International Journal of Plant & Soil Science

Volume 37, Issue 7, Page 164-177, 2025; Article no.IJPSS.138976
ISSN: 2320-7035

Genetic Variability and Correlation Studies in Tomato (*Lycopersicon esculentum* Mill.) Genotypes for Quality Contributing Traits

Sunil Kumar [a], Lila Bora [b] and Shubham [c*]

[a] Centre of Excellence for Vegetables (Indo-Israel Agricultural Project), Department of Horticulture, Government of Haryana, Ghraunda, 132114, India.
[b] Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana 125004, India.
[c] Department of Vegetable Science, Maharana Partap Horticultural University, Karnal, Haryana 132001, India.

Authors' contributions

This work was carried out in collaboration among all authors. Author SK was responsible for the methodology, investigation, conceptualization, and original draft preparation. Authors LB and Shubham reviewed and edited the manuscript. Authors SK and LB also contributed to reviewing and editing the final draft. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.9734/ijpss/2025/v37i75561

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://pr.sdiarticle5.com/review-history/138976

Original Research Article

Received: 23/04/2025
Accepted: 25/06/2025
Published: 02/07/2025

ABSTRACT

Plant traits are influenced by both genetics and environmental factors. For traits governed by quantitative inheritance, the total observed variation includes both heritable (additive) and non-heritable (dominance and epistasis) components. Tomato (*Solanum lycopersicum* L.) is an

**Corresponding author: E-mail: shubhammalik123@hau.ac.in;*

Cite as: *Kumar, Sunil, Lila Bora, and Shubham. 2025. "Genetic Variability and Correlation Studies in Tomato (Lycopersicon Esculentum Mill.) Genotypes for Quality Contributing Traits". International Journal of Plant & Soil Science 37 (7):164-77. https://doi.org/10.9734/ijpss/2025/v37i75561.*

important horticultural crop in the Solanaceae family, with a chromosome number of 2n = 2x = 24. It is widely consumed in various forms—fresh, in salads, as a cooking ingredient, or processed into products such as tomato paste, peeled or diced tomatoes, juices, and soups. Tomatoes are a rich source of vital nutrients, including vitamins, minerals, and antioxidants, which are essential for a healthy and balanced diet. Due to its nutritional and commercial value, there is a growing need to identify suitable genotypes that exhibit superior quality traits. The present study explores about genetic variability and correlation studies in tomato (*Lycopersicon esculentum* Mill.) genotypes for quality contributing traits. To explore different genotypes, a field experiment was conducted at the Regional Research Station, Karnal and Laboratory of the Department of Vegetable Science, CCS Haryana Agricultural University, Hisar, during the rabi season of 2016-17. Among all genotypes, maximum Fruit Firmness (1.75 kg/cm^2) found in Punjab Upma, Specific Gravity (1.30 g/cm^3) in genotype DVRT-5, Total Soluble Solids (5.50%) in genotype PNR-7, Ascorbic acid (26.39 mg/100g) in genotype DVRT-3 and Acidity (0.84%) in genotype DVRT-6. Based on this study, these genotypes can be used for sustainable tomato production. Thus, this study provides valuable insights for tomato growers and researchers. High heritability estimates for traits like acidity, specific gravity, fruit firmness, and ascorbic acid content indicate that these are largely controlled by genetic factors and can be effectively improved through selection. These findings provide valuable insights for the development of tomato genotypes with enhanced internal fruit quality.

Keywords: Tomato growers; horticultural crop; genotype; polyploidy.

1. INTRODUCTION

Genetic diversity is the range of different inherited traits within a species, which is the prerequisite of the breeding program. Genetic diversity leads to the selection of superior cultivars and their traits. Genetic variability is well defined as the formation of individuals varying in genotype (Rasheed et al., 2023). Tomato (*Solanum lycopersicum* L.) is a widely cultivated and economically important crop from the Solanaceae family, with a chromosome number of 2n = 2x = 24. Originally found in the wild regions of the Andes—spanning modern-day Peru, Ecuador, and Bolivia—tomatoes have since spread across the globe and are now grown in nearly every agricultural region (Patel & Udit, 2021). 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 (Zannat et al., 2023). Tomatoes are incredibly versatile. They're consumed fresh, featured in salads, cooked into meals, or processed into products like tomato paste, canned tomatoes, juices, and soups. Nutritionally, tomatoes are packed with essential vitamins, minerals, and antioxidants, which contribute significantly to a healthy diet (Dadi et al., 2024). They have been linked to various health benefits, including the management of chronic conditions such as diabetes, hypertension, and even certain cancers. Their high fiber content, low calories, and abundance of vitamins A, C, and E—as well as potent antioxidants like lycopene and β-carotene—make them a standout among functional foods (Omoyeni et al., 2024). Despite once being mistakenly thought poisonous, tomatoes have become one of the most consumed vegetables worldwide. Their appeal as a crop is due not only to their flavor and utility but also to their biological traits: a small genome, self-fertility, and low natural mutation rates. Tomato plants are largely self-pollinating and highly homozygous, making them easier to breed (Gautham et al., 2024).

