



Variability Analysis for Growth and Yield Contributing Traits in Tomato (*Lycopersicon esculentum* Mill.) Grown in Karnal Conditions of Haryana

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Authors' contributions

This work was carried out in collaboration among all authors. Author SK performed methodology, investigated the work, conceptualized the study, wrote and prepared the draft of the manuscript. Authors Lb and Shubham reviewed and edited of the manuscript. Authors SK and LB reviewed the final draft and edited of the manuscript. All authors read and approved the final manuscript.

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ABSTRACT

Tomato (*Solanum lycopersicum* L.) is a major crop in the Solanaceae family with a chromosome number of $2n = 2x = 24$, is widely consumed in multiple forms—fresh, in salads, as a culinary ingredient, or processed into products like tomato paste, diced or peeled tomatoes, juices, and

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soups. It is a rich source of essential nutrients such as vitamins, minerals, and antioxidants, contributing significantly to a balanced and healthy diet. Given its nutritional importance and commercial value, identifying high-performing genotypes with desirable growth and yield traits is crucial. The present study estimated the variability analysis for Growth and Yield Contributing Traits in Tomato (*Lycopersicon esculentum* Mill.) Grown in Karnal Conditions of Haryana. A field experiment was conducted during the rabi season of 2016–17 at the Regional Research Station, Karnal, and the Laboratory of the Department of Vegetable Science, CCS Haryana Agricultural University, Hisar. Among the evaluated genotypes, Punjab Upma recorded the highest plant height (60.78 cm), NT-8 had the maximum number of branches per plant (7.00), Punjab Chhuhara showed the largest polar diameter (6.76 cm), and Castle Rock had the highest equatorial diameter (5.11 cm). The thickest pericarp (7.44 mm) was observed in DVRT-8, while DVRT-5 produced the highest number of marketable fruits per plant (38.53). The maximum marketable fruit weight per plant (1356.70 g) was found in PNR-7. Additionally, the minimum number of unmarketable fruits per plant (7.90) was recorded in S-12, and the earliest flowering (36.67 days to 50% flowering) was observed in Pusa Ruby. These findings highlight the potential of certain genotypes for improving tomato productivity and sustainability. Most traits showed high heritability and genetic advance, particularly those related to yield and plant architecture, suggesting the presence of additive gene action and good potential for genetic improvement through selection. These results underline the importance of exploiting superior genotypes for enhancing tomato productivity in breeding programs. The study offers useful insights for both researchers and growers in selecting suitable genotypes for enhanced tomato cultivation.

Keywords: *Lycopersicon esculentum*; antioxidants; phenolic compounds; functional food.

1. INTRODUCTION

“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. 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). “Tomato (*Lycopersicon esculentum* Mill.) is a significant crop belonging to the Solanaceae family, with a chromosome number of $2n = 2x = 24$. It originated in its wild form in the Andean region of South America, specifically in Peru, Ecuador, and Bolivia, and is now cultivated worldwide” (Patel and Udit, 2021). “Tomato contains a number of nutritive elements, almost double compared to apple. Tomatoes are a good source of vitamins A, C and E and minerals that are very good for the body and protect the body against diseases. The tomato is composed mainly of

water (approximately 90%), soluble and insoluble solids (5-7%), citric and other organic acids, and vitamins and minerals” (Akhter & Najnine, 2022). “Tomatoes are eaten fresh on their own, used in salads, included as ingredients in numerous recipes, or processed into various products such as tomato paste, whole peeled tomatoes, diced varieties, and different types of juices and soups. It consists of essential nutrients, including vitamins, minerals, and antioxidants, all of which play a vital role in maintaining a well-balanced human diet” (Dadi et. al., 2024). “It offers significant health benefits and plays a role in disease prevention. It is used in managing conditions such as diabetes, hypertension, and cancer. Additionally, it is commonly incorporated into stews and vegetable salads. With its low calorie content and high levels of fiber, minerals, phenolic compounds, and vitamins A, C, and E, along with powerful antioxidants like lycopene and β -carotene, it is considered an excellent functional food that meets essential nutritional requirements” (Omoyeni et. al., 2024). “Tomatoes are one of the most widely consumed vegetables globally and hold significant importance as a processing crop due to their remarkable qualities. Although once mistakenly believed to be poisonous, tomatoes are now cultivated across nearly every continent and are a staple ingredient in a wide variety of dishes, thanks to their unique characteristics. Tomato plants possess a small genome, are self-fertile,

