



# Selection of Elite Lines in Triple Cross F<sub>1</sub> Population of Tomato (*Solanum lycopersicum* L.) through Principal Component Analysis

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## ABSTRACT

The study was conducted during August, 2024–February, 2025 at the ICAR-Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh, India to select superior lines from early segregating population. Principal component analysis was conducted to identify major contributing agro-horticultural traits and superior lines in a selected triple cross tomato population. Tomato, one of the most important vegetable crops worldwide due to its high economic value, nutritional significance and wide adaptability. The scree plot revealed that the first five principal components (PCs) accounted for 86.7% of the total variability, with PC1 and PC2 explaining 36.7% and 20.6%, respectively. Together, these two components captured 57.3% of the overall variation, indicating their effectiveness in summarizing population diversity. The biplot and loading matrix demonstrated that fruit length, fruit diameter, fruit weight and pericarp thickness exhibited strong positive loadings on PC1, identifying it as the primary yield and fruit size axis. Total soluble solids and number of locules showed moderate positive association with PC1 and strong loading on PC5 (0.770), indicating partial independence of fruit quality traits from yield components. Genotypic distribution in the biplot identified TCH-55, TCH-125 and TCH-57 as superior for yield attributes, while TCH-13 and TCH-7 were promising for quality improvement. The clear separation of yield, vegetative, and quality traits across principal components highlighted the multidimensional variability generated through triple cross breeding and provided a strategic framework for simultaneous selection of high-yielding and quality genotypes.

**KEYWORDS:** Scree plot, principal components, biplot, triple cross breeding

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**Data Availability Statement:** Legal restrictions are imposed on the public sharing of raw data. However, author have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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## 1. INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the most economically important vegetable crops worldwide and serves as a model species for genetic and genomic studies among horticultural crops (Kumar et al., 2020). It is cultivated extensively for its high nutritional value, being a rich source of lycopene,  $\beta$ -carotene, vitamins (A and C), minerals, and antioxidants (Kandasamy, 2017; Yadav et al., 2021). Despite its importance, modern cultivated tomato possesses a relatively narrow genetic base due to domestication bottlenecks and intensive selection, which limits the scope for further yield and quality enhancement (Ashrafi et al., 2009). Hybrid breeding has played a pivotal role in tomato improvement programs, particularly through the exploitation of heterosis (Yerasu et al., 2025a). Conventional single cross hybrids involve two inbred parents, whereas triple cross hybrids are developed by crossing a single cross hybrid with a third genetically diverse parent (Labroo et al., 2021). This strategy increases genetic recombination and allows the accumulation of favourable alleles from three distinct parental lines. Triple cross  $F_1$  hybrids are expected to express enhanced hybrid vigour, wider adaptability, and improved trait combinations due to the interaction of additive, dominance, and epistatic gene effects (Fujimoto et al., 2018). Such breeding designs are particularly useful when integrating disease resistance genes from diverse genetic backgrounds (Yerasu et al., 2025b). Characterization of early segregating populations such as triple cross  $F_1$  s is a crucial step in determining the extent of genetic variability and identifying superior genotypes for selection. In complex hybrid populations such as triple cross  $F_1$  s, multiple agronomic, morphological, and quality traits are evaluated simultaneously. These traits are often correlated; interpreting univariate statistical methods is inadequate. Therefore, multivariate statistical techniques are essential to effectively summarise and interpret large datasets (Hair, 2011). Among multivariate approaches, Principal Component Analysis (PCA) is one of the most widely used tools in plant breeding and genetic diversity studies (Jolliffe and Cadima, 2016). PCA transforms a set of correlated variables into a smaller number of orthogonal (uncorrelated) principal components, each explaining a portion of the total variance present in the dataset (Zhao et al., 2020). In tomato, PCA has been extensively employed to assess genetic diversity among germplasm lines, breeding populations and hybrids based on morphological, yield, and biochemical traits (Bhattarai et al., 2016; Khan et al., 2024). It facilitates the identification of trait associations, grouping of genotypes, and visualisation of genetic relationships through biplots and scatter diagrams. Moreover, PCA aids in reducing redundancy among variables and helps breeders focus on key traits that contribute most to variability and

heterosis expression. In the context of triple cross  $F_1$  hybrid populations, PCA becomes particularly valuable because these populations often exhibit broad phenotypic variation resulting from the involvement of three genetically diverse parents (Elhaik, 2022; Jassim et al., 2025). The multivariate structure of such populations may reveal distinct trait combinations and heterotic patterns that are not apparent through conventional statistical analyses (Lubke and McArtor et al., 2014). By identifying major principal components and their associated trait loadings, breeders can determine which yield and quality attributes predominantly influence variability and can design more efficient selection strategies (Harini et al., 2025). Therefore, the present study aimed to characterise a triple cross  $F_1$  hybrid population of tomato using principal component analysis to quantify the magnitude of phenotypic variability, identify key traits contributing to total variation and identify superior hybrid lines for effective breeding decisions.