Over the past five decades, significant breeding efforts have led to major improvements in tomato yield, quality, and adaptability. Hundreds of new varieties have been developed to suit diverse growing conditions and market needs. To develop varieties that perform well under specific environmental conditions or for targeted uses, it's essential to understand the existing genetic diversity within the crop. Without adequate variability, breeding progress is limited. Therefore, strategies like hybridisation, mutation breeding, and polyploidy are often used to broaden the genetic base. Plant traits are influenced by both genetics and environmental factors. For traits governed by quantitative inheritance, the total observed variation includes both heritable (additive) and non-heritable (dominance and epistasis) components. Hence, it's crucial to assess traits using tools like the genotypic and phenotypic coefficient of variation,

heritability estimates, and genetic advance. These parameters help predict the potential success of selection in breeding programs. Tomato yield is a complex trait, affected by several interrelated components. Effective breeding must consider not just yield itself, but also the individual traits contributing to it. The correlation coefficient assesses how closely different traits are related to each other and identifies the constituent traits from which genetic improvement for yield and yield traits that contribute to increasing yield (Arya et al., 2023; Ingole et al., 2024). Correlation and path coefficient analyses are valuable tools in this context. Correlation analysis shows the strength and direction of relationships between traits, while path analysis breaks these correlations down into direct and indirect effects. This helps breeders identify which traits to target for the greatest improvement in yield. The use of F1 hybrids is widespread in tomato cultivation. Identifying genetically diverse parents is key to maximising hybrid vigor (heterosis). Studying genetic divergence among existing varieties and germplasm collections allows breeders to select the best combinations for crossing. Traits linked to yield and quality are especially important when planning hybridisation strategies. Improving yield and quality in a self-pollinated crop like tomato typically involves selecting plants that naturally express desirable traits or creating new combinations through crossbreeding. For any effective breeding program, detailed information is needed on existing genetic variability, heritability, and the relationships between traits. Vegetable breeding focuses on both quantitative and qualitative improvements, so a solid understanding of genetics is essential. The success of breeding efforts depends on the level of variability present in the germplasm. Evaluating germplasm not only helps identify promising lines for traits like yield and quality but also opens the door to developing new, better-performing varieties that outperform their parents (Sekhar et al., 2008).

2. MATERIALS AND METHODS

2.1 Trial Location

The field trial was conducted at the Regional Research Station, Karnal and Laboratory of the Department of Vegetable Science, CCS Haryana Agricultural University, Hisar, during rabi season of 2016-17. The experimental field is situated at latitude of 29º 43' North and a longitude of 76º 58' East, with an elevation of 253 meters above mean sea level. It is located 5 kilometers north of the district headquarters in Karnal and 132 kilometers from the state capital, Chandigarh, positioned on the eastern side of the Jammu-Delhi Grand Trunk (GT) Road.

2.2 Properties of the Soil Prior to the Experiment Conducted

The soil of the experimental field was analysed for mechanical and chemical properties, and cropping history details are given below in Table 1.

Experimental details: The particulars of the present experiment entitled “Evaluation of tomato (*Lycopersicon esculentum* Mill.) genotypes for growth, yield and quality traits” are given below:

Number of genotypes investigated	: 22 along with one standard check
Experimental design	: Randomized block design (RBD)
Plot size	: 3 rows of 4.5 meter length
Spacing (row x plant)	: 60 cm x 45 cm
Replications	: Three
Crop season	: Rabi 2016-17

Observations:

Fruit firmness (kg/cm^2): Fruit firmness was determined after the rate of penetration of a needle driven into the fruits with the help of a digital penetrometer. Two readings were taken at two different positions on the flesh of each fruit.

Specific gravity (g/cm^3): A weighed number of fruits were placed in a graduated cylinder, and their volume was determined by water displacement. Specific gravity of fruits was obtained by dividing the weight of fruits (g) to the volume of fruit (ml).

Total soluble solid (%): The total soluble solids (TSS) of the fruit juice samples was determined with the help of refractrometer and expressed in percent at room temperature. The refractrometer was washed with distilled water and dried with blotting paper after every use.

Ascorbic acid (mg/100g fruit juice): The ascorbic acid content of fruit juice was estimated by 2, 6-dichlorophenol indophenols visual titration method of A.O.A.C (1975).

Acidity (%): Acidity was determined by titrating 5 ml of juice against 0.1 N sodium hydroxide (NaOH) using 1-2 drops of phenolphthalein as an indicator. NaOH was added slowly to the sample until finally one drop gave a pink colour lasting for a minute or longer. Appearance of pink colour was taken as end-point of titration. The acidity expressed in percent citric acid was estimated using the following formula:

$$Acidity\ (\%)\ = \frac{Titre\ x\ normality\ of\ alkali\ x\ Volume\ made\ x\ Eq.wt.of\ acid\ x100}{Vol.of\ sample\ taken\ for\ estimation\ x\ vol.of\ sample\ taken\ for\ titration\ x\ 1000}$$

2.3 Statistical Analysis

The collected data were systematically compiled and analyzed statistically to determine the extent of variability using variances and coefficients of variation (Burton and Devane, 1953). Correlation coefficient analysis will be carried out following the method of Al-Jibouri, et. al. (1958), while path coefficient analysis will be performed according to Dewey and Lu, (1959). Hierarchical cluster analysis was conducted using the approach proposed by Romesburg (1990).