and exhibit a low rate of genetic mutations. Their ease of breeding is further supported by their self-pollinating nature and high level of homozygosity" (Gautham et. al., 2024). "So far, the efforts of many vegetable breeders have resulted in spectacular improvements in yield and quality characters. As a result of these efforts, hundreds of new cultivars have been developed in last 50 years to meet the diverse needs. Considering the potential of this crop, there is a need to develop varieties suitable for cultivation under specific agroecological conditions and also for specific end use. A thorough knowledge of the amount of genetic variability existing for various characters is essential for initiating the crop improvement programme. With limited variability, much improvement cannot be achieved; hence, the breeder will have to enrich the germplasm or create greater variability through hybridization, mutation and polyploidy breeding. The phenotypic expression of plant characters is mainly controlled by the interaction genetic makeup of a plant and the environment in which it is grown. Further, the genetic variance of any quantitative trait is composed of additive (heritable) and non-additive variance including dominance and epistasis (non-allelic interaction), hence, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance" (Dadi et. al., 2024). "The genetic advance can also be used to predict the efficiency of selection. Yield is a complex character, and selection for yield and yield components deserves considerable attention. A crop-breeding programme aimed at increasing the productivity requires consideration not only of yield but also of its components that have a direct or indirect bearing on yield. For any effective selection programme, it would be desirable to consider the relative magnitude of various characters associated with yield. Correlation and path coefficient analysis give an insight into the genetic variability present in the population. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which the selection can be based for improvement in yield. Path analysis splits the correlation coefficients into direct and indirect effects of a set of dependent variables on the independent variable, thereby aids in the selection of elite genotype. Based on these studies, the quantum importance of

individual characters is marked to facilitate the selection programme for better gains. The commercial F1 hybrids are common in tomato and the selection of new parents for higher heterosis is a continuous process. Generally, the genetically diverse plants are expected to give high hybrid vigour. Hence, it necessitates the study of genetic divergence among the 2 existing varieties and germplasm for the identification of parents for the hybridisation programme" (Dadi et. al., 2024). "The information on genetic divergence of various traits, particularly of those that contribute to yield and quality, would be of most useful in planning the breeding programme. An improvement in yield and quality in a self-pollinated crop like tomato is normally achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridisation. Information on the nature and extent of variability present in genetic stocks, heritability, genetic advance and interrelationship among various characters is prerequisite for framing any selection programme. The breeding of vegetable crops is primarily concerned with the improvement of both quantitative and qualitative plant characters; thus, complete knowledge of genetics is very essential in a vegetable breeding programme for obtaining desired results. The success of vegetable breeding depends on the extent and the magnitude of variability existing in the germplasm. Variability is the basic requirement for successful genetic improvement in a crop. Germplasm evaluation studies would help in the identification of genetic material for quality and yield traits in crop plants, effectively to generate noble variants having adaptation and yielding potential far better than parental types" (Sekhar et. al., 2008).

2. MATERIALS AND METHODS

2.1 Trial Location

The field trial was conducted at 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 29° 43' North and a longitude of 76° 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.

2.1.1 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

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°C (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 <i>et al.</i> , 1954)
6	Available potassium (kg/ha)	197	N NH ₄ OAC extraction and Flame photometry method, (Jackson 1973)

2.2 Observations

Plant height (cm): The height of five randomly selected individual plants was measured at final harvest stage from the ground to tip of the plant and replication-wise wise the average plant height of each genotype was worked out.

Number of branches per plant: The total number of fruiting branches of five plants was counted at the time of final picking and then averaged for the number of branches per plant.

Days to 50% flowering: The number of days taken from transplanting to the anthesis of first flowers on 50% plants of each genotype per

replication was recorded and the average was expressed as days to 50% flowering.