## 2. MATERIALS AND METHODS

### 2.1. Plant materials and field experiments

The study was conducted during August, 2024–February, 2025 at the ICAR-Indian Institute of Vegetable Research, Varanasi (25.18° N latitude and 82.83° E longitude). Three donor lines, including Kashi Amul, AVTO1219 and LA4025, were utilised as parental sources to develop a triple cross  $F_1$  population in tomato (*Solanum lycopersicum* L.). The donor lines were selected based on their desirable agronomic performance and potential to contribute favourable alleles governing growth and yield traits. Initially, a single cross was made between two selected parents, followed by crossing the resultant  $F_1$  with the third donor line to generate the triple cross  $F_1$  population (Kashi Amul $\times$ AVTO1219) $\times$ LA4025, thereby enhancing genetic recombination and variability. A total of 150 triple-cross  $F_1$  population were raised and evaluated under open field conditions following standard agronomic practices. The evaluation aimed to identify individuals exhibiting superior performance with respect to yield contributing and growth-related attributes. Based on overall phenotypic performance, yield potential and desirable horticultural characteristics, 22 superior plants were selected. The selection criteria emphasised early flowering, higher fruit number, improved fruit size and weight and overall plant robustness.

Field experiment was conducted during the crop season under a paired-row planting system at the ICAR-Indian Institute of Vegetable Research, Varanasi (25.18° N latitude and 82.83° E longitude). Seeds were sown in Mid-August, and seedlings were transplanted during the mid-September. Ten individual plants per row were established under the paired row system on raised beds, maintaining a spacing of 60 $\times$ 45 cm<sup>2</sup>. The crop was managed in accordance with the

recommended package of practices for tomato cultivation.

## 2.2. Data collection

Ten horticultural traits were recorded on every plant including plant height (cm), number of primary branches, days to 50% flowering, number of flowers inflorescence<sup>-1</sup>, fruit weight (g), fruit length (cm), fruit diameter (cm), number of locules, pericarp thickness (cm) and total soluble solids (TSS) (°Brix). Pericarp thickness was measured with a Vernier calliper. The average fruit weight was calculated from the mean weight of five fruits. TSS was determined using a hand refractometer.

## 2.3. Statistical analysis

Principal component analysis was carried out by using the GRAPES software, version 1.0.0. (Gopinath et al., 2020).

# 3. RESULTS AND DISCUSSION

## 3.1. Assessment of contribution variability in the scree plot

Principal component analysis was performed to assess the extent of variability and to identify major contributing agro-horticultural traits in the triple cross F<sub>1</sub> tomato population (Shoba et al., 2019). The scree plot revealed that the first five principal components explained 86.7% proportion of the total variability (Figure 1). The first principal component (PC1) accounted for approximately 36.7% of the total variation, indicating that a substantial portion of phenotypic variability among the genotypes was governed by traits associated with this component. The second principal component (PC2) contributed around 20.6% of the variation. Together, PC1 and PC2 explained nearly 57.3% of the total variability, suggesting that these two components effectively summarized the diversity present in the population.

The third and fourth principal components contributed 11.7 and 10.1% proportions of the variation, respectively. Subsequent components showed a sharp decline in eigenvalues, each contributing less than 5% of the total

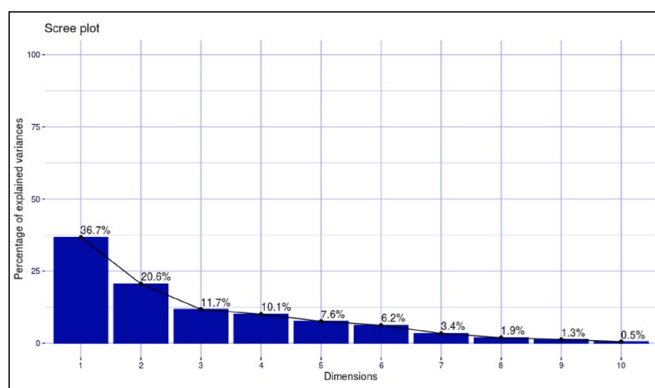


Figure 1: Scree plot for eigenvalues and cumulative variability explained by principal components in triple cross F<sub>1</sub> hybrids

variance (Table 1). The scree plot exhibited a clear elbow after the second or third principal component, indicating that only the first few components were significant in explaining the majority of variation. Ten principal components, only the first four (PC1, PC2, PC3 and PC4) produced eigenvalues greater than one, suggesting that the detected features had a greater impact on the phenotype of the genotypes being studied (Nachimuthu et al., 2014). These findings were similar to the findings of Williams and Anbuselvam (2023).