2.4 Analysis of Variance

The analysis of variance was carried out for individual characters to test the significance of differences among the genotypes following the method given by Fischer and Yates (1963) and described by Panse and Sukhatme (1967). The following model was used:

$Y_{ij} = \mu + a_i + b_j + e_{ij}$

Where,

Y_{ij} = Observation for the i^{th} treatment in j^{th} block
μ = General mean
a_i= Effect of i^{th} treatment
b_j= Effect of j^{th} block
e_{ij}= Random error (uncontrolled variation) associated with i^{th} treatment in j^{th} block

List 1. Analysis of variance

Source of variation	d. f.	Mean Squares	Expected mean squares	F value
Replications	(r-1)	M_r	$\sigma_e^2 + g\sigma_r^2$	
Genotypes	(g-l)	M_g	$\sigma_e^2 + r\sigma_g^2$	M_g / M_e
Error	(r-l)(g-l)	M_e	σ_e^2	

Where,

r = Number of replications
g = Number of genotypes

Assumptions of the model:

The following assumptions were made during analysis of variance-

1. All the observations should be independent.
2. The different effects in the model should be additive.
3. Error involved in the population should be normally and independently distributed with mean zero and variance σ_e^2.

The significance of M_r and M_g was tested against M_e by 'F' test at 5 and 1 per cent level of significance.

2.5 Parameters of Variability

Mean

The mean value of each character was calculated by summing up of all the observations and dividing the total by corresponding number of observations:

$$\bar{x} = \frac{\sum Xij}{N}$$

Where,

$\sum x_{ij}$: Summation of i^{th} treatment in j^{th} replication
N: Total number of observations

Range

The minimum and maximum value of observation means for each character was taken as range.

Standard error (SE)

$$S.E.(d) = \sqrt{\frac{2MSe}{r}}$$

Where,

SE (d) = Standard error of difference of two means
MSe = Error mean sum of squares
r = Number of replications

Critical Difference (CD)

Critical difference was calculated for all the traits to compare the treatment means using difference of two means and tabulated value of t (p=0.05) at error degree of freedom using the following formula:

CD =SE(d) X 't' value at error degree of freedom

Where,

SE (d) = Standard error (difference of two means)

Coefficient of variation (CV)

The coefficient of variation as percentage of mean was estimated as mentioned bellow:

$$CV\ (\%) = \frac{S.D}{Mean} \times 100$$

Where,

CV (%) = Coefficient of variation in per cent,
S.D. = Standard deviation

Variances

Genotypic and phenotypic variances were computed as follows:

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{Treatment MSS} - \text{Error MSS}}{r}$$

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

Where,

r = Number of replications
M_g= Mean squares due to genotypes
M_e = Mean squares due to error
σ^2_g = Genotypic variance
σ^2_e = Environmental variance
σ^2_p = Phenotypic variance

2.6 Estimation of Coefficient of Variation

Genotypic and phenotypic coefficients of variation for different characters were calculated by the formula as suggested by Burton and Devane (1953).

$$\text{Genotypic coefficient of variability (GCV \%)} = \frac{\sigma^2 g\ X\ 100}{\bar{X}}$$

$$\text{Phenotypic coefficient of variability (PCV \%)} = \frac{\sigma^2 p\ X\ 100}{\bar{X}}$$

Where,

GCV = Genotypic coefficient of variation
PCV= Phenotypic coefficient of variation
$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

GCV and PCV was classified as low (0-10%), moderate (10-20%) and high (>20%) as suggested by Sivasubramanium and Madhavamenon, (1973).

2.7 Heritability (Broad Sense)

Heritability (broad sense) in per cent was estimated as per the formula given by Burton and Devane (1953), Johnson, et. al. (1955) and Hanson, et. al. (1956).

$h^2_{bs} = \frac{\sigma_g}{\sigma_p} \times 100$

Heritability was classified in following categories as suggested by Robinson, 1966

Low: 0-50%
Moderate: 50-70%
High: >70%

2.8 Genetic Advance

The expected genetic advance was calculated by the formula as suggested by Johnson, et. al. (1955).

Genetic advance (G.A.) = $k\sigma_p h^2$

Where,

GA= Genetic advance
σ_p = Phenotypic standard deviation
h^2 = heritability in broad sense
k = selection intensity

Genetic advance was classified as low (0-10%), moderate (10-30%) and high (>30%) (13).

2.9 Estimation of Correlation Co-efficient

Genotypic and phenotypic coefficients of correlation were determined by using the variance and covariance components as suggested by Al-Jibouri, et al., 1958.

$$r_{ij}(G) = \frac{\sigma^2 gij}{\sqrt{\sigma^2 gii \times \sigma^2 gjj}}$$

Where,

σ^2_{gij} = Genotypic co-variance of character x_i and x_j
σ^2_{gii} = Genotypic variance of character x_i
σ^2_{gjj} = Genotypic variance of character x_j

$$r_{ij}(P) = \frac{\sigma^2 pij}{\sqrt{\sigma^2 pii \times \sigma^2 pjj}}$$

Where,

σ^2_{pij}= Phenotypic co-variance of character x_i and x_j
σ^2_{pii}= Phenotypic variance of character x_i
σ^2_{pjj}= Phenotypic variance of character x_j

2.10 Path Coefficient Analysis

Path analysis was originally developed by Wright, 1921 and elaborated by Dewey and Lu, 1959. Path coefficient analysis splits the genotypic correlation coefficient into the measure of direct and indirect effects. It measures the direct and indirect contribution of independent variables on dependent variable.

