

## Research Article

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# Evaluation of tomato hybrid lines adapted to lowland

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**Abstract:** Improving tomato fruit characteristics is a crucial step to address the decline in production, which is primarily caused by biotic stress and the limited adaptability of existing varieties in lowland areas. This improvement can be achieved through plant breeding programs involving crossbreeding techniques. The primary objective of developing superior varieties is to produce tomatoes with high fruit quality and excellent productivity. The selection criteria were further refined using both principal component analysis (PCA) and path analysis. PCA was employed to identify the primary traits contributing to variability, while path analysis helped establish the strength and direction of relationships between key traits and supporting characteristics. The most significant direct impact will be incorporated into the index value to determine the genotype with the best overall performance. The findings identified 12 F1 tomato breeding lines deemed suitable for progression to the next generation, offering significant potential for enhancing tomato production. This study underscores the effectiveness of targeted breeding strategies. It contributes to developing more sustainable and efficient approaches to tomato cultivation, paving the way for improved productivity and quality in future varieties.

**Keywords:** compatible ability, hybrid tomato, path analysis, PCA, *Solanum lycopersicum*

## 1 Introduction

Tomato (*Solanum lycopersicum*) is one of the important horticultural crops in several countries in the world because it is a commodity that can provide essential nutrients in the form of phosphorus, iron, and vitamin A. In addition, tomatoes also contain a number of essential compounds, such as flavonoids and lycopene [1]. Tomatoes are also useful as a vegetable and are widely used by people to treat several diseases, such as anti-inflammatory, hypertension, coronary heart disease, and anti-cancer [2]. Tomatoes have a unique taste with sweet and sour flavors that can be consumed directly. They play a crucial role as an industrial raw material, making them popular because of their extraordinary benefits [3]. However, the growth of tomato production is considered slow. Tomato production in Indonesia in 2022 was 1,168,744 tons and decreased in 2023 to 1,143,788 tons. The decrease in production was caused by several problems, such as pest and disease attacks and varieties less adaptive to the environment [4]. Therefore, developing the productivity and quality of tomatoes in line with the population rate is one of the keys to stabilizing the rate of production and demand.

The common problem encountered in tomato cultivation in Indonesia is the lack of superior varieties with high yields, good fruit quality, and resistance to pests and diseases. This decline is partly due to biotic stress, such as pests and diseases, as well as the limited adaptability of existing tomato varieties to local agroecological conditions. This effort not only addresses local agricultural challenges but also contributes to breeding programs in tropical and subtropical regions where similar conditions prevail [5–7]. This highlights the pressing need for superior varieties that combine high yield potential, good fruit quality, and resistance to environmental stresses. In contrast to prior research focusing primarily on conventional varieties, this study specifically evaluates F1 hybrid tomato lines, which have heterosis advantages offering better yield and disease resistance potential [8,9].

One way to develop tomato varieties is by improving the varieties [10]. Variety improvement is an important

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step in efforts to increase the declining tomato production. This can be done through a plant breeding program involving crossbreeding techniques. In the process of assembling superior varieties, the main goal is to create tomato varieties that not only have high quality and good productivity but also meet consumer needs and preferences. Thus, the resulting varieties are expected to be well accepted by the community to benefit farmers and the agricultural industry as a whole [11,12]. Hybrids result from the first-generation (F1) crosses from a pair or more pure lines of parents with superior characteristics. The heterozygous genetic composition of hybrid varieties causes these varieties to have more advantages compared to non-hybrid varieties, which generally have homozygous genetic compositions [13]. A plant breeding program's success in producing superior varieties is based on the diversity of plant populations.

The formation of tomato diversity from crossbreeding is greatly influenced by the method of crossbreeding. In general, there are several cross-breeding methods such as a single cross, double cross, three-way cross, multiple crosses, backcross, and diallel mating [14–16]. Crossing a pair of inbred lines will produce a single-cross hybrid, and crossing two unrelated single-cross hybrids can create a double-cross hybrid variety. Crossing is done to improve yield by selecting the offspring from the cross [17]. Crossbreeding will improve tomato genetics to improve yield through the selection of crossbred offspring. Assembling superior varieties is directed to increase yield potential and quality, so that superior varieties have high competitive power. In addition, assembling new varieties is still important to increase genetic variation that can be used as a plant breeding material [11].

Genetic diversity and heritability are absolute requirements for the success of a plant breeding program. Genetic diversity can increase the possibility of obtaining better genotypes through selection. Character diversity and genotype diversity are helpful in determining the pattern of genotype grouping in a particular population based on observed characters. They can be used as a basis for selection activities. Characters with high heritability and genetic values can be used as selection criteria in the early generations. The characteristics observed include measuring variations in observable traits (*phenotypic diversity*). Genetic correlation between one character and another can be beneficial if the character covers one that is closely related to the results [17]. Testing must first determine the characteristics of plants, yield, and quality of cross-bred lines. This must be carried out under stable environmental conditions, i.e., under conditions of the place where the variety will be cultivated [18]. Diversity

analysis can be done with various types of markers; one of the marker types is the morphology of the plant; it is the indicator that the character is genetically controlled based on heritability values [19]. This study aimed to produce tomato strains that have good fruit quality and high productivity in the lowlands.

## 2 Materials and methods

The study was carried out in the Experimental Farm of the Faculty of Agriculture, Hasanuddin University, Tamalanrea District, Makassar City, South Sulawesi, from June to September 2024. The location has an altitude of 22.4 m above sea level with an average minimum and maximum temperature of 24 and 32°C.

### 2.1 Experimental design

This study used determinate tomatoes by crossing three types of tomato fruit types, consisting of Karina (Grape), Mawar (Beffstreak), and Chung (Cherry) varieties. This first trial evaluated the diversity of tomato F1 hybrids using a randomized complete block design with three replications. Sixteen F1 hybrid genotypes consisting of G1 (KM30.5.2.6 × MC74.12.6.3), G2 (MC12.3.1.12 × MC74.12.5.6), G3 (MC10.4.5.7 × MC10.7.2.9), G4 (MC8.3.2.6 × KM30.5.2.6), G5 (KM30.5.2.6 × MC10.4.6.3), G6 (MC74.12.8 × MC10.10.1), G7 (MC27.12.6 × KM23.3.3), G8 (MC74.12.8 × KM23.3.3), G9 (KM5.3.6.6 × MC74.12.8.9), G10 (MC12.3.1.12 × MC10.4.5.5), G11 (MC10.4.6.3 × MC10.4.5.5), G12 (MC10.4.5.5 × MC29.4.5.10), G13 (MC10.4.5.7 × MC12.3.5.11), G14 (MC10.4.5.7 × MC74.12.6.3), G15 (MC10.7.2.9 × KM69.6.2.1), and G16 (KM30.5.2.6 × MC8.3.2.6), and three check varieties (Mawar, Natavi, Servo) were used to focus on productivity and other key traits (Figure 1). This setup enabled comprehensive comparisons across genotypes and varieties.

