{def}	4.20 ^{gh}	27.63 ^{gh}	45.92 ^{hi}	9.50 ^{def}	4.20 ^{c}	2.50 ^{k}	1.26 ^{lm}	40.32 ^{jk}
LS-014	58.00 ^{bcdef}	103.50 ^{abcd}	85.60 ^{ghij}	6.16 ^{ab}	5.33 ^{bcde}	56.97 ^{a}	50.24 ^{gh}	12.60 ^{ab}	5.06 ^{ab}	0.58 ^{l}	2.90 ^{b}	92.80 ^{b}
LS-015	60.00 ^{abcde}	100.50 ^{bcdef}	92.50 ^{efgh}	4.80 ^{efg}	4.90 ^{cdefg}	37.03 ^{def}	55.30 ^{fg}	8.40 ^{fg}	3.20 ^{e}	42.58 ^{b}	1.95 ^{fg}	62.65 ^{g}
STM-001	53.50 ^{f}	92.50 ^{f}	134.50 ^{b}	5.10 ^{def}	4.80 ^{cdefg}	33.90 ^{f}	80.33 ^{a}	12.67 ^{ab}	5.16 ^{ab}	40.80 ^{bc}	2.57 ^{c}	77.10 ^{de}
STM-002	55.43 ^{ef}	93.40 ^{def}	165.20 ^{a}	3.30 ^{i}	3.10 ^{i}	29.84 ^{g}	42.17 ^{i}	7.00 ^{gh}	5.23 ^{a}	10.30 ^{g}	1.25 ^{m}	37.50 ^{k}
STM-003	56.10 ^{def}	94.10 ^{def}	111.50 ^{c}	5.16 ^{cdef}	5.10 ^{cdef}	41.43 ^{c}	62.80 ^{e}	11.00 ^{bcd}	3.20 ^{e}	22.03 ^{d}	2.47 ^{cd}	75.60 ^{e}
STM-004	55.40 ^{ef}	93.10 ^{ef}	77.60 ^{jk}	4.33 ^{fgh}	4.80 ^{cdefg}	45.39 ^{b}	63.33 ^{de}	7.00 ^{gh}	4.10 ^{cd}	54.50 ^{a}	2.91 ^{b}	87.30 ^{c}
STM-005	56.17 ^{def}	98.03 ^{def}	110.50 ^{c}	6.36 ^{a}	5.36 ^{bcde}	41.36 ^{c}	74.67 ^{b}	8.00 ^{fg}	4.20 ^{c}	11.83 ^{fg}	3.07 ^{ab}	93.00 ^{b}
STM-006	57.09 ^{cdef}	97.73 ^{def}	108.30 ^{c}	5.00 ^{defg}	4.80 ^{cdefg}	35.84 ^{ef}	69.52 ^{c}	11.33 ^{bcd}	5.46 ^{a}	11.33 ^{fg}	2.54 ^{c}	76.20 ^{de}
STM-007	55.78 ^{ef}	92.87 ^{f}	81.83 ^{ij}	4.43 ^{fgh}	4.10 ^{gh}	25.41 ^{hi}	61.01 ^{ef}	7.66 ^{fg}	5.13 ^{ab}	40.60 ^{c}	1.51 ^{jkl}	45.02 ^{ij}
STM-008	59.50^{abcdef}	93.13 ^{ef}	112.10 ^{c}	4.76 ^{efg}	3.33 ^{i}	41.36 ^{c}	33.72 ^{j}	11.67 ^{abc}	5.26 ^{a}	7.47 ^{hi}	1.33 ^{lm}	39.60 ^{k}
STM-009	56.08 ^{def}	93.77 ^{def}	104.50 ^{cd}	3.76 ^{hi}	4.26 ^{gh}	37.72 ^{cdef}	61.69 ^{e}	5.66 ^{hi}	5.16 ^{ab}	6.10 ^{ij}	2.26 ^{de}	67.80 ^{f}
STM-010	59.40^{abcdef}	92.07 ^{f}	94.57 ^{efg}	4.16 ^{gh}	3.66 ^{hi}	34.96 ^{f}	41.50 ^{i}	11.67 ^{abc}	4.80 ^{abc}	12.84 ^{f}	1.41 ^{lm}	42.00 ^{jk}
Mean	58.96	99.23	104.30	5.08	4.84	36.26	61.0 4	9.94	4.41	16.27	2.17	67.79
CV (%)	4.26	1.92	8.13	6.45	7.94	11.45	5.06	3.77	4.31	6.33	0.23	6.11

DTF: days to 50% flowering, DTH: days to the first harvest, PH: plant height, FL: fruit length, FD: fruit diameter, NFP: number of fruits/plants, FW: fruit weight, SL: shelf life, TSS: total soluble solids, TYLCV: tomato yellow leaf curl virus infestation, FYP: fruit yield/plant, FYH: fruit yield/hectare.
Different letters indicate a significant difference according to Tukey's HSD test ($p \leq 0.05$).