Days to first picking: The number of days taken from transplanting to picking of first ripened fruits of each genotype per replication was recorded and the average was expressed as days to first picking.

Days to last picking: The number of days taken from transplanting to the picking of last ripened of each genotype per replication was recorded and the average was expressed as days to last picking.

Polar Diameter (cm): Fruits polar diameter was measured from stalk end to blossom end with the help of digital Vernier calliper.

Equatorial diameter (cm): Fruits equatorial diameter was measured from fruit breadth at highest bulged portion of the fruit with the help of digital Vernier calliper.

Pericarp thickness (mm): Fruit pericarp thickness was measured after cutting the fruits transversely with the help of digital Vernier calliper.

Number of marketable fruits per plant: Fruits of good quality were identified and counted from five marked plants and their average was calculated.

Weight of marketable fruits per plant: Fruits of good quality were identified and collected from five marked plants and their weight was calculated and their average was taken.

Number of unmarketable fruits per plant: Fruits of inferior quality and diseased one were identified and counted from five marked plants and their average was calculated.

Weight of unmarketable fruits per plant: 18 Fruits of inferior quality and diseased one were identified and collected from five marked plants and their weight was calculated and their average was taken.

Total number of fruits per plant: The fruits harvested from five selected plants of each genotype from all the pickings were summed up separately and then averaged per plant.

Yield of fruits per plant (g): The yield of fruits per plant of individual genotypes was counted by adding up the weight of marketable fruits per plant into the weight of unmarketable fruits per plant obtained from all pickings and averaged.

Yield of fruits per hectare (q): The weight of fruits collected from each plot all plants in all replications, was recorded and then converted into quintal per hectare.

Number of locules per fruit: The randomly five fruits of each genotype were selected and

dissected transversely. The number of locules per fruit was counted and averaged.

Fruit firmness (kg/cm²): 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 fruits.

Specific gravity (g/cm³): 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).

2.3 Statistical Analysis

The collected data were systematically compiled and analysed 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).

2.3.1 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

Chart 1. Analysis of variance

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

2.3.2 Parameters of variability

Mean

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

$$\bar{x} = \frac{\sum X_{ij}}{N}$$

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:

$$CD = SE(d) \times 't' \text{ value at error degree of freedom}$$

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 below:

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

Where,

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

2.3.3 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

2.3.4 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).

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

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

Where,

GCV = Genotypic coefficient of variation
 PCV = Phenotypic coefficient of variation
 σ^2_g = Genotypic variance
 σ^2_p = Phenotypic variance

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

2.3.5 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%

2.3.6 Genetic advance

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

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

2.4.1 Setting up of simultaneous equations

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

$$\begin{aligned} r_{1y} &= P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \dots + P_{1k} P_{ky} \\ r_{2y} &= r_{21} P_{1y} + P_{2y} + r_{23} P_{3y} + \dots + r_{2k} P_{ky} \\ r_{iy} &= r_{i1} P_{1y} + P_{iy} + r_{i3} P_{3y} + \dots + r_{ik} P_{ky} \\ r_{ky} &= r_{k1} P_{1y} + P_{k2} P_{2y} + r_{k3} P_{3y} + \dots + r_{kk} P_{ky} \end{aligned}$$

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).

2.3.7 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

2.4 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.

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 (C)
12.	Punjab Kesari		

2.4.2 Solution of simultaneous equations

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

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

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

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

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,

$$\begin{aligned} i &= 1, 2, \dots, n \\ j &= 1, 2, \dots, n \text{ and} \\ P_{jy} &= P_{1y}, P_{2y}, \dots, P_{ny} \end{aligned}$$

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

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

Where,

$$R^2 = P_{1y} r_{1y} + P_{2y} r_{2y} + \dots + P_{ny} r_{ny}$$

R^2 = Squared multiple correlation coefficients and the amount of variation in yield that can

be accounted for by the yield component characters.

