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

**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 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/cm2) found in Punjab Upma, Specific Gravity (1.30 g/cm3) 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

**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).

**Materials and Methods**

**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.

**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/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 fruit.

**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).

**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 (%) = 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

**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).

**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:

Yij = μ+ ai + bj+ eij

Where,

Yij = Observation for the ith treatment in jth block

μ = General mean

ai= Effect of ith treatment

bj= Effect of jth block

eij= Random error (uncontrolled variation) associated with ith treatment in jth block

**List 1: Analysis of variance**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Source of variation** | **d. f.** | **Mean Squares** | **Expected mean squares** | **F value** |
| Replications | (r-1) | Mr | σe2 + gσr2 |  |
| Genotypes | (g-l) | Mg | σe2 + rσg2 | Mg / Me |
| Error | (r-l)(g-l) | Me | σe2 |  |

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 *σe2*.

The significance of Mr and Mg was tested against Me by ‘F’ test at 5 and 1 per cent level of significance.

**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:

Where,

∑ xij : Summation of ith treatment in jth 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)**

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 (%) =

Where,

CV (%) = Coefficient of variation in per cent,

S.D. = Standard deviation

**Variances**

Genotypic and phenotypic variances were computed as follows:

Where,

r = Number of replications

Mg= Mean squares due to genotypes

Me = Mean squares due to error

σ2g = Genotypic variance

σ2e = Environmental variance

σ2p = Phenotypic variance

**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).

Where,

GCV = Genotypic coefficient of variation

PCV= Phenotypic coefficient of variation

σ2g = Genotypic variance

σ2p = Phenotypic variance

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

**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).

h2bs= x 100

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

Low : 0-50%

Moderate : 50-70%

High : >70%

**Genetic advance**

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

Genetic advance (G.A.) = kσph2

Where,

GA= Genetic advance

σp = Phenotypic standard deviation

h2 = heritability in broad sense

k = selection intensity

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

**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.

rij(G) =

Where,

σ2gij = Genotypic co-variance of character xi and xj

σ2gii = Genotypic variance of character xi

σ2gjj = Genotypic variance of character xj

rij (P) =

Where,

σ2pij= Phenotypic co-variance of character xi and xj

σ2pii= Phenotypic variance of character xi

σ2pjj= Phenotypic variance of character xj

**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.

|  |  |  |
| --- | --- | --- |
| r1y | = | P1y + r12 P2y + r13P3y+ + P1kPky |
| r2y | = | r21 P1y + P2y + r23P3y+ + r2kPky |
| riy | = | ri1 P1y + Pi2 P2y + ri3 P3y+ + r ikPky |
| rky | = | rk1 P1y + Pk2 P2y +rk3Pky+ +. rkkPky |

**Solution of simultaneous equations**

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

r1y r11 r12 r13 ……r1j

r2y r21 r22 r23 ……r2j

r3y r31 r32 r33 ……r3j

riy ri1 ri2 ri3 …….rij

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

Pjy = (B-1) x (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.

Indirect effect = rij x Pjy

Where,

i = 1, 2…………..n

j = 1, 2…………..n and

Pjy = P1y, P2y......Pny

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

Residual factor (x) = 1-R2

Where,

R2 = P1y r1y + P2y r2y + ………..Pny rny

R2 = Squared multiple correlation coefficients and the amount of variation in yield

that can be accounted for by the yield component characters.

**Genetic divergence**

**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.

**City Block Distance (X,Y)** = **∑ │Xi – Yi│**

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.

**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).

**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.

**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%.

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).

**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.

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**Author Contribution**

Methodology, Investigation, Conceptualization, writing-original and draft preparation was done by SK. Reviewing and Editing was done by LB and S. Reviewing the final draft and editing was done by SK and LB. All authors contributed to the article and approved the submitted version.

**Conflict of interest**

There is no conflict of interest among authors.

**Disclaimer (Artificial intelligence)**

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**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 250C  (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 | NaHCO3 extraction and colorimetry method (Olsen *et al.*, 1954) |
| 6 | Available potassium (kg/ha) | 197 | N NH4OAC 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 (C) |
| 12. | Punjab Kesari |  |  |

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Observations**  **Treatments** | **Fruit firmness**  **(kg/cm2)** | **Specific gravity**  **(g/cm3)** | **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 |