### 2.2 Research procedure

Plant maintenance consists of several components: watering, replanting, fertilizing, pruning, weeding, and managing pest and disease control. Watering was done twice daily, in the morning and evening, using either a watering can or sprinklers. For tomato plants that exhibited abnormal growth, wilting, or signs of pest or disease damage, replanting was conducted. This process involved

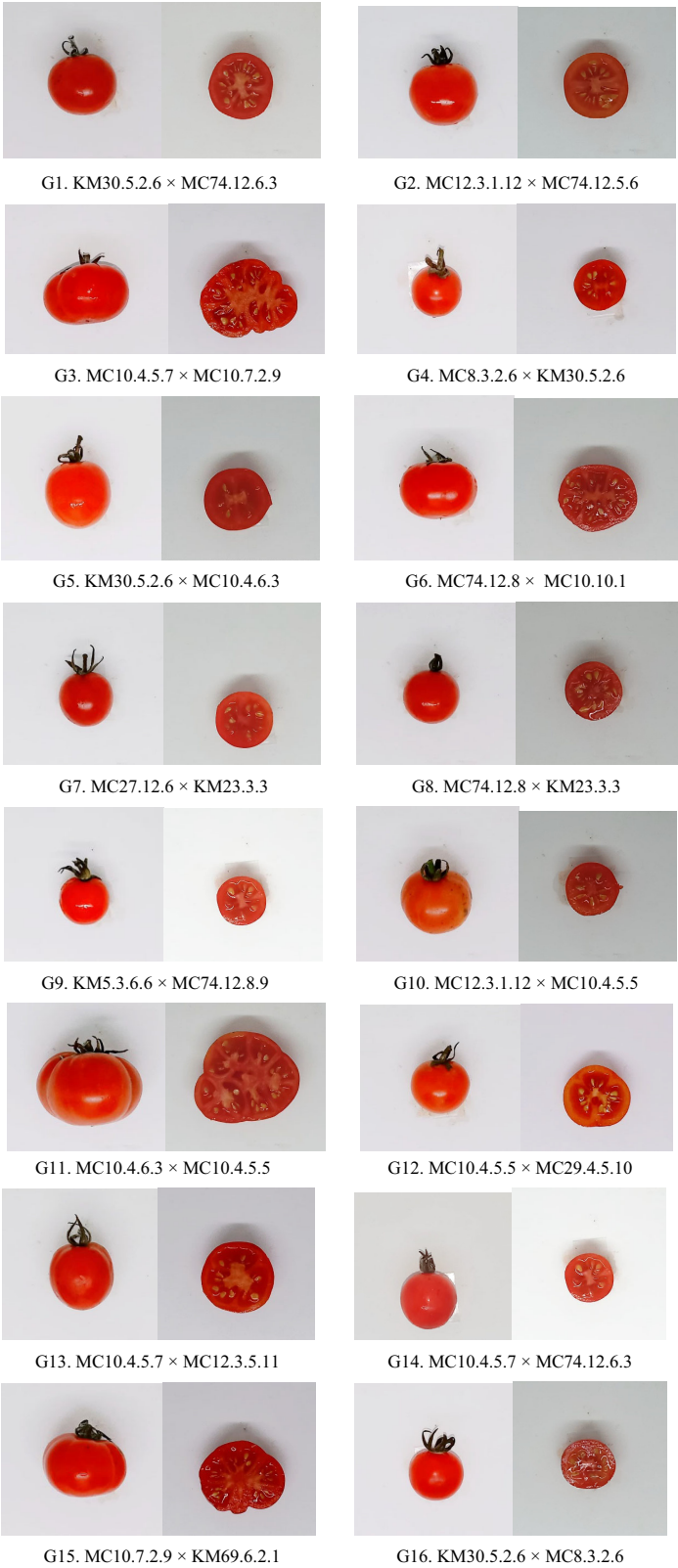


Figure 1: Fruit appearance of all genotypes.

replacing the affected plants with seedlings of the same age and genetic code precisely 1 week after planting (WAP) and typically in the afternoon to prevent wilting. Fertilization began at one WAP and continued weekly, using an NPK Mutiara fertilizer solution (10 g/L) at a rate of 250 mL per plant. For subsequent applications, KNO<sub>3</sub> was added at a concentration of 5 g/L. Additionally, NPK Mutiara was applied as a root zone solution during the plant's reproductive stage, and Gandasil B was used during the generative phase.

Pruning was performed at least once a week to remove small or early shoots on the lower stem and other branches, ensuring the plant's growth was directed toward the main stem. Weeding was also done to eliminate unwanted plants that could hinder tomato growth. Weeds within the planting holes were removed by hand, while those outside the planting beds were cleared using a hoe.

Pest and disease control was conducted weekly, using a mixture of the insecticide Curacron 500 E and the fungicide Antracol 70 WP C at concentrations of 2 cc/L and 2 g/L of water, respectively. Dithane M-45 WP was used at a concentration of 2 g/L of water as a substitute for Antracol 70 WP for more effective results. Pesticides were applied by spraying them onto the plant surfaces while harvesting twice weekly. Fruits were considered ready for harvest when they reached a reddish-yellow color, meeting the desired maturity criteria.