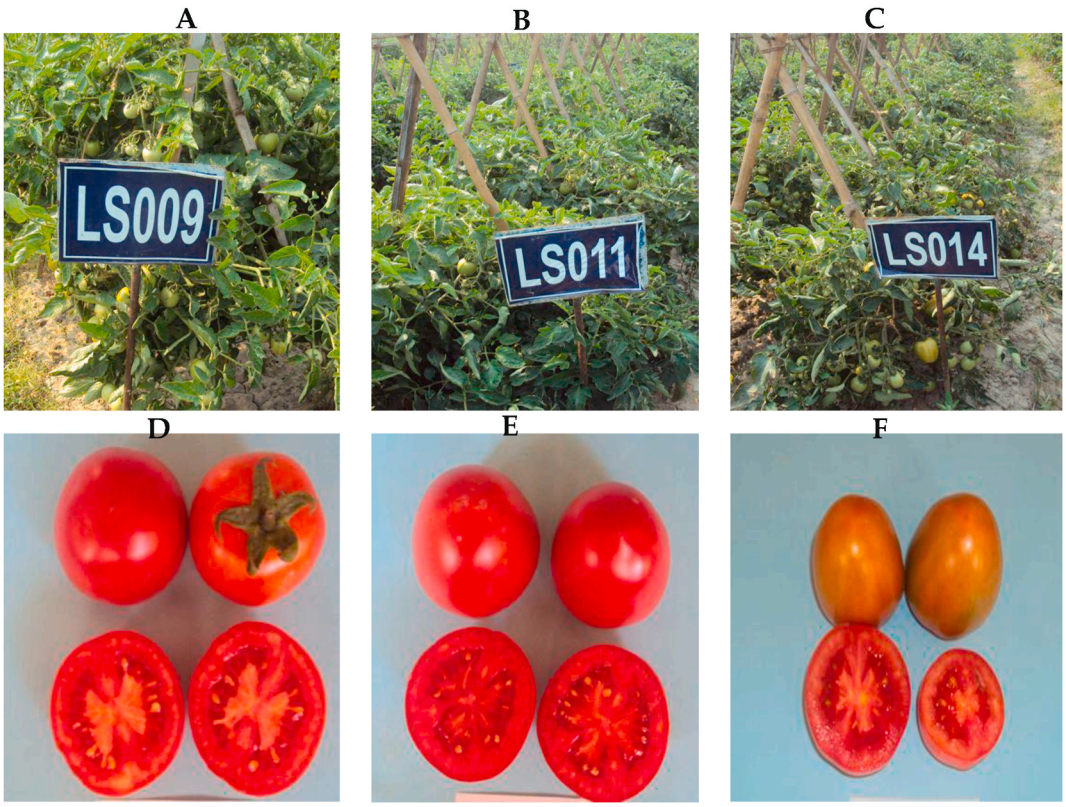

Fig. 3. Agronomic performance of some promising tomato genotypes in terms of fruit yield and resistance to YLCV infestation. A, B, and C are growth of the promising genotypes LS009, LS011, and LS014 in the same order. D, E and F are fruits of the promising genotypes LS009, LS011, and LS014 respectively.

Table 4
Correlation analysis among different yield-associated characters of selected tomato genotypes.