2.5 Genetic Divergence

2.5.1 Hierarchical cluster analysis

This analysis was performed using SPSS statistical software (version 20.0). Cluster analysis was employed to assess the similarity and divergence among genotype pairs within the dataset. The hierarchical clustering method, specifically the agglomerative approach, was applied in this study. In this method, each genotype initially starts as an individual cluster, and clusters are progressively merged based on their similarity until all genotypes are grouped into a single cluster. This approach facilitates the identification of relatively homogeneous groups of genotypes.

Among various clustering techniques—such as between-group linkage, within-group linkage, nearest neighbor, furthest neighbor, centroid clustering, median clustering, and Ward's method—the between-group linkage method, also known as UPGMA (Unweighted Pair Group Method Using Arithmetic Averages), was selected for this study, following the recommendation of Romesburg, (1990).

UPGMA calculates the distance between two clusters as the average of all pairwise distances between members of one cluster and those of the other. These distances are computed using the Proximity procedure in SPSS. To measure similarity and dissimilarity, the City Block distance (also known as Manhattan distance) was used, which is defined as the sum of the absolute differences between corresponding values of all variables for two given cases.

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

After computing the distance matrix, clustering was initiated by merging the two cases with the smallest absolute distance between them. The distance between any two clusters was then calculated as the average of all pairwise distances between members of one cluster and members of the other. For instance, if cases 1 and 2 form Cluster A, and cases 3, 4, and 5 form Cluster B, the distance between Clusters A and B is determined by averaging the distances between the following pairs: (1,3), (1,4), (1,5), (2,3), (2,4), and (2,5). This agglomerative process continued until all cases were merged into a single cluster. At each stage, either individual cases were added to existing clusters or clusters were combined. Once a cluster was formed, it remained intact and could only merge with other clusters—it could not be separated or reassigned.

Following the clustering process, a dendrogram was generated using rescaled distances. This scaling preserved the ratio between steps and minimised issues related to large distance values, thereby enhancing the visualisation of similarities and differences among the objects. The dendrogram displayed the sequence of cluster combinations and the corresponding distance coefficients at each step.

Determining the optimal number of clusters is inherently subjective. However, selecting a point on the dendrogram within a broad range of resemblance coefficients where the number of clusters remains stable. A wide range suggests well-separated clusters and reduces sensitivity to error (Romesburg, 1990). This guideline was followed to decide the final number of clusters retained in the analysis.

3. RESULTS AND DISCUSSION

Under field conditions plant height (cm), number of branches per plant, number of fruits per plant, fruit diameter(cm), fresh fruit yield per plant (kg/ha), and marketable fresh fruit yield per hectare (ton) were measured.

The results of this study showed that most growth and yield-related traits were significantly influenced by the different genotypes. As presented in Table 3, plant height exhibited a highly significant variation among genotypes. The tallest plants (145.22 cm) were observed in the genotype Pusa Ruby, which was statistically

comparable to PNR-7. In contrast, the shortest plants were recorded in the genotype Punjab Upma (60.78 cm). The number of branches per plant was maximum in genotype NT-8 (7.00), which was statistically at par with S-12 (6.67) and minimum was reported in genotypes Castle Rock and P.H.S. (3.89). The maximum and minimum polar diameter was observed in genotypes Punjab Chhuhara (6.76 cm) and Sel-7 (3.36 cm), respectively. Whereas, the maximum and the minimum equatorial diameters were observed in genotypes Castle Rock (5.35 cm) and DVRT-8 (3.47 cm). Pericarp thickness was observed to be maximum in genotype DVRT-8 (7.44 cm) and minimum in genotype Pusa Ruby (3.24 cm). These differences in growth parameters are likely attributed to the genetic variation among the genotypes. Similar findings were reported by Dadi et al. (2024), who observed variation in plant height among four tomato varieties, suggesting that genetic differences played a key role.