## 2.3 Observations

### 2.3.1 Observation of quantitative parameter evaluation of the F1 hybrid

The quantitative characters observed were based on [20] the following:

1. Plant height (cm) is measured from the ground level to the growing point of the plant at the time of harvest.
2. Dichotomous height (cm) was observed from the base of the root to the first branching of the plant.
3. Stem diameter (mm) was observed at the upper base of the root.
4. Day to flower (DAP), which is calculated from the blossoming of flowers from the day after planting under flowering conditions, had at least one open flower (50%).
5. Day to harvest (DAP) was observed when the tomatoes were reddish in color; harvesting was done four times during the harvesting period.
6. Number of branches (branch) is the number of branches observed from the average of the three flowering bunches in each bunch.
7. Number of flowers per bunch (flower) is the number of flowers observed from the average of three flowering bunches in each bunch.
8. Number of fruits per bunch (fruit) is the number of fruits per bunch formed and calculated as the average of three bunches of fruits observed from each sample.
9. Number of inflorescences (fruit) is the number of bunches observed from the average of the three flowering bunches in each cluster.
10. Weight of fruit sample per plant (g) is the weight of 10 fruits observed in a plant.
11. Total fruit weight per plant (g) is the total of fruit weights observed in a plant throughout during life cycle.
12. Fruit thickness (mm) is measured at the largest part of the fruit using a caliper.
13. Fruit diameter (mm) is measured at the longest part of the fruit using a caliper.
14. Fruit weight (g) is measured at the largest part of the fruit using an analytical balance.
15. Number of cavities (cavity) is counted in the cavity of the fruit after splitting it into two parts.
16. Total soluble solids (Brix) (%), measured scale determined the refractive index as total soluble solids.
17. Number of seeds per fruit (seed) is the number of seeds obtained from the extracted sample.
18. Yield (ton/ha) is calculated by the fruit's weight in the genotype sample.

## 2.4 Data analysis

The field evaluation data were analyzed using analysis of variance (ANOVA), which provided the foundation for estimating the heritability of various plant traits. The selection criteria were systematically developed through correlation analysis. Correlation analysis is calculated using the Pearson Product Moment correlation technique equation using the following formula:

$$r = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum (x_i - \bar{x})^2} \sqrt{\sum (y_i - \bar{y})^2}},$$

where  $r$  is the Pearson's correlation coefficient,  $x_i$  is the  $i$ th observation of variable  $x$ ,  $y_i$  is the  $i$ th observation of variable  $y$ ,  $\bar{x}$  is the mean of variable  $x$ ,  $\bar{y}$  is the mean of variable  $y$ , and  $\Sigma$  is the summation symbol.

Cross-sectional analysis was calculated based on the simultaneous equation using the following formula [21]:

$$\begin{pmatrix} R_{11} & R_{12} & \dots & R_{1p} \\ R_{21} & R_{22} & \dots & R_{2p} \\ \dots & \dots & \dots & \dots \\ R_{p1} & R_{p2} & \dots & R_{pp} \end{pmatrix} \begin{pmatrix} C_1 \\ C_2 \\ \dots \\ C_p \end{pmatrix} = \begin{pmatrix} R_{1y} \\ R_{2y} \\ \dots \\ R_{py} \end{pmatrix}.$$

Based on this equation, the value of  $C$  (direct effect) can be calculated using the following formula:

$$C = R_x^{-1} \times R_y.$$

$R_x$  is the correlation matrix between independent variables,  $R_x^{-1}$  is the inverse of the  $R_x$  matrix,  $C$  is the cross coefficient vector that shows the direct effect of each standardized independent variable on the independent variable,  $R_y$  is the correlation coefficient vector between  $X_i$  variables and independent variables.

Initially, the traits identified as significant were integrated into a selection index based on the yield values derived from the principal component analysis (PCA). Subsequently, the yield values were adjusted using the proportionate contributions of the PCA components and correlation analysis, as referenced in previous studies [22–24]. The selection criteria were further refined using both PCA and path analysis. PCA was employed to identify the primary traits contributing to variability [25], while path analysis helped establish the strength and direction

of relationships between key traits and supporting characteristics [26]. Combining these methods, a comprehensive selection index was developed, highlighting the traits most strongly associated with yield and other desirable attributes, enabling systematic and informed selection decisions [27]:

$$S_n = \frac{xi - \bar{x}}{SD},$$

where  $S_n$  is the standardization,  $xi$  is the value of genotype in characters,  $\bar{x}$  is the average value of all genotypes, and  $SD$  is the standard deviation.

### 3 Results

#### 3.1 Average standard deviation

The results of the standard deviation analysis in Tables 1 and 2 show the variation of plant genotypes based on growth parameters and fruit characteristics. Regarding growth, the highest plant height was found in genotype G1 (363.67 cm), while the lowest was T3 (312.85 cm). The number of days until harvest ranged from 171 to 210 days, with differences in the number of branches and fruits per bunch in each genotype. Meanwhile, based on the fruit characteristics, fruit number and weight, fruit thickness and diameter, sweetness level