Setting up of simultaneous equations

For estimation of various direct and indirect effects, a set of simultaneous equations were formed.

$r_{1y} = P_{1y} + r_{12} P_{2y} + r_{13}P_{3y} + \ldots\ldots\ldots\ldots\ldots + P_{1k}P_{ky}$
$r_{2y} = r_{21} P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots\ldots\ldots\ldots\ldots + r_{2k}P_{ky}$
$r_{iy} = r_{i1} P_{1y} + P_{i2} P_{2y} + r_{i3} P_{3y} + \ldots\ldots\ldots\ldots\ldots + r_{ik}P_{ky}$
$r_{ky} = r_{k1} P_{1y} + P_{k2} P_{2y} + r_{k3}P_{ky} + \ldots\ldots\ldots\ldots\ldots +. r_{kk}P_{ky}$

Solution of simultaneous equations

The above equations were written in a matrix form as under.

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ r_{iy} \end{pmatrix} \quad \begin{pmatrix} r_{11} & r_{12} & r_{13} & \ldots\ldots r_{1j} \\ r_{21} & r_{22} & r_{23} & \ldots\ldots r_{2j} \\ r_{31} & r_{32} & r_{33} & \ldots\ldots r_{3j} \\ r_{i1} & r_{i2} & r_{i3} & \ldots\ldots r_{ij} \end{pmatrix}$$

The technique given by Goulden, 1954 was followed for inversion (B-1) of B matrix. Path coefficients P_{jy} were obtained as follows:

$$P_{jy} = (B\text{-}1) \times (A)$$

The indirect effect for a particular character through other character was obtained by multiplication of direct path and particular correlation coefficient between those two characters, respectively.

$$\text{Indirect effect} = r_{ij} \times P_{jy}$$

Where,

i = 1, 2……..n
j = 1, 2……..n and
$P_{jy} = P_{1y}, P_{2y}.....P_{ny}$

The residual factor, *i.e.* the variation in yield unaccounted for (by such traits which could not be studied) was calculated as:

$$\text{Residual factor (x)} = 1\text{-}R^2$$

Where,

$R^2 = P_{1y}\, r_{1y} + P_{2y}\, r_{2y} + \ldots\ldots\ldots P_{ny}\, r_{ny}$
R^2 = Squared multiple correlation coefficients and the amount of variation in yield that can be accounted for by the yield component characters.

2.11 Genetic Divergence

2.11.1 Hierarchical cluster analysis

The data analysis was conducted using SPSS statistical software (version 20.0). To explore the relationships among the different genotypes, cluster analysis was used to evaluate both their similarities and differences. A hierarchical clustering approach, specifically the agglomerative method, was employed. In this approach, each genotype begins as its cluster, and similar clusters are gradually merged step by step until all genotypes form a single group. This technique helps in identifying relatively uniform groups within the overall dataset.

Among the various clustering strategies available—such as nearest and furthest neighbour, within- and between-group linkage, centroid and median clustering, and Ward's method—the between-group linkage method was chosen for this study. Also known as UPGMA (Unweighted Pair Group Method Using Arithmetic Averages), this method was selected based on the guidelines provided by Romesburg (1990).

UPGMA determines the distance between two clusters by averaging all pairwise distances between the genotypes in one cluster and those in another. In SPSS, these distances are calculated using the Proximity procedure. To quantify similarity and dissimilarity, the City Block distance (or Manhattan distance) was applied. This metric sums the absolute differences between the corresponding values of all variables for each pair of genotypes.

$$\text{City Block Distance } (X,Y) = \sum \left| X_i - Y_i \right|$$

Once the distance matrix was calculated, the clustering process began by identifying and merging the two genotypes with the smallest absolute distance between them. From there, the distance between clusters was computed as the average of all pairwise distances between the members of one cluster and those of another. For example, if cases 1 and 2 are grouped into Cluster A, and cases 3, 4, and 5 make up Cluster B, the distance between Clusters A and B would be the average of the distances between each pair: (1,3), (1,4), (1,5), (2,3), (2,4), and (2,5).

This agglomerative approach continued step-by-step, progressively merging genotypes or clusters based on their similarities until all entries were grouped into a single overarching cluster. Once a cluster was formed, it remained fixed and could only merge with other clusters—it couldn't be broken apart or reassigned.

After completing the clustering, a dendrogram was produced to visually represent the clustering process. This diagram was created using rescaled distances to maintain proportionality between steps, ensuring that even large distance values did not distort the overall structure. The dendrogram effectively illustrated the order in which genotypes were combined and showed the corresponding distance values at each stage of merging.