Table 1: Eigenvalues and percentage of variance in principal components

| Principal Components | Eigenvalue | Percentage of variance | Cumulative percentage of variance |
|----------------------|------------|------------------------|-----------------------------------|
| PC1                  | 3.67       | 36.67                  | 36.67                             |
| PC2                  | 2.06       | 20.56                  | 57.24                             |
| PC3                  | 1.17       | 11.74                  | 68.98                             |
| PC4                  | 1.01       | 10.05                  | 79.03                             |
| PC5                  | 0.76       | 7.62                   | 86.64                             |
| PC6                  | 0.62       | 6.24                   | 92.89                             |
| PC7                  | 0.34       | 3.38                   | 96.27                             |
| PC8                  | 0.19       | 1.91                   | 98.17                             |
| PC9                  | 0.13       | 1.31                   | 99.48                             |
| PC10                 | 0.05       | 0.52                   | 100                               |

## 3.2. Identification of major trait contributions and associations through biplot

The PCA biplot revealed substantial dispersion of progenies across different quadrants, indicating the presence of considerable genetic variability within the population. Traits such as fruit length, fruit diameter, fruit weight and pericarp thickness exhibited strong positive loadings along PC1, indicating their major contribution toward yield potential. The close angular proximity among these vectors suggested strong positive correlations among fruit size and yield-contributing traits. This implied that improvement in one of these traits was likely to result in a simultaneous increase in others. Total soluble solids and number of locules were positioned in the lower right quadrant, showing their association with fruit quality parameters. Their moderate alignment with yield traits suggested the possibility of concurrent improvement of yield and quality through careful selection. Plant height and number of primary branches showed higher loadings along PC2, indicating their significant contribution to vegetative vigour. The close association between these two traits suggested that taller plants tend to produce more branches. Days to 50% flowering (DFPF) were oriented in a direction opposite to

fruit size traits, indicating a negative association, suggesting that early flowering lines might differ in fruit development characteristics (Gautam et al., 2024). These findings were similar to the reports of Carbonell et al. (2026), Seid et al. (2021) in tomato and Harini et al. (2025) in dolichos bean.

### 3.3. Genotypic distribution and identification of superior lines

Progenies located in the positive region of PC1 and closer to fruit-related vectors were identified as promising for yield improvement. Lines such as TCH-55, TCH-125, and TCH-57 were positioned near FW, FD, FL, and PT vectors, indicating superior performance for fruit size and weight attributes (Figure 2). Progenies positioned nearer to TSS and NL vectors, including TCH-13 and TCH-7, appeared promising for fruit quality improvement. Lines associated with PH and NPB, such as TCH-44 and TCH-76, demonstrated strong vegetative vigour and may serve as potential parents for breeding programs targeting plant architecture. TCH-55 was placed away from the origin. Progenies located farther from the origin exhibited greater divergence and could be considered genetically diverse. The Progenies that were present in the same quadrant, along with TCH-55 considered superior and highly diversified and the progenies that were located in the opposite direction to these vectors could be considered as inferior progenies for these traits (Lakshmi et al., 2022). In our study, most of the progenies were highly distributed in the biplot this indicated high variability among the genotypes (Harini et al., 2025).

### 3.4. Correlation of agro-horticultural traits with principal components

Principal component analysis (PCA) was performed to dissect the multivariate structure of variability with in the triple cross  $F_1$  population. The loading matrix and correlation plot collectively revealed the magnitude and direction of association between agro-horticultural traits and principal components, thereby enabling biological interpretation of each dimension.

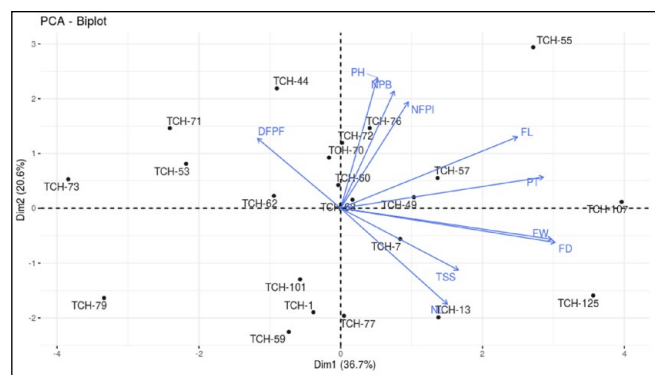


Figure 2: Biplot between PC1 (36.7%) and PC2 (20.6%) scores of triple cross  $F_1$  hybrids and their variables