The yield and yield contributing characters like the maximum number of marketable fruits per plant, were found in genotype DVRT-5 (38.53) and number of unmarketable fruits per plant in genotype P.H.S. (13.22). Weight of marketable fruits per plant was observed to be maximum in genotype PNR-7 (1356.70 g) and the weight of unmarketable fruits per plant in genotype Castle Rock (660.34 g). The yield of fruits per plant and yield of fruits per hectare was recorded as maximum in genotype Castle Rock (1388.74 g and 462.91 q) and minimum was recorded in genotype S-12 (981.33 g and 327.11 q). The differences in yield and yield-contributing traits may be attributed to the genetic variability among the varieties, as each possesses a distinct genetic makeup. Similar observations were made by Hossain et al. (2014) and Dadi et al. (2024), who reported variations in fruit diameter and fruit number while assessing different tomato varieties.

3.1 Coefficient of Variation

Genotypic coefficient of variation: The highest magnitude of genotypic coefficient of variation (GCV) was observed for traits plant height (32.50%) followed by number of marketable fruits per plant (23.90%). Moderate estimates of GCV was observed for traits total number of fruits per plant (19.15%), number of branches per plant (17.86%), weight of unmarketable fruits per plant (15.49%), yield of fruits per plant (15.09%), yield of fruits per hectare 34 (14.93%), number of

unmarketable fruits per plant (13.36%), weight of marketable fruits per plant (13.08%), days to 50% flowering (11.59%).

Phenotypic coefficient of variation: The highest estimates of phenotypic coefficient of variation (PCV) was observed for traits plant height (32.88%) followed by number of marketable fruits per plant (28.62%), total number of fruits per plant (23.02%) and polar diameter (21.81%) whereas, the moderate PCV was observed for traits number of branches per plant (19.48%), number of unmarketable fruits per plant (18.18%), weight of unmarketable fruits per plant (16.59%), yield of fruits per plant (15.36%), yield of fruits per hectare (15.16%), weight of marketable fruits per plant (13.21%), days to 50% flowering (12.55%).

From the results of the present investigation (Table 4), it is clear that it is not always necessary for high heritability to be associated with high genetic advance. Phenotypic coefficient of variation (PCV) was always higher than the corresponding genotypic coefficient of variation (GCV) for all the traits, denoting environmental factors influencing their expression to some degree or other on these traits. Shankar et al., (2013) and Meitei et al., (2014) also observed higher PCV value than GCV values for all the traits. Wide difference between PCV and GCV for some of the traits implied that they are more susceptible to environmental fluctuations than others. In the present investigation high magnitude of GCV and PCV was observed for almost all traits. Similar results were also observed by Islam et al., (2012) and Kumar et al., (2017). The efficacy of selection for any character depends not only on the magnitude of variability present for the character but also on the extent to which it can be transferred from parents to the offspring i.e. heritability of the trait.

Heritability and Genetic Advance: The uniformity between parents and their progeny is governed by heritability. The magnitude of heritability in the broad sense indicates the reliability with which a genotype can be recognised by its phenotypic expression. According to Burton and DeVane (1953), heritability is a measure of heritable variation and is helpful in predicting expected amount of improvement to be achieved through selection together with the genotypic coefficient of variation. Heritability acts as an index of transmissibility of a particular character to its

offsprings. However, the knowledge of heritability alone does not help in formulating concrete breeding programme. Genetic advance along with heritability helps to ascertain the possible genetic control for any particular trait and provide the knowledge about the expected gain for a particular trait after selection. The nature and extent of the inherent ability of a genotype for a character is an important parameter determining the extent of improvement of any crop species. The heritability in a broad sense and genetic advance as per cent of the mean were worked out for all the characters presented in (Table 4).

Based on above characterization, it was evaluated from Table 4 that the high magnitude of heritability (broad sense) was noticed in almost all characters like weight of marketable fruits per plant (98.11%) followed by plant height (97.72%), yield of fruits per hectare (97.04%), yield of fruits per plant (96.48%), days to 50% flowering (85.22%), number of branches per plant (84.06%), equatorial diameter (76.71%), weight of unmarketable fruits per plant (71.24%), number of marketable fruits per plant (69.75%) and total number of fruits per plant (69.24%) whereas, the moderate heritability was observed for total soluble solids (57.24%), number of unmarketable fruits per plant (54.03%).