**Table 1:** Average and standard deviation of several growth parameters from lowland tomato hybrid

Genotype	PH	DHe	SD	DF	DH	NB	NFB	NFpB	NI
G1	363.67 ± 9.19	118.67 ± 5.11	32.84 ± 1.74	105 ± 2.65	171 ± 0	17.75 ± 0.56	13.54 ± 1.37	7.76 ± 0.40	52.08 ± 1.75
G2	365.27 ± 4.43	108.2 ± 6.21	30.19 ± 0.66	106 ± 1.15	189 ± 5.20	18.4 ± 1.01	16.54 ± 0.98	7.39 ± 0.20	60.14 ± 2.00
G3	359.00 ± 2.73	123.6 ± 2.88	32.12 ± 1.64	104 ± 2.52	198 ± 0	20 ± 1.01	13.46 ± 0.55	8.05 ± 0.48	44.17 ± 1.42
G4	342.08 ± 2.67	127 ± 6.10	27.7 ± 0.32	103 ± 2.08	171 ± 0	11.5 ± 0.76	15.74 ± 0.67	10.99 ± 0.03	40.14 ± 3.12
G5	388.16 ± 5.39	121.92 ± 2.86	23.65 ± 0.46	102 ± 2	171 ± 0	18.34 ± 0.86	20 ± 0.2	10.62 ± 0.64	36.95 ± 0.33
G6	333.83 ± 6.54	126.07 ± 2.92	24.13 ± 0.59	99 ± 1	171 ± 0	15.93 ± 0.87	15.40 ± 0.52	10.02 ± 0.26	41.67 ± 1.39
G7	345.83 ± 2.81	102.17 ± 8.48	30 ± 1.26	99 ± 1	180 ± 5.20	20.01 ± 0.33	19.27 ± 0.19	9.91 ± 0.09	56.00 ± 0.50
G8	314.84 ± 10.72	121.25 ± 7.97	32.75 ± 2.13	99 ± 1	171 ± 0	16.63 ± 0.39	18.07 ± 0.27	17.25 ± 0.15	48.015 ± 0.33
G9	331.67 ± 1.64	123.25 ± 4.02	27.38 ± 0.59	99 ± 1	180 ± 5.20	16.17 ± 1.13	19.07 ± 0.66	9.87 ± 0.39	51.74 ± 1.26
G10	363.50 ± 13.57	128.08 ± 3.21	29.67 ± 2.02	104 ± 3.06	171 ± 0	19.08 ± 1.05	16.87 ± 0.51	7.93 ± 0.95	38.33 ± 1.43
G11	346.24 ± 3.46	108.54 ± 3.45	28.27 ± 0.71	106 ± 2.89	198 ± 0	17.76 ± 1.40	15.93 ± 0.47	4.20 ± 0.08	44.09 ± 2.60
G12	291.75 ± 12.97	116 ± 6.66	30.56 ± 0.59	108 ± 3.61	180 ± 5.20	17.67 ± 0.76	13.87 ± 0.17	5.42 ± 0.44	47.91 ± 1.57
G13	338.7 ± 5.61	126.77 ± 3.77	26.32 ± 1.30	107 ± 2.52	209 ± 6.35	14.12 ± 0.53	15.4 ± 1.27	6.69 ± 0.07	46.11 ± 6.52
G14	345.25 ± 12.90	125.67 ± 5.83	28.79 ± 0.34	107 ± 3.51	198 ± 0	13 ± 0.34	13.8 ± 0.84	3.75 ± 0.28	44.17 ± 1.70
G15	354.83 ± 14.56	121.48 ± 2.61	31.59 ± 1.11	110 ± 4.04	189 ± 5.20	19.42 ± 0.65	11.40 ± 0.29	10.8 ± 0.17	35.02 ± 1.16
G16	361 ± 8.97	123.34 ± 2.69	31.07 ± 2.27	107 ± 3.21	180 ± 5.20	15.83 ± 0.77	14.13 ± 0.79	14.67 ± 0.43	38.39 ± 0.87
T1	329.64 ± 9.19	92.84 ± 6.26	27.62 ± 0.78	105 ± 3	210 ± 3.46	16.10 ± 0.62	10.94 ± 0.50	5.6 ± 0.13	24.57 ± 2.99
T2	239.6 ± 6.18	126.42 ± 5.05	22.7 ± 0.64	104 ± 1.15	189 ± 5.20	7.13 ± 0.40	15.2 ± 1.10	4.60 ± 0.12	17.08 ± 1.23
T3	312.85 ± 9.35	131.5 ± 1.01	27.55 ± 1.44	107 ± 3.21	195 ± 0	7.65 ± 0.40	14.46 ± 1.04	4.61 ± 0.17	25.00 ± 1.28

Note: PH: plant height (cm); DHe: dichotomous height (cm); SD: steam diameter (mm); DF: day to flower (DAP); DH: day to harvest (DAP); NB: number of branches (branch); NFB: number of flowers per bunch (flower); NFpB: number of fruits per bunch (fruit); NI: number of inflorescences (fruit).



**Table 2:** Continued average and standard deviation of growth parameters of hybrid lowland tomatoes

Genotype	WFSP	TFWP	FT	FD	NFC	FW	Brix	NSF	Yield
G1	134.08 ± 6.02	804.5 ± 36.10	74.28 ± 2.05	75.54 ± 2.07	10.5 ± 0.33	31.45 ± 0.47	9.95 ± 0.73	122.67 ± 3.79	56.30 ± 2.93
G2	148.2 ± 6.77	829 ± 6.51	68.9 ± 0.91	72.31 ± 0.93	10.53 ± 0.43	26.42 ± 1.13	10.13 ± 0.13	105.57 ± 6.81	48.59 ± 1.75
G3	117.17 ± 3.29	703 ± 1.76	76.67 ± 6.12	83.99 ± 7.45	19.56 ± 0.20	33.59 ± 1.34	8.767 ± 0.32	186 ± 2.65	52.35 ± 2.17
G4	147.00 ± 1.40	862 ± 10.69	61.74 ± 0.98	63.62 ± 1.11	8.52 ± 0.17	18.75 ± 0.50	10.07 ± 0.49	115.58 ± 7.20	35.97 ± 1.34
G5	131.17 ± 8.95	817 ± 9.29	63.45 ± 1.50	66.56 ± 0.34	8.18 ± 0.15	24.189 ± 0.86	8.77 ± 0.23	127.17 ± 3.40	43.93 ± 1.74
G6	139.67 ± 7.71	838 ± 46.23	67.82 ± 2.57	72.62 ± 3.30	13.33 ± 0.59	27.95 ± 0.91	9.83 ± 0.47	150.5 ± 6.67	52.60 ± 4.63
G7	185.00 ± 3.22	1,110 ± 19.31	55.17 ± 5.21	56.64 ± 5.24	7.00 ± 0.34	18.75 ± 0.59	7.5 ± 0.26	114.67 ± 1.29	46.39 ± 2.23
G8	276.17 ± 4.17	1,677 ± 16.52	51 ± 1.84	52.64 ± 1.79	9.67 ± 0.58	14.00 ± 0.64	10.2 ± 0.40	97.65 ± 6.75	52.12 ± 2.18
G9	169.34 ± 2.31	992 ± 8.14	58.7 ± 1.92	60.08 ± 1.84	10 ± 0.88	16.78 ± 0.66	10.63 ± 0.35	102.67 ± 3.29	36.96 ± 1.35
G10	99.00 ± 8.69	564 ± 14	75 ± 2.56	78.77 ± 3.22	12.83 ± 0.69	34.66 ± 0.81	12.7 ± 0.58	179 ± 4.42	43.37 ± 1.13
G11	61.57 ± 3.44	369.4 ± 20.64	64.59 ± 1.77	67.47 ± 1.99	12.27 ± 0.50	22.09 ± 0.36	10.93 ± 0.73	77.2 ± 2.53	18.06 ± 0.78
G12	85.42 ± 4.56	512.5 ± 27.39	75.66 ± 3.90	78.63 ± 3.88	13.33 ± 0.51	26.12 ± 0.92	10.78 ± 0.66	153.22 ± 9.53	29.87 ± 2.12
G13	102.17 ± 13.58	613 ± 14.01	53.96 ± 4.03	55.52 ± 4.21	8.53 ± 0.73	18.86 ± 0.57	11.47 ± 0.24	165.83 ± 4.84	25.61 ± 0.46
G14	54.92 ± 3.89	339 ± 8.54	60.93 ± 1.12	62.6 ± 0.98	7.25 ± 0.52	19.23 ± 0.68	9.72 ± 0.10	183.92 ± 1.72	14.43 ± 0.36
G15	126.08 ± 4.63	756 ± 8.19	78.03 ± 0.49	87.01 ± 0.64	14.25 ± 0.04	39.31 ± 0.76	9.03 ± 0.48	216.25 ± 6.00	66.02 ± 1.39
G16	187.34 ± 4.76	1,123 ± 10.69	62.23 ± 0.54	64.8 ± 0.30	10.33 ± 0.19	17.83 ± 1.25	10.67 ± 0.34	130 ± 6.12	44.57 ± 3.32
T1	46.67 ± 6.87	280 ± 14.74	79.60 ± 6.53	82.45 ± 7.59	18.16 ± 0.46	48.15 ± 0.26	12.38 ± 0.21	233.76 ± 8.90	29.94 ± 1.52
T2	26.17 ± 1.97	157 ± 11.84	75.8 ± 0.60	80.67 ± 0.42	7.46 ± 0.17	54.71 ± 0.86	8.27 ± 0.80	120.32 ± 4.33	19.03 ± 1.34
T3	38.50 ± 2.50	231 ± 6.76	87.02 ± 1.70	90.57 ± 0.93	6.7 ± 0.23	65.97 ± 1.03	12.84 ± 0.73	174.35 ± 4.56	33.96 ± 1.51