Trait	DTF	DTH	PH	FL	FD	NFP	FW	SL	TSS	TYLCV	FYP
DTH	0.59**										
PH	−0.01	−0.19									
FL	0.39*	0.43*	−0.10								
FD	0.23	0.41*	−0.17	0.81**							
NFP	−0.33	0.10	−0.38	0.19	0.15						
FW	−0.09	0.05	−0.01	0.51**	0.77**	−0.04					
SL	0.01	0.19	−0.27	0.19	0.05	0.31	−0.02				
TSS	−0.28*	−0.30	0.07	−0.16	−0.29	0.22	−0.08	0.21			
TYLCV	−0.32	−0.34	−0.02	−0.22	−0.05	−0.08	0.06	−0.42	−0.20		
FYP	−0.38	0.16	−0.34*	0.44*	0.57**	0.77**	0.51**	0.20	0.02	0.01	
FYH	−0.30	0.24	−0.35*	0.48*	0.61**	0.76**	0.51**	0.23	−0.02	−0.03	0.99**

DTF: days to 50% flowering, DTH: days to the first harvest, PH: plant height, FL: fruit length, FD: fruit diameter, NFP: number of fruits/plants, FW: fruit weight, SL: shelf life, TSS: total soluble solids, TYLCV: tomato yellow leaf curl virus infestation, FYP: fruit yield/plant, FYH: fruit yield/hectare. * and ** indicates Pearson correlation coefficient value significant at 5% and 1% levels of probability.

highest performance (depicted in blue for most characters), while STM010, STM-008, and STM-002 were grouped with the lowest performance (red values for most characters).

4. Discussion

Exploring genotypic diversity is a fundamental approach for developing novel genotypes with the desired traits to improve tomato production, particularly under the fast-growing global population and abrupt global climate change. The present study focused on understanding the genetic variation of different tomato genotypes to provide information that could improve tomato fruit yield and quality. The detected genotypic difference for all evaluated traits implies the presence of adequate genetic variability among the tested

Table 5
Direct (bold) and indirect effects of different yield contributing traits of tomato on fruit yield/hectare through path coefficient analysis.

Trait	DTF	DTH	PH	FL	FD	NFP	FW	SL	TSS	TYLCV	FYP
DTF	**0.059**										
DTH	0.008	**0.142**									
PH	0.001	0.001	**−0.002**								
FL	−0.002	−0.004	0.001	**0.027**							
FD	−0.008	−0.019	0.001	0.004	**0.136**						
NFP	0.051	0.123	−0.002	−0.023	0.118	**0.865**					
FW	0.045	0.109	−0.002	−0.021	0.105	0.666	**0.770**				
SL	0.001	0.002	0.001	0.001	0.002	0.013	0.012	**0.015**			
TSS	0.003	0.007	0.001	−0.001	−0.007	0.045	0.040	0.001	**0.052**		
TYLCV	0.006	0.013	0.001	−0.003	−0.013	0.081	0.072	0.001	0.005	**0.094**	
FYP	0.058	0.139	−0.002	0.026	0.133	0.844	0.752	0.015	0.051	0.092	**0.976**
Residual effect: 0.157											

Independent variables: DTF: days to 50% flowering, DTH: days to the first harvest, PH: plant height, FL: fruit length, FD: fruit diameter, NFP: number of fruits/plants, FW: fruit weight, SL: shelf life, TSS: total soluble solids, TYLCV: tomato yellow leaf curl virus infestation, and FYP: fruit yield/plant. Dependent variables: FYH: fruit yield/hectare.

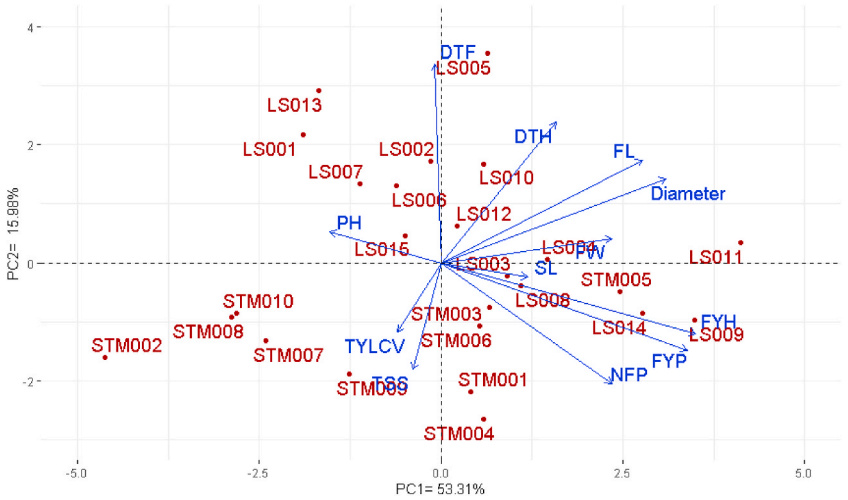

Fig. 4. Biplot of PCA for the evaluated twenty-five tomato genotypes based on studied growth, yield, and quality characters. DTF: days to 50% flowering, DTH: days to the first harvest, PH: plant height, FL: fruit length, Diameter: fruit diameter, NFP: number of fruits/plants, FW: fruit weight, SL: shelf life, TSS: total soluble solids, TYLCV: tomato yellow leaf curl virus infestation, FYP: fruit yield/plant, FYH: fruit yield/hectare.