Determining the ideal number of clusters is somewhat subjective. However, one practical approach is to examine a portion of the dendrogram where the number of clusters remains unchanged across a broad range of similarity coefficients. A wide plateau in this region typically indicates separated clusters and makes the result less sensitive to minor data

variations. This method, as recommended by Romesburg (1990), was used to determine the final number of clusters in the analysis.

3. RESULTS AND DISCUSSION

Under laboratory conditions, several key quality parameters were evaluated, including fruit firmness (kg/cm³), specific gravity (g/cm³), total soluble solids (TSS, %), ascorbic acid content (mg/100g of fruit juice), and titratable acidity (%).

The findings revealed that most of these quality traits varied significantly across the different tomato genotypes. As shown in Table 3, fruit firmness demonstrated highly significant variation. The highest firmness value (1.75 kg/cm³) was recorded in the genotype 'Punjab Upma', which was statistically comparable to 'Castle Rock' (1.51 kg/cm³). On the other hand, the lowest firmness was observed in 'Punjab Tropics' (0.69 kg/cm³).

In terms of specific gravity, the genotype 'DVRT-5' had the highest value (1.30 g/cm³), followed by 'Pusa Sadabahar' (1.16 g/cm³), while 'Punjab Upma' showed the lowest (0.97 g/cm³). The total soluble solids content was also genotype-dependent, with 'PNR-7' exhibiting the highest TSS (5.50%) and 'Punjab Upma' the lowest (3.77%).

Ascorbic acid content, a key nutritional trait, ranged significantly among genotypes. 'DVRT-3' recorded the highest concentration (26.39 mg/100g), whereas 'Punjab Ratta' had the lowest (20.48 mg/100g).

Titratable acidity ranged from 0.54% to 0.84%. The highest acidity level was observed in 'DVRT-6' (0.84%), closely followed by 'H-86' (0.81%), while the lowest was recorded in 'DVRT-1' (0.54%). Among these traits, fruit firmness plays a particularly important role in determining internal fruit quality. It is closely linked to the thickness of the pericarp and has a direct influence on shelf life, marketability, and consumer acceptance. Firmness affects both the commercial value of the tomato and how it is perceived in terms of texture and overall eating quality (Khan et al., 2017).

3.1 Coefficient of Variation

In the current study, the highest genotypic coefficient of variation (GCV) was observed for fruit firmness, registering at 23.90%. Traits such as titratable acidity showed moderate GCV (11.50%), while lower GCV values were noted for ascorbic acid (6.65%), specific gravity (6.78%), and total soluble solids (8.13%).

Similarly, the phenotypic coefficient of variation (PCV) was also highest for fruit firmness (28.03%), followed by the number of marketable fruits per plant (28.62%), total number of fruits per plant (23.02%), and polar diameter (21.81%). Moderate PCV was observed for acidity content (12.33%), whereas lower PCV values were recorded for ascorbic acid (7.88%), specific gravity (7.89%), and total soluble solids (10.75%).

These results (Table 4) indicate that high heritability does not always correlate with high genetic advance. Across all traits, PCV values were consistently higher than their corresponding GCV values, suggesting that environmental influences play a role in the expression of these characteristics. Similar findings were reported by Shankar et al. (2013) and Meitei et al. (2014), who also noted higher PCV values than GCV across traits.

A large gap between PCV and GCV for certain traits implies they are more susceptible to environmental variation. In this investigation, both GCV and PCV values were generally high for most traits, indicating the presence of substantial genetic variability—an observation supported by earlier studies such as those by Islam et al. (2012) and Kumar et al. (2017).

Ultimately, the success of selection in a breeding program depends not only on the extent of variability in a trait but also on how effectively that trait can be passed on to the next generation. This makes heritability a critical factor in determining the efficiency of genetic improvement.

3.2 Heritability and Genetic Advance

Heritability reflects the degree to which traits are passed from parents to their offspring and plays a key role in determining the consistency between genotypes and their phenotypic expression. The broad-sense heritability provides insight into how reliably a trait can be identified based on phenotype alone. According to Burton and DeVane (1953) and Mitra et. al. (2023), heritability not only measures the extent of genetic variation but, when considered alongside the genotypic coefficient of variation (GCV),

helps predict the potential for improvement through selection. Essentially, heritability serves as an index of how effectively a particular trait can be transmitted to the next generation.

However, relying on heritability alone is not sufficient when designing a breeding strategy. To gain a clearer understanding of how a trait is genetically controlled and what improvement can be expected from selection, heritability must be considered together with genetic advance. Genetic advance, especially when expressed as a percentage of the mean, indicates the potential for achieving measurable progress in the desired trait.

In the current study, both broad-sense heritability and genetic advance as a percentage of the mean were calculated for all observed traits and are presented in Table 4.

The results showed that high heritability estimates were observed for acidity content (86.41%), specific gravity (79.44%), fruit firmness (72.53%), and ascorbic acid content (71.27%). Total soluble solids showed a moderate heritability of 57.24%.