In the present investigation, the magnitude of genetic advance as percentage of mean was observed high for plant height (66.19%) followed by polar diameter (42.45%), number of marketable fruits per plant (41.12%), number of branches per plant (33.74%), total number of fruits per plant (32.84%), yield of fruits per plant (31.28%) and yield of fruits per hectare (30.30%). It was recorded as moderate for weight of marketable fruits per plant (28.11%), days to 50% flowering (22.03%), weight of unmarketable fruits per plant (29.36%), number of unmarketable fruits per plant (20.20%) and equatorial diameter (19.36%).

Heritability estimates together with genetic advance is more important than heritability alone to predict the effects of selection. In reality, heritability and genetic advance are two complementary aspects of crop improvement through selection. In the present investigation, high heritability coupled with high genetic advance as percent of mean and high GCV was observed for yield attributing traits. These results are in accordance with the findings of Sahanur et al., (2011); Madhurina and Paul (2012) and Tasisa et al., (2012).

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

Observations Treatments	Plant height (cm)	Number of branches per plant	Days to 50% flowering	Polar diameter (cm)	Equatorial diameter (cm)	Number of marketable fruits per plant	Weight of marketable fruits per plant (g)	Number of un-marketable fruits per plant	Yield of fruit per plant (g)	Yield of fruit per plant (g)
DVRT-1	64.22	4.33	52.00	4.36	4.30	17.71	849.89	11.85	1191.63	1191.63
DVRT-2	73.67	4.44	56.33	4.49	5.11	20.76	1117.05	10.53	1549.28	1549.28
DVRT-3	61.67	6.33	50.67	3.76	3.65	30.73	931.68	12.33	1157.78	1157.78
DVRT-5	70.78	5.00	47.33	3.55	3.63	38.53	1100.78	16.82	1421.14	1421.14
DVRT-6	68.55	4.45	46.67	5.67	4.60	18.49	1126.87	11.24	1590.71	1590.71
DVRT-8	65.33	4.56	45.00	5.37	3.47	20.11	1047.69	11.98	1493.97	1493.97
Arka Vikas	81.11	5.23	40.00	4.10	4.67	20.18	958.93	11.36	1311.44	1311.44
Castle Rock	62.33	3.89	43.00	5.61	5.35	13.11	1139.72	8.98	1800.06	1800.06
NT-8	64.33	7.00	45.00	3.99	4.29	19.78	1151.15	11.07	1512.38	1512.38
Punjab Chhuhara	70.44	4.44	44.33	6.76	3.64	24.62	1066.01	10.71	1336.84	1336.84
P.H.S	66.22	3.89	39.33	3.50	4.15	22.47	911.14	13.22	1224.29	1224.29
Punjab Kesari	63.55	4.89	53.67	3.60	4.38	25.29	988.75	12.98	1297.13	1297.13
PNR-7	144.66	5.00	52.33	4.01	5.05	19.02	1356.70	10.45	1756.57	1756.57
Palam Pink	67.22	4.00	37.67	4.43	4.52	15.02	801.79	11.40	1144.41	1144.41
Punjab Ratta	80.22	4.33	49.00	5.44	4.56	17.44	1093.54	9.62	1465.26	1465.26
Pusa Ruby	145.22	5.00	36.67	3.41	4.20	25.76	932.14	12.31	1283.38	1283.38
Punjab Tropics	70.56	4.56	45.67	3.51	4.44	23.22	916.35	12.98	1333.52	1333.52
Pusa Uphar	131.00	4.78	43.00	3.44	3.93	26.20	1036.81	10.00	1331.75	1331.75
Punjab Upma	60.78	4.56	51.67	5.40	4.59	17.40	1067.39	12.13	1477.76	1477.76
Sel-7	66.29	6.41	38.00	3.36	4.08	19.46	835.64	11.53	1177.02	1177.02
S-12	66.89	6.67	44.00	3.66	3.99	18.51	745.59	7.90	981.33	981.33
H-86	76.89	4.11	41.67	4.20	4.68	16.98	1169.79	12.27	1733.43	1733.43
Pusa Sadabahar (C)	69.22	4.11	46.33	4.25	4.60	21.69	1045.71	10.98	1369.96	1369.96
General mean	77.88	4.87	45.62	4.34	4.34	21.41	1017.00	11.51	1388.74	1388.74
C.D. @ 5%	6.38	0.63	3.64	0.37	0.42	5.56	32.10	2.33	65.41	65.41
SE(m)	2.23	0.22	1.27	0.13	0.15	1.95	11.23	0.82	22.87	22.87
SE(d)	3.16	0.31	1.80	0.18	0.21	2.75	15.88	1.15	32.34	32.34
C.V.	4.96	7.78	4.83	5.10	5.91	15.74	1.91	12.27	2.85	2.85