genotypes. However, some traits overwhelmingly represented their genetic diversity through genotypic, and phenotypic variations along with their high heritability and genetic advance. In general, genotypic and phenotypic variation reveals the extent of genetic variation in the evaluated germplasm [42–44]. Moreover, the genetic advance was estimated for the assessed traits to reflect the best traits for future hybridization programs of tomatoes. Similarly, earlier published reports on tomato manifested high genotypic and phenotypic variations, strong heritability, and genetic advance for the number of fruits per plant, plant height, and fruit weight [42,43,45,46]. Hybrids and parents are selected based on genetic advance, h^2, and genetic variability. Therefore, traits with high h^2 magnitudes are highly heritable for developing improved varieties of tomatoes which is crucial [47]. For making a selection, genetic variability components like h^2 and genetic advance (GA) are essential biometric tools to improve tomato germplasm through breeding [48]. Moreover, the hybridization scheme among diverse genotypes generates desirable novel allele combinations owing to their genetic diversity. To explore the genetic diversity of the studied traits, it is crucial to investigate the genetic divergence of assessed genotypes. The principal coordinate analysis usually renders clusters among genotypes to indicate their genetic distance. This study delivered five different clusters among the evaluated genotypes. If the cluster distance is high, the genetic divergence of those cluster components will be higher, along with the highest heterosis when crossing occurs in each pair of genotypes in each cluster. Moreover, the highest intra-cluster difference pointed to varied genetic diversity because of forces of natural and artificial selection [49]. The highest inter and intra-cluster distance between clusters V and IV reveals higher genetic diversity and heterosis, which also supports focusing on those tomato genotypes and their traits for further hybridization programs. Similarly, Prakash and Vijay [49] detected clustering distances for different characteristics of tomato genotypes.

Correlation analysis usually paves the way to understanding the relationship among studied traits and facilitating better insight regarding the contribution of each trait to improving the crop's genetic makeup. Accordingly, correlation studies indicate the most suitable traits needed to be prioritized in the future breeding program. The obtained results alluded to number of fruits/plant, fruit