Table 1. Detailed description of Mechanical, and chemical analysis of soil and cropping history

Mechanical analysis of the soil			
Sr. No.	**Soil parameters**	**Proportion in percentage**	**Methods and reference**
1	Sand	56	International pipette method (Piper, 1950)
2	Silt	32	
3	Clay	12	
4	Soil texture	Sandy – loam	
Chemical analysis of the soil at the start of the experiment			
S. No.	Soil Parameters	Value	Methods and reference
1	pH (1:2 soil: water suspension)	7.86	Potentiometric method (Jackson, 1973)
2	EC (ds/m) at 25^0C (1:2 soil: water suspension)	0.12	Conductometric method (Jackson, 1973)
3	Organic Carbon (%)	0.40	Wet oxidation method (Walkley and Black, 1934)
4	Available nitrogen (kg/ha)	158	Kjeldhal- distillation method (Subbiah and Asija, 1956)
5	Available phosphorus (kg/ha)	11	$NaHCO_3$ extraction and colorimetry method (Olsen et al., 1954)
6	Available potassium (kg/ha)	197	N NH_4OAC extraction and Flame photometry method, (Jackson 1973)

Table 2. List of germplasm lines and standard released varieties included in the research programme

Sr. No.	**Genotype**	**Sr. No.**	**Genotype**
1.	DVRT-1	13.	PNR-7
2.	DVRT-2	14.	Palam Pink
3.	DVRT-3	15.	Punjab Ratta
4.	DVRT-5	16.	Pusa Ruby
5.	DVRT-6	17.	Punjab Tropics
6.	DVRT-8	18.	Pusa Uphar
7.	Arka Vikas	19.	Punjab Upma
8.	Castle Rock	20.	Sel-7
9.	NT-8	21.	S-12
10.	Punjab Chhuhara	22.	H-86
11.	P.H.S	23.	Pusa Sadabahar ©
12.	Punjab Kesari		

Table 3. Mean performance of different genotypes for various traits in tomato

Observations / Treatments	Fruit firmness (kg/cm^2)	Specific gravity (g/cm^3)	TSS (%)	Ascorbic acid (mg/100g)	Acidity (%)
DVRT-1	0.96	1.01	4.83	22.19	0.54
DVRT-2	0.91	1.03	4.03	21.09	0.56
DVRT-3	0.96	1.02	4.23	26.39	0.77
DVRT-5	0.77	1.30	4.70	22.35	0.80
DVRT-6	0.99	1.10	4.43	22.58	0.84
DVRT-8	1.02	1.21	4.17	22.70	0.78
Arka Vikas	0.95	1.13	4.97	21.52	0.73
Castle Rock	1.51	1.02	4.50	23.59	0.61
NT-8	1.09	1.04	4.06	22.55	0.72
Punjab Chhuhara	1.16	0.97	4.30	24.38	0.59
P.H.S	0.77	1.17	5.03	26.38	0.76
Punjab Kesari	0.87	1.14	4.83	25.42	0.69
PNR-7	0.87	1.07	5.50	22.57	0.71
Palam Pink	0.87	1.11	4.83	23.40	0.63
Punjab Ratta	1.22	1.08	5.07	20.48	0.78
Pusa Ruby	0.97	1.20	4.77	20.80	0.62
Punjab Tropics	0.69	1.20	4.43	23.66	0.68
Pusa Uphar	0.95	1.14	4.83	23.36	0.79
Punjab Upma	1.75	1.07	3.77	24.95	0.69
Sel-7	0.80	1.09	4.17	23.47	0.68
S-12	0.62	1.03	4.76	24.62	0.75
H-86	0.94	1.16	4.17	23.44	0.81
Pusa Sadabahar (C)	1.16	1.16	4.43	22.42	0.72
General Mean	0.99	1.11	4.56	23.36	0.71
C.D. @ 5%	0.24	0.07	0.53	1.63	0.05
SE(m)	0.08	0.02	0.19	0.57	0.02
SE(d)	0.12	0.03	0.26	0.81	0.03
C.V.	14.70	3.57	7.03	4.22	4.55

Table 4. Range, mean, coefficient of variations, heritability and genetic advance as % of mean for 6 characters in tomato

Characters	Mean	Range		Variance		Coefficient of variation		Heritability% (broad sense)	Genetic advance
		Min	max	Genotypic	Phenotypic	Genotypic	Phenotypic		As *percent* of mean
Number of locules per fruit	3.68	2.44	5.22	0.69	0.95	22.55	26.42	72.83	39.66
Fruit firmness (kg/cm2)	0.99	0.62	1.75	0.06	0.08	23.90	28.03	72.53	41.91
Specific gravity (g/cm3)	1.11	0.97	1.30	0.01	0.01	6.78	7.89	79.44	12.75
Total Soluble Solids (%)	4.56	3.77	5.50	0.14	0.24	8.13	10.75	57.24	12.67
Ascorbic acid (mg/100g)	23.36	20.48	26.39	2.41	3.39	6.65	7.88	71.27	11.57
Acidity (%)	0.71	0.54	0.84	0.01	0.01	11.50	12.33	86.41	21.98

In terms of genetic advance as a percentage of the mean, fruit firmness recorded the highest value (41.91%), suggesting a strong potential for improvement through selection. Moderate genetic advance was noted for titratable acidity (21.98%), specific gravity (12.75%), total soluble solids (12.67%), and ascorbic acid content (11.57%).