Note: WFSP: weight of fruit sample per plant (10 fruits) (g); TFWP: total fruit weight per plant (g); FT: fruit thickness (mm); FD: fruit diameter (mm); FW: fruit weight (g); NFC: number of fruit cavities (cavity); NSF: number of seeds per fruit (seed).

(Brix), and number of seeds varied among genotypes. The genotype with the highest yield was G15 (66.02), while the lowest was G14 (25.61). These data can be used to evaluate and determine the best genotypes based on the desired growth and yield characteristics.

### 3.2 ANOVA

The ANOVA results (Table 3) indicate that the variance attributed to lines had a significant effect on multiple traits, including the plant height, dichotomous height, stem diameter, days to flower, days to harvest, number of branches, number of flowers per bunch, number of fruits per bunch, total fruit weight per plant, fruit thickness, fruit diameter, fruit weight, number of fruit cavities, Brix, number of seeds per fruit, and yield. Genotype variance demonstrated highly significant effects (\*\*) on several traits, including the plant height (354.39), stem diameter (2.98), days to harvest (57.96), number of branches (4.72), number of flowers per bunch (2.06), number of fruits per bunch (4.29), number of inflorescences (39.62), number of fruits per plant (1264.61), the total number of fruits (45638.96), fruit thickness (32.82), fruit diameter (42.27), number of fruit cavities (65.76), fruit weight (4.37), Brix (0.70), number of seeds per fruit (598.56), and yield (89.24). The only trait that significantly affected genotype variance (\*) was days to flower (3.73). Additionally, the coefficient of variation (CV) showed that the character with the highest variability was the number of

**Table 3:** ANOVA and genetic parameters of the observed characters

Parameter	MSG	VG	VP	CV	H (%)
PH	354.39**	100.12	118.13	6.52	84.75
DHi	33.08	2.36	11.03	12.79	21.41
SD	2.98**	0.73	0.99	9.35	73.16
DF	3.73*	0.61	1.24	3.98	48.85
DH	57.96**	15.39	19.32	5.56	79.67
NB	4.72**	1.42	1.57	12.88	90.10
NFB	2.06**	0.52	0.69	13.62	76.15
NFPB	4.29**	1.38	1.43	13.37	96.71
NI	39.62**	11.57	13.21	15.96	87.60
WFSP	1264.61**	407.44	421.54	16.29	96.66
TFWP	45638.96**	15094.68	15212.99	7.91	99.22
FT	32.82**	8.08	10.94	12.94	73.84
FD	42.27**	10.58	14.09	13.69	75.07
NFC	65.76**	21.68	21.92	8.58	98.93
FW	4.37**	1.38	1.46	12.79	95.00
Brix	0.70**	0.16	0.23	13.61	69.14
NSF	598.56**	189.24	199.52	11.48	94.85
Yield	89.24**	28.40	29.75	15.27	95.47

Note: \*\* significant effect on 1% level, \* considerable impact on 5%, ns: not significant; MSg: means square genotypes; Vg: variance of genotypes; Vp: variance of phenotypes; CV: coefficient of variance (%); H: heritability (%); PH: plant height (cm); DHi: dichotomous height (cm); SD: stem diameter (mm); DF: day to flower (DAP); DH: day to harvest (DAP); NB: number of branches (branch); NFB: number of flowers per bunch (flower); NFPB: number of fruits per bunch (fruit); NI: number of inflorescences (fruit); WFSP: weight of fruit sample per plant (10 fruits) (g); TFWP: total fruit weight per plant (g); FT: fruit thickness (mm); FD: fruit diameter (mm); FW: fruit weight (g); NFC: number of fruit cavities (cavity); NSF: number of seeds per fruit (seed).

**Table 4:** Correlation analysis of tomato production based on characters significantly correlated with the yield

	DHe	SD	DF	DH	NB	NFB	NFPB	NI	WFSP	TFWP	FT	FD	NFC	FW	Brix	NSF	Yield
PH	-0.09ns	0.25*	0.05ns	-0.04ns	0.5**	0.02ns	0.19ns	0.35**	0.25*	0.25*	-0.2ns	-0.18ns	-0.35ns	0.12ns	-0.13ns	0.02ns	0.32**
DHi	1	-0.08ns	0ns	-0.28ns	-0.27ns	-0.06ns	0.05ns	-0.13ns	-0.02	0ns	0.14ns	0.14ns	0.04ns	-0.2ns	-0.06ns	0.01ns	0ns
SD		1	-0.26ns	-0.02ns	0.48**	-0.17ns	0.18ns	0.35**	0.3*	0.31**	-0.02ns	0ns	-0.16ns	0.23*	-0.04ns	0.05ns	0.32**
DF			1	0.35**	-0.24ns	-0.41ns	-0.17ns	-0.14ns	-0.22	-0.26ns	0.13ns	0.11ns	0.16ns	0.1ns	0.16ns	0.26*	-0.1ns
DH				1	-0.18ns	-0.41ns	-0.46ns	-0.12ns	-0.43	-0.47ns	0.1ns	0.11ns	0.24*	0.22ns	0.24*	0.35**	-0.39ns
NB					1	0.12ns	0.25*	0.5*	0.38**	0.39**	-0.12ns	-0.08ns	-0.41ns	0.42**	-0.17ns	0.01ns	0.48**
NFB						1	0.27*	0.17ns	0.32**	0.36**	-0.45ns	-0.46ns	-0.38ns	-0.43ns	-0.09ns	-0.5ns	-0.01ns
NFPB							1	0.19ns	0.9**	0.9**	-0.4ns	-0.37ns	-0.47ns	-0.04ns	-0.12ns	-0.25ns	0.63**
NI								1	0.58**	0.52**	-0.36ns	-0.36ns	-0.66ns	-0.03ns	-0.21ns	-0.41ns	0.28*
WFSP									1	0.98**	-0.49ns	-0.47ns	-0.63ns	-0.09ns	-0.21ns	-0.42ns	0.61**
TFWP										1	-0.5ns	-0.47ns	-0.65ns	-0.1ns	-0.23ns	-0.42ns	0.62**
FT											1	0.99**	0.72**	0.33**	0.15ns	0.42**	0.14ns
FD												1	0.72**	0.37**	0.11ns	0.43**	0.19ns
NFC													1	0.14ns	0.19ns	0.47**	-0.03ns
FW														1	0.09ns	0.46**	0.26*
Brix															1	0.22ns	-0.19ns
NSF																1	0.06ns