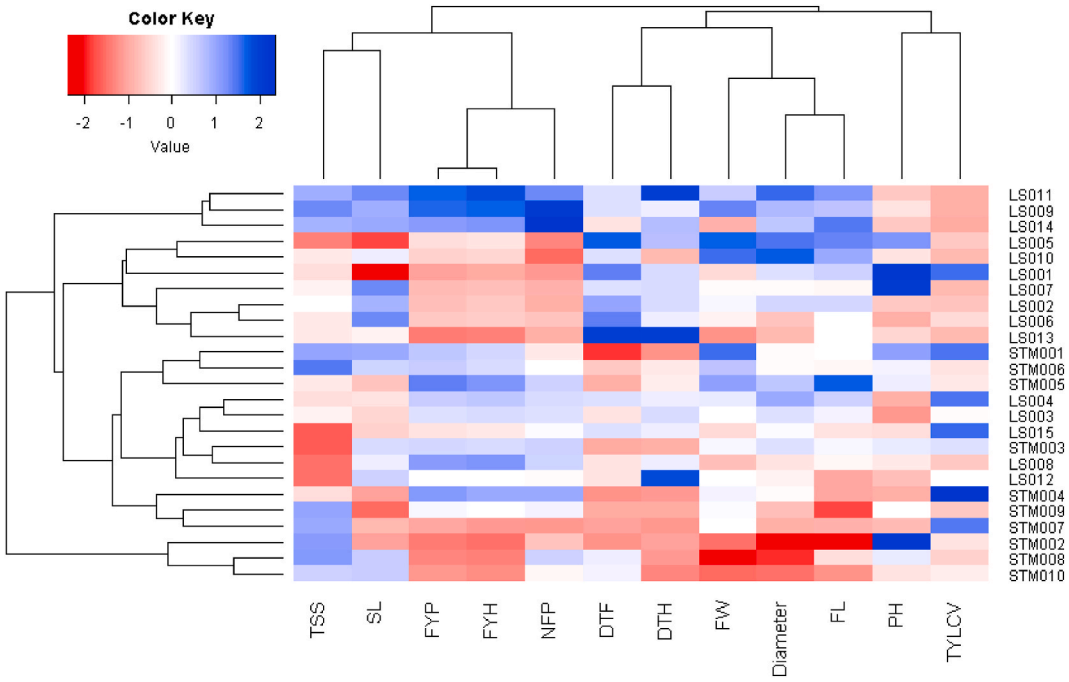

Fig. 5. Heatmap and hierarchical clustering divide the evaluated genotypes into different clusters based on growth, yield, and quality characters. Red and blue colors imply low and high performance for the corresponding characters, respectively. DTF: days to 50% flowering, DTH: days to the first harvest, PH: plant height, FL: fruit length, Diameter: fruit diameter, NFP: number of fruits/plants, FW: fruit weight, SL: shelf life, TSS: total soluble solids, TYLCV: tomato yellow leaf curl virus infestation, FYP: fruit yield/plant, FYH: fruit yield/hectare.

diameter, and fruit weight reflected strong positive associations with fruit yield. Consequently, these traits are important in breeding programs to improve fruit yield [50]. Similarly, Reddy et al. [46] and Kumar et al. [42] deduced that the number of fruits/plant, fruit weight, and fruit diameter have significant correlations with tomato fruit yield. Even though correlation studies are supportive to identify related traits to fruit yield, while makes it perplexing to have a clear understanding of the direct and indirect contribution of each trait. Under such a scenario, path analysis assists in breakdown the correlation coefficients into their direct as well as indirect effects, which reflect the relative importance of each character. Any trait's direct and indirect effects can positively or negatively influence the performance of another trait. In this study, positive direct and indirect effects were detected for the number of fruits per plant, fruit weight, and fruit diameter on tomato fruit yield. It reveals that these traits are more suitable for effective selection in the future breeding program for enhancing the fruit yield of tomatoes. Similarly, Kumar et al. [42] disclosed that the number of fruits/plant, fruit weight, and fruit diameter illustrated a strong direct and positive effect on the fruit yield of tomatoes.

Principal component analysis can address more relevant variables and grouping suitable traits into different components [51]. The principal component analysis differentiates between poor and high-performing genotypes from the selected tomato genotypes in this study. Among 25 tomato genotypes, 14 genotypes showed good performance on PC1, while 11 genotypes belonged to poor-performing genotypes on PC2. Remarkably, LS-009, LS011, and LS014 genotypes were strongly associated with yield traits, which brings our attention to those high-yielding genotypes. Besides, these aforementioned genotypes exhibited a negative relationship with tomato yellow leaf curl virus infestation.

Furthermore, these tomato genotypes were validated through heatmap analysis with high-yielding and adequate resistance to yellow leaf curl virus (YLCV) infestation. Several studies have demonstrated that yellow leaf curl virus has a remarkable effect on yield quality [52]. These findings confirm the best performance of those three genotypes among the evaluated 25 genotypes. Therefore, this study reveals that LS-009, LS011, and LS014 would be high-performing tomato genotypes and resistant to yellow leaf curl virus infestation, accordingly, could be considered for future hybridization tomato breeding programs. Besides, the fruit diameter, number of fruits per plant, and fruit weight are important traits that could be used to indirectly select fruit yield to improve tomato productivity in breeding programs.

Author contribution statement

Md. Ismail Hossain; Md. Saifullah; Md Sazzad Hossain; Abu Habib Md Abdullah; Md. Arif Hussain; Arova Zannat: Conceived and designed the experiments; Performed the experiments; Contributed reagents, materials, analysis tools or data.

Fatmah A. Safhi; Khalid S. Alshallash; Elsayed Mansour; Abdelaleim I. ElSayed: Analyzed and interpreted the data; Wrote the paper.

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Data availability statement

The data presented in this study are available upon request from the corresponding author.

Additional information

No additional information is available for this paper.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.heliyon.2023.e18958.

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