Table 4. Range, mean, coefficient of variations, heritability and genetic advance as % of mean for 21 characters in tomato

Characters	Mean	Range		Variance		Coefficient of variation		Heritability% (broad sense)	Genetic advance As percent of mean
		Min	max	Genotypic	Phenotypic	Genotypic	Phenotypic		
Plant height (cm)	77.88	60.78	145.22	640.80	655.74	32.50	32.88	97.72	66.19
Number of branches per plant	4.87	3.89	7.00	0.76	0.90	17.86	19.48	84.06	33.74
Days to 50% flowering	45.62	36.67	56.33	27.94	32.78	11.59	12.55	85.22	22.03
Days to first picking	101.55	92.33	109.44	21.82	29.89	4.60	5.38	73.01	8.10
Days to last picking	136.62	127.33	144.33	22.02	30.01	3.43	4.01	73.38	6.06
Polar diameter (cm)	4.34	3.36	6.76	0.85	0.90	21.20	21.81	94.53	42.45
Equatorial diameter (cm)	4.34	3.47	5.35	0.22	0.28	10.73	12.26	76.71	19.36
Pericarp thickness (mm)	5.33	3.24	7.44	1.11	1.16	19.76	20.23	95.42	40.10
Number of marketable fruit per plant	21.41	13.11	38.53	26.19	37.54	23.90	28.62	69.75	41.12
Weight of marketable fruits per plant (g)	1071.00	745.59	1356.70	19630.37	20007.92	13.08	13.21	98.11	28.11
Number of unmarketable fruits per plant	11.51	7.90	16.82	2.37	4.38	13.36	18.18	54.03	20.20
Weight of unmarketable fruits per plant (g)	371.74	226.11	660.34	9696.05	9770.21	26.49	26.59	99.24	54.36
Total number of fruits per plant	32.92	22.09	55.36	39.76	57.43	19.15	23.02	69.24	32.84
Yield of fruit per plant (g)	1388.74	981.33	1800.06	43928.62	45530.16	15.09	15.36	96.48	31.28
Yield of fruit per hectare (q)	462.91	327.11	600.01	4777.50	4923.07	14.93	15.16	97.04	30.30

It may be due to the presence of additive gene action for these characters and hence, simple selection would be the most appropriate breeding method for their improvement. Traits like plant height, number of marketable fruits per plant and polar diameter revealed high heritability associated with high genetic advance as percent of the mean and moderate GCV indicated lesser variability but they can be improved through selection. Similar findings were also observed by Dar and Sharma (2011); Mohamed et al., (2012) and Saleem et al., (2013).

4. CONCLUSION

The current study demonstrated considerable genetic variability among the assessed tomato genotypes in terms of growth, yield, and associated traits. Significant differences were found in characteristics such as plant height, number of branches, fruit size, and pericarp thickness, reflecting a wide genetic base. Genotypes like Pusa Ruby, NT-8, DVRT-8, and Castle Rock excelled in specific traits, with 'Castle Rock' achieving the highest yield per plant and per hectare, and DVRT-5 recording the greatest number of marketable fruits per plant. High genotypic and phenotypic coefficients of variation, especially for plant height and marketable fruit number, indicated strong genetic diversity. Most traits showed high heritability and genetic advance, particularly those related to yield and plant architecture, suggesting the presence of additive gene action and good potential for genetic improvement through selection. These results underline the importance of exploiting superior genotypes for enhancing tomato productivity in breeding programs.

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.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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