Note: \*\*highly significant effect; \*significant effect; ns: not significant; PH: plant height (cm); DHe: dichotomous height (cm); SD: stem diameter (mm); DF: day to flower (DAP); DH: day to harvest (DAP); NB: number of branches (branch); NFB: number of flowers per bunch (flower); NFPB: number of fruits per bunch (fruit); NI: number of inflorescences (fruit); WFSP: weight of fruit sample per plant (10 fruits) (g); TFWP: total fruit weight per plant (g); FT: fruit thickness (mm); FD: fruit diameter (mm); FW: fruit weight (g); NFC: number of fruit cavities (cavity); NSF: number of seeds per fruit (seed).

fruits per plant (16.29%). In comparison, the lowest variability was observed for days to flower (3.98%). These findings highlight the genetic contributions to these traits and provide a foundation for evaluating and selecting lines with desirable attributes in breeding programs.

The ANOVA and genetic parameters for various tomato characteristics revealed significant differences in most traits, including plant height, number of fruits, fruit weight, and yield, all of which demonstrated high heritability. This indicates that genetic factors play a major role in determining these traits. Conversely, traits such as dichotomous height and days to flower exhibited lower heritability, suggesting that their variation is more influenced by environmental factors. These findings emphasize the importance of traits like fruit number and yield for selection in breeding programs, particularly in lowland environments. Furthermore, the table illustrates an asymmetry in variance, with genotype variance being significantly greater than phenotype variance for the majority of traits.

### 3.3 Heritability

The identification of genetic parameters is concentrated on heritability (Table 3). In general, the heritability analysis results indicated a high heritability level. The heritability results align with the results obtained from ANOVA, in which the plant height, stem diameter, day to harvest, number of branches, number of flowers per bunch, number of fruits per bunch, number of inflorescences, number of fruits per plant, total number of fruits, fruit thickness, fruit

diameter, fruit weight, number of fruit cavities, brix, number of seeds per fruit and yield show high percentages, except for the dichotomous height and day to flower parameter, which shows a moderate rate.

### 3.4 Correlation analysis

The correlation analysis results (Table 4) reveal that the plant height, stem diameter, number of branches, number of fruit per bunches, number of inflorescences, number of fruits per plant, the total number of fruits, and number of fruit cavities are very significantly and positively correlated with production, with correlation values of 0.32, 0.32, 0.48, 0.63, 0.28, 0.61, 0.62, and 0.26, respectively. These traits will serve as key considerations for identifying tomato genotypes capable of achieving the desired production levels. Other characteristics did not show significant relationships with yield attributes, indicating that changes in these characteristics did not significantly affect the yield.

### 3.5 Path analysis

Based on the correlation analysis, observation parameters showing a positive correlation with productivity were further evaluated using path analysis (Table 5). The path analysis revealed highly significant positive direct effects on yield from key traits, including the number of fruits per bunch (1.28), the total fruit weight per plant (0.55), and the number of inflorescences (0.49). These results emphasize

**Table 5:** Path analysis of tomato production based on characters significantly correlated with the yield

Parameter	Direct effect	Indirect effect							Residual
		PH	SD	NB	NFpB	NI	WFSP	TFWP	NFC
PH	0.02		0.02	0.06	0.24	0.17	−0.35	0.14	0.02
SD	0.07	0.01		0.06	0.23	0.17	−0.43	0.17	0.04
NB	0.12	0.01	0.03		0.32	0.24	−0.54	0.21	0.08
NFpB	1.28	0.00	0.01	0.03		0.09	−1.28	0.49	−0.01
NI	0.49	0.01	0.02	0.06	0.24		−0.82	0.28	−0.01
WFSP	−1.42	0.01	0.02	0.04	1.15	0.28		0.54	−0.02
TFWP	0.55	0.01	0.02	0.05	1.15	0.25	−1.39		−0.02
NFC	0.18	0.00	0.02	0.05	−0.05	−0.01	0.13	−0.05	
		0.05	0.14	0.34	3.30	1.20	−4.68	1.78	0.09

Note: PH: plant height (cm); SD: steam diameter (mm); NB: number of branches (branch); NFpB: number of fruits per bunch (fruit); NI: number of inflorescences (fruit); WFSP: weight of fruit sample per plant (10 fruits) (g); TFWP: total fruit weight per plant (g); NFC: number of fruit cavities (cavity).

the strong direct influence of these traits on yield, making them critical factors for selection in crop improvement programs.

### 3.6 PCA

The PCA findings are summarized in Table 6 and Figure 2. According to the study, the proportion of variance explained by the first principal component (PC1) is 0.47 (47%), followed by PC2 at 0.23 (23%), PC3 at 0.11 (11%), PC4 at 0.08 (8%), PC5 at 0.06 (6%), PC6 at 0.03 (3%), PC7 at 0.02 (2%), PC8 at 0.01 (1%), and PC9 at 0.00 (0%). The eigenvector coefficients for the plant traits contributing to PC1

are as follows: plant height (−0.31), stem diameter (−0.31), number of branches (−0.39), number of fruits per bunch (−0.16), number of inflorescences (−0.37), number of fruits per plant (−0.42), total number of fruits (−0.42), number of fruit cavities (−0.08), and yield (−0.37). These values indicate the relative influence of each trait on the variability captured by PC1. Among the components, PC1 accounts for the largest share of the observed variability, making it the most significant in explaining differences within the dataset. This implies that the traits with high eigenvector coefficients in PC1 are critical for distinguishing the plant performance. Therefore, in this study, the selection index was primarily based on PC1, emphasizing its importance in identifying traits most strongly associated with variability in plant characteristics.