Heritability estimates alone provide a general idea of trait transmission, but when paired with genetic advance, they offer a much more reliable prediction of how effective selection will be. In this study, traits showing high heritability along with high genetic advance and high GCV—such as yield-related traits—indicate that additive gene effects are likely responsible. This suggests that straightforward selection would be an effective breeding approach for improving these traits. These findings are consistent with those reported by Sahanur et al. (2011), Madhurina and Paul (2012), and Tasisa et al. (2012).

Furthermore, traits like plant height, number of marketable fruits per plant, and polar diameter exhibited high heritability combined with high genetic advance as a percentage of the mean, and moderate GCV. Although these traits display less genetic variability, their improvement through selection remains quite feasible. Similar results were also reported by Dar and Sharma (2011), Mohamed et al. (2012), and Saleem et al. (2013).

4. CONCLUSION

The present study revealed considerable genetic variability among the tomato genotypes for various quality traits. Punjab Upma recorded the highest fruit firmness, while Punjab Tropics showed the lowest. DVRT-5 had the maximum specific gravity, and DVRT-3 was superior in ascorbic acid content. Fruit firmness exhibited the highest genotypic and phenotypic coefficients of variation, as well as the greatest genetic advance, suggesting its high potential for selection in breeding programs. High heritability estimates for traits like acidity, specific gravity, fruit firmness, and ascorbic acid content indicate that these are largely controlled by genetic factors and can be effectively improved through selection. These findings provide valuable insights for the development of tomato genotypes with enhanced internal fruit quality.

FUNDING

This research did not receive any specific funding from public, commercial, or non-profit funding agencies.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

ACKNOWLEDGEMENTS

The authors sincerely appreciate the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar, for providing the opportunity to conduct this research.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

A.O.A.C. (1975). Official Methods of Analysis. Publication of the Association of Analytical Chemists, Washington DC, USA., 401-404 and 829-831.

Al-Jibouri, H.A., Miller, P.A. and Robinson, H.F. (1958). Genotypic and environmental variances and co-variances in upland cotton crosses of inter specific origin. *Agronomy Journal*, 50: 633-637.

Arya, Dhaneshvari, Akhilesh Kumar Pal, Anand Kumar Singh, Bajrang Kumar, and Avneesh Rathour. 2023. “Studies of Correlation and Path Coefficients for Tomato Yield and Quality Attributes (*Solanum Lycopersicum* L.)”. International Journal of Environment and Climate Change 13 (10):381-88.

Burton, G.W. and Devane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundi-nancea*) from replicated clonal materials. *Agronomy Journal,* 45: 478-481.

Dadi, T.L., Dejene, T.B., Habtamu G.M. and Damtew A. (2024). Evaluation and participatory variety selection of tomato (*Lycopersicum esculentum* Mill.) for yield and related traits. *Cross Current International Journal of Agriculture and Veterinary Sciences*. 6(1): 1-5.

Dar, R.A. and Sharma, J.P. (2011). Genetic variability studies of yield and quality traits in tomato (*Solanum lycopersicum* L.). *International Journal of Plant Breeding and Genetics*, 5: 168-174.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of yield components of the crested wheat grass seed production. *Agronomy Journal*, 51: 515-518.

Fischer, R.A. and Yates, F. (1963). Statistical Tables for Biological, Agricultural and Medical Research, Oliver and Boyd Edinburgh. pp. 55-57.

Gautham, S.S.P., Shashikanth, E., Fakrudin B., Raveendra, J., Vasudeva, KR, Basavarajappa, M.P. and Vinay, K.M.M. (2024). Exploring genetic variability in tomato for yield and quality traits. *International Journal of Research in Agronomy*, 7(12): 321-325.

Goulden, C.H. (1954). Methods of statistical analysis. John Wiley and Sons. Inc., New York, 2nd Edition.

Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating population of Korean Lespedeza. *Agronomy Journal,* 48: 268-272.

Hossain, M.F., Ara, N., Islam, M.R., Hossain, J. and Ahkter, B. (2014). Effect of different sowing dates on yield of tomato genotypes. *International Journal of Agricultural Research Innovation and Technology,* 4(1): 40-43.

Ingole, D.B., Shinde B.D., Karmarkar M.S., Sanap P.B., and Kadam J.J. 2024. "Studies on Seasonal Incidence and Correlation of Tomato Aphids, Aphis Gossypii (Glover) in Konkan Region". Journal of Experimental Agriculture International 46 (12):589-96. https://doi.org/10.9734/jeai/2024/v46i123165.

Islam, M.S., Mohanta, H.C., Rafii, M.Y. and Malek, M.A. (2012). Genetic variability and trait relationship in cherry tomato (*Solanum lycopersicum* L.). *Bangladesh Journal Botany*, 41(2): 163-167.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Journal of Agronomy*, 47: 314-318.

Khan, M.A., Butt, S.J., Nadeem, F., Yousaf, B. and Javed, H.U. (2017). Morphological and physico biochemical characterization of various tomato cultivars in a simplified soilless media, 62(2): 139-143.

Kumar, V., Sahay, S., Nirgude, V., Kumari, A., Singh, R.S., Mir, H., Mahesh, S.S., Kumar, V. (2017). Assessment of genetic variability among different genotypes of Cape gooseberry (*Physalis peruviana* L.) in India. *Journal of Applied and Natural Science*, 9(3): 1735-1739.