**Table 6:** PCA of tomato production character F1 generation

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
PH	−0.31	−0.13	−0.56	−0.21	−0.61	0.36	−0.08	0.16	0.00
SD	−0.31	−0.29	0.27	0.59	−0.20	0.06	0.54	0.23	0.01
NB	−0.39	−0.25	−0.36	−0.07	0.33	−0.12	0.31	−0.66	−0.03
NFpB	−0.16	0.57	−0.29	−0.19	0.29	−0.09	0.49	0.44	0.02
NI	−0.37	0.12	−0.30	0.53	0.17	−0.34	−0.55	0.17	0.03
WFSP	−0.42	0.24	0.33	−0.08	0.08	0.32	−0.16	−0.07	−0.72
TFWP	−0.42	0.24	0.34	−0.09	0.08	0.35	−0.13	−0.15	0.69
NFC	−0.08	−0.60	−0.01	−0.24	0.54	0.24	−0.13	0.46	0.02
Yield	−0.37	−0.16	0.31	−0.46	−0.26	−0.67	−0.02	0.14	0.02
Eigen values	4.21	2.09	0.95	0.73	0.52	0.23	0.19	0.08	0.00
Proportion	0.47	0.23	0.11	0.08	0.06	0.03	0.02	0.01	0.00
Cumulative	0.47	0.70	0.81	0.89	0.95	0.97	0.99	1.00	1.00

Note: PH: plant height (cm); SD: steam diameter (mm); NB: number of branches (branch); NFpB: number of fruits per bunch (fruit); NI: number of inflorescences (fruit); WFSP: weight of fruit sample per plant (10 fruits) (g); TFWP: total fruit weight per plant (g); NFC: number of fruit cavities (cavity); PCx is a latent variable, which is a new character consisting of the components of the observed characters.



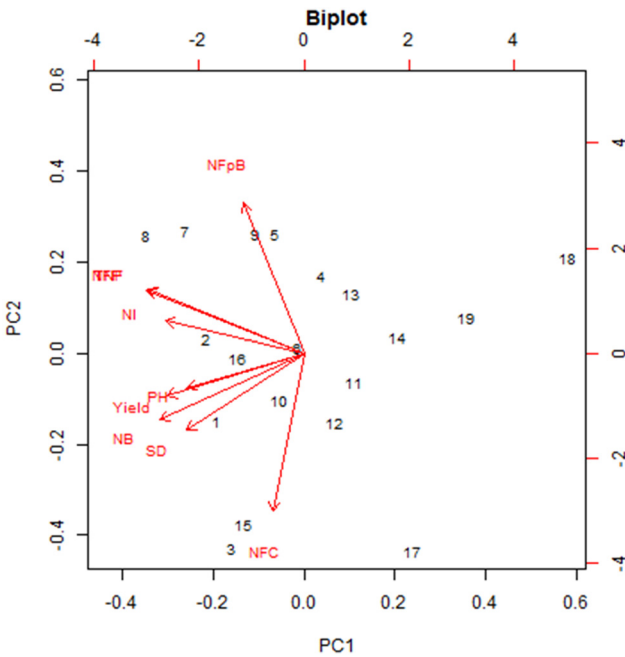


Figure 2: Biplot graph of PCA in relation to all genotypes.

3.7 Index analysis

The analysis results (Table 7) showed 12 F1 tomato plant lines with positive selection index values and were better

than their parents. Selection criteria include heritability, path analysis, and PCA to assess the potential of plant lines. These results have implications for the selection of plant lines for breeding programs, improving the quality and productivity of tomato plants. However, it is necessary to validate and monitor the performance of selected plant lines under different environmental conditions.

4 Discussion

ANOVA revealed significant differences among genotypes, enabling comparisons of genetic diversity, heritability, trait correlations, and regression analysis to identify specific characteristics with substantial to highly significant effects [20,28,29]. These findings highlighted that overall growth and production traits significantly influenced the F1 tomato population, including their variation within the population. Genetic diversity is crucial in selecting populations and enhancing desirable characteristics, as evidenced by the varied responses between tolerant and sensitive genotypes under different environmental conditions. This underscores the importance of these traits in determining the effectiveness of selection. Significant variance is a critical indicator of the potential success of selection for specific traits, with diversity within lines and comparisons

Table 7: Selection of F1 tomato lines based on the index value

Rank	Genotype	Actual value				Standardization				Index
		NFpB	NI	TFWP	Yield	NFpB	NI	TFWP	Yield	
1	G8	6.02	16.00	559.00	17.37	1.09	0.60	2.67	0.92	1.25
2	G7	6.42	18.67	370.00	15.46	1.59	1.35	1.10	0.50	0.96
3	G2	5.51	20.05	276.33	16.20	0.46	1.74	0.32	0.66	0.67
4	G9	6.36	17.25	330.67	12.32	1.51	0.95	0.77	-0.18	0.56
5	G1	4.51	17.36	268.17	18.77	-0.78	0.98	0.25	1.22	0.49
6	G5	6.67	12.32	272.33	14.64	1.89	-0.44	0.28	0.32	0.48
7	G6	5.13	13.89	279.33	17.53	-0.01	0.00	0.34	0.95	0.41
8	G15	3.80	11.67	252.00	22.01	-1.67	-0.63	0.11	1.93	0.27
9	G16	4.71	12.80	374.33	14.86	-0.54	-0.31	1.13	0.37	0.23
10	G3	4.49	14.72	234.33	17.45	-0.81	0.24	-0.03	0.93	0.20
11	G10	5.62	12.78	188.00	14.46	0.60	-0.31	-0.42	0.28	0.07
12	G4	5.25	13.38	287.33	11.99	0.13	-0.14	0.41	-0.26	0.01
13	G13	5.13	15.37	204.33	8.54	-0.01	0.42	-0.28	-1.01	-0.35
14	G12	4.62	15.97	170.83	9.96	-0.64	0.59	-0.56	-0.70	-0.41
15	G11	5.31	14.70	123.13	6.02	0.21	0.23	-0.96	-1.55	-0.69
16	T3	4.82	8.33	77.00	11.32	-0.40	-1.57	-1.34	-0.40	-0.78
17	G14	4.60	14.72	113.00	4.81	-0.67	0.24	-1.04	-1.82	-0.97
18	T1	3.65	8.19	93.33	9.98	-1.86	-1.61	-1.21	-0.69	-1.14
19	T2	5.07	5.69	52.33	6.35	-0.09	-2.32	-1.55	-1.48	-1.26

Note: NFpB: number of fruits per bunch (fruit); NI: number of inflorescences (fruit); TFWP: total fruit weight per plant (g).

between lines and control varieties being essential components for evaluating and refining line selection processes [16,30,31].