Madhurina, M. and Paul, A. (2012). Studies on genetic variability and characters association of fruit quality parameters in tomato. *Horticulture Flora Research Spectrum*, 1(2): 110-116.

Meitei, K.M., Bora, G.C., Senjam, J.S. and Anjan, K.S. (2014). Morphology based genetic variability analysis and identification of important characters for tomato (*Solanum lycopersicum* L.) crop improvement. *American Eurasian Journal of Agricultural and Environmental Sciences*, 14(10): 1105-1111.

Mitra, D.S., Kumar, S., Yadav, S., Verma, S. and Yadav, L. (2023). Assessment of Genetic Variability, Heritability and Genetic Advance among Different Characters in Tomato [*Solanum lycopersicum* (Mill.) Wettsd]. *International Journal of Environment and Climate Change*, 13(11): 2742–2750.

Mohamed, S.M., Ali, E.E. and Mohamed, T.Y. (2012). Study of heritability and genetic variability among different plant and fruit characters of tomato (*Solanum lycopersicum* L.). *International Journal of Science and Technology Research*, 1(2): 55-58.

Olsen, S.R., Cole, C.V., Watanabe, F.S. and Dean, L.A. (1954). Estimation of available phosphorous in soils by extraction with sodium bicarbonate. *Circulation from United States Department of Agriculture*, 939. USDA, Washington, D.C.

Omoyeni D.I., Fayeun, L.S., Odiyi, A.C., Olatunji, O.S. and Oluwadare, L.V. (2024). Genetic diversity studies for quantitative traits of twenty Six tomato (*Solanum lycopersicon* M.) genotypes using principal component analysis and single linkage cluster analysis. *Nigerian Journal of Horticultural Science*, 28(3): 1118-2733.

Panse, V.G. and Sukhatme, P.V. (1967). Statistical methods for agricultural workers. ICAR, New Delhi.

Patel, P. and Kumar, U. (2021). Studies on correlation and path coefficient analysis for yield and quality traits in tomato. *The Pharma Innovation Journal*, 10(9): 1914-1918.

Piper, C.S. (1950). Soil and water analysis. Published by University Adelaide, Australia.

Rasheed, A., Ilyas, M., Khan, T. N., Mahmood, A., Riaz, U., Chattha, M. B., ... & Qari, S. H. (2023). Study of genetic variability, heritability, and genetic advance for yield-related traits in tomato (Solanum lycopersicon MILL.). Frontiers in Genetics, 13, 1030309.

Robinson, H.F. (1966). Quantitative genetics in relation to breeding on centennial of Mendelism. *Indian Jounal of Genetics*. 26: 171-187.

Romesburg, H.C. (1990). Cluster Analysis for Researchers. Krieger Publishing Co., Malabar, Florida.

Sahanur R., Lakshman, S.S. and Maitra, N.J. (2012). Genetic variability and heritability studies in tomato (*Lycopersicon esculentum* Mill.). *International Journal of Plant Science,* (Muzaffarnagar), 7(1): 58-62.

Saleem, M.Y., Iqbal, Q. and Asghar, M. (2013). Genetic variability, heritability, character association and path analysis in F1 Hybrids of tomato. *Pakistan Journal of Agricultural Sciences,* 50(4): 649-653.

Sekhar, L., Prakash, B.G., Salimath, P.M., Sridevi, O. and Patil, A.A. (2008). Genetic diversity among some productive hybrids of tomato (*Lycopersicon esculentum* Mill.). *Karnataka Journal of Agricultural Science,* 21(2): 264-265.

Shankar, A., Reddy, R.V.S.K., Sujatha, M. and Pratap, M. (2013). Genetic variability studies in F1 generation of tomato (*Solanum lycopersicum* L.). *IOSR Journal of Agriculture and Veterinary Science,* 4(5): 31-34.

Sivasubramanium, J. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. *Madras Agriculture Journal,* 12: 15-16.

Subbaiah, B.V. and Asija, G.L. (1956). A rapid procedure for the determination of available nitrogen in the soil. *Current Science*, 25: 259-260.

Tasisa, J., Belew, D. and Bantte, K. (2011). Variability, heritability and genetic advance in tomato (*Lycopersicon esculentum* Mill.). genotypes in West Shoa, Ethiopia, American- Eurasian. *Journal of Agriculture and Environment Science*, 11(1): 87-94.

Walkley, A. and Black C.A. (1934). An examination of the digtjareff method for determination of soil organic matter and a proposed modification of chronic acid titration method. *Soil Science*, 37: 29-39.

Wright, S. (1921). Correlation of causation. *Journal of Agriculture Research*, 20: 257-287.

Zannat, A., Hussain, M. A., Abdullah, A. H. M., Hossain, M. I., Saifullah, M., Safhi, F. A., ... & Hossain, M. S. (2023). Exploring Genotypic Variability and Interrelationships among Growth, Yield, and Quality Characteristics in Diverse Tomato Genotypes. Heliyon, 9(8).

Peer-review history:
The peer review history for this paper can be accessed here:
https://pr.sdiarticle5.com/review-history/138976