Based on the standard deviation analysis shown in Tables 1 and 2, there is significant variation among the genotypes regarding growth and fruit characteristics. In terms of growth, genotype G1 showed the highest plant height (363.67 cm), while genotype T3 had the lowest height (312.85 cm). According to research conducted by Zhu *et al.* [32] and Da Silva Oliveira *et al.* [33], the plant height is influenced by genetic and environmental factors, such as the availability of light and nutrients, which regulate growth hormones such as auxin and gibberellin. In addition, the time taken to harvest ranged from 171 to 210 days, indicating differences in the ripening speed between genotypes, an essential factor in determining crop production efficiency [34,35].

On the other hand, fruit characteristics also showed considerable differences between genotypes in fruit number and weight, fruit thickness and diameter, sweetness level (Brix), and the number of seeds in each fruit. Genotype G15 recorded the highest yield (66.02), while G14 had the lowest yield (25.61), indicating variations in productivity between genotypes. According to Rasheed *et al.* [36], yield is influenced by genetic factors and the environment, such as water availability, nutrients, and cultivation techniques applied. In addition, Brix content, which varies among genotypes, is an essential indicator in assessing fruit quality, especially in terms of flavor and marketability, as the level of sweetness is influenced by sugar accumulation during the ripening process [37,38].

Heritability values in Table 3 ranged from 21.41 to 99.22%, falling into medium to high categories. Among the traits analyzed, 16 exhibited high heritability values, while one trait displayed medium heritability. Traits with the highest heritability included the plant height (84.75%), stem diameter (73.16%), days to harvest (79.67%), number of branches (90.1%), number of flowers per bunch (76.15%), number of fruits per bunch (96.71%), number of inflorescences (87.6%), weight of fruit sample per plant (96.66%), the total fruit weight per plant (g) (99.22%), fruit thickness (73.84%), fruit diameter (75.07%), fruit weight (98.93%), number of fruit cavities (95%), Brix (69.14%), number of seeds per fruit (94.85%), and yield (95.47%). In contrast, traits such as dichotomous height (21.41%) and days to flower (48.85%) exhibited medium heritability. High heritability indicates that traits are predominantly influenced by genetic factors rather than environmental conditions, making them valuable selection criteria. According to Del Medico *et al.* [39] and Singh *et al.* [40], traits with high heritability are more likely to be inherited and can benefit from additive genetic effects, further enhancing selection efficiency.

Path analysis was used to measure the direct effects of specific traits on yield variation, complementing correlation analysis, which was insufficient for this study. The number of fruits per bunch (1.28), the total fruit weight per plant (g) (0.55), and the number of inflorescences (0.49) suggested that direct selection for these traits could enhance yield per plant [41,42]. Based on path analysis parameters that have a high direct effect, namely the number of fruits per bunch, the number of inflorescences, and the total fruit weight per plant, will be used in the index value to see which genotype has the best performance.

Based on the PCA results, PC1 emerged as the most suitable dimension for forming the selection index, supported by its eigenvalue exceeding 1, whereas PC2 and PC3 had eigenvalues below 1. An eigenvalue of 1 is a critical threshold for determining the effectiveness of a dimension in accumulating multi-trait diversity in PCA [27,43,44]. The selection index derived from the eigenvector values on PC1 was calculated as follows: selection index = 0.31 (plant height) + 0.31 (stem diameter) + 0.39 (number of branches) + 0.16 (number of fruits per bunch) + 0.37 (number of inflorescences) + 0.42 (weight of fruit sample per plant) + 0.42 (total fruit weight per plant) + 0.08 (number of fruit cavities) + 0.37 (yield). However, this index requires further refinement to incorporate factors such as gene action and its correlation with the primary trait.

Primary characters still dominate the selection process, indicating the need to adjust the selection index for secondary characters using PCA variance, path analysis, and correlation analysis. Though correlation analysis is rough, it remains effective for a few secondary characters and can be optimized through the determination value. The corrected index can characterize the optimal conditions in the lineage selection. Therefore, the determination value must be incorporated into the development of the selection index in this study, relying on the correlation determination value. Based on the correlation determination value, the selection index formed is as follows:

Selection Index =  $(0.42 \times 0.47 \times 0.55)$  total fruit weight per plant (g) +  $(0.37 \times 0.47 \times 0.49)$  number of inflorescences +  $(0.16 \times 0.47 \times 1.28)$  number of fruits per bunch.

The selection index analysis identified 16 lines for advancement based on their positive index values and performance relative to the control variety. These criteria align with methodologies reported in previous studies [45,46]. The analysis ultimately recommended 12 F1 tomato breeding lines for advancement, although further testing through within-family ANOVA is needed to evaluate the potential for transgressive segregation. The positive index value is a critical selection criterion at this stage of the F1 generation, where approximately 50% of the lines were selected. Early-

generation selection should remain flexible to ensure that promising lines are more likely to succeed, facilitating consistent progress in subsequent generations [27,47].

## 5 Conclusions

In conclusion, based on heritability analysis, correlation analysis, path analysis, and PCA, 12 tomato plant lines had higher growth and productivity than the parents and other targeted lines. The novelty of this research lies in its integrated use of heritability, correlation, path analysis, and PCA to identify critical yield-related traits. By employing these advanced analytical methods, the study provides a more targeted and efficient breeding strategy for improving tomato yield and quality, particularly in tropical and subtropical lowland regions. These findings provide valuable insights for improving tomato production through targeted breeding strategies and contribute to a more targeted and efficient approach to plant breeding, paving the way for sustainable improvements in tomato cultivation. However, this study has certain limitations. The evaluation was conducted under a single environmental condition, which may limit the applicability of the findings across varying agroecological regions. To build on these findings, future research should include multilocation trials to assess the stability and adaptability of the selected lines. This approach could be extended to support tomato biofortification programs, focusing on increasing the content of essential nutrients such as lycopene, beta-carotene, vitamin C, and minerals. This would not only improve yield and plant resilience but also contribute significantly to food and nutritional security, particularly in lowland.

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