Both the loading table and correlation plot (Figure 3) clearly indicated that PC1 was predominantly governed by fruit size and yield-related traits. High positive loadings were observed for fruit diameter (0.475), fruit weight (0.468), pericarp thickness (0.449), and fruit length (0.391). The correlation plot further confirmed strong positive correlations of these traits with PC1, as represented by large blue circles. The close clustering of FL, FD, FW, and PT in both analyses indicated strong positive interrelationships among fruit size parameters. Moderate positive contributions of the number of locules (0.236) and total soluble solids (0.261) suggest partial alignment of fruit quality with yield traits (Table 2). In contrast, days to first flowering (-0.184) showed a slight negative loading, implying that early flowering genotypes might not necessarily possess larger fruit size. Thus, PC1 could be interpreted as a primary yield and fruit size axis, explaining a substantial portion of total variability in the population. These findings were similar to the reports of Zahid et al. (2024).

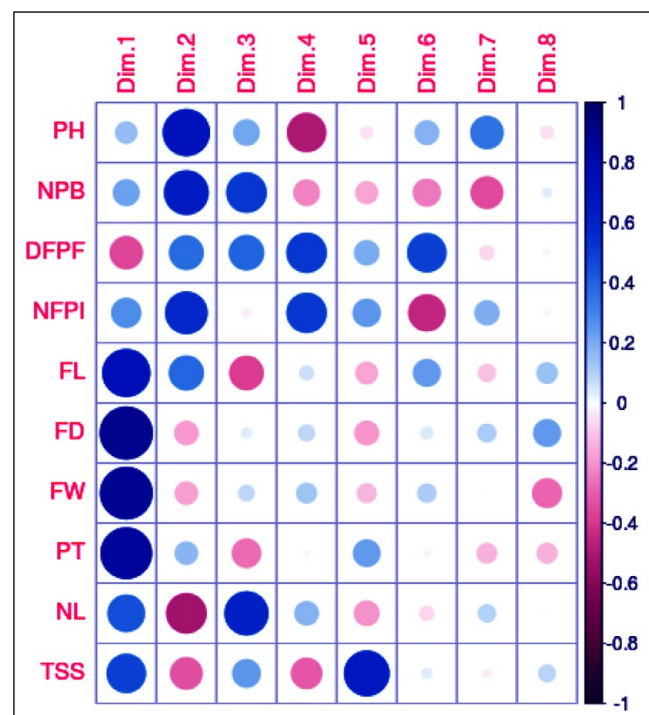


Figure 3: Contribution of the individual trait in the first 8 major principal components

PC2 exhibited strong negative loadings for plant height (-0.500), number of primary branches (-0.449), and number of fruits inflorescence<sup>-1</sup> (-0.407). The correlation plot corroborated these findings by showing significant associations of PH and NPB with PC2. The grouping of vegetative traits in PC2 indicated that plant architecture contributed independently of fruit size traits. Interestingly, the number of locules (0.368) and total soluble solids (0.236) showed positive loadings in PC2, suggesting partial

Table 2: Loading eigenvalues and variation of triple cross F1 hybrid lines for different principal components

| Variables                                  | PC1   | PC2   | PC3   | PC4   | PC5   | PC6   | PC7   | PC8   | PC9   | PC10  |
|--------------------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Plant height (cm)                          | 0.08  | -0.50 | -0.20 | 0.49  | -0.06 | -0.24 | 0.61  | -0.13 | 0.09  | -0.01 |
| Number of primary branches                 | 0.12  | -0.45 | -0.49 | 0.22  | -0.19 | 0.32  | -0.59 | 0.07  | -0.09 | 0.09  |
| Days to 50% flowering                      | -0.18 | -0.27 | -0.37 | -0.52 | 0.23  | -0.63 | -0.12 | 0.04  | 0.04  | 0.14  |
| No. of flowers inflorescence <sup>-1</sup> | 0.15  | -0.41 | 0.02  | -0.52 | 0.29  | 0.56  | 0.34  | 0.03  | -0.11 | -0.09 |
| Fruit length (cm)                          | 0.39  | -0.27 | 0.35  | -0.06 | -0.18 | -0.31 | -0.17 | 0.33  | -0.09 | -0.61 |
| Fruit diameter (cm)                        | 0.48  | 0.13  | -0.03 | -0.09 | -0.22 | -0.06 | 0.19  | 0.55  | -0.06 | 0.59  |
| Fruit weight (g)                           | 0.47  | 0.12  | -0.08 | -0.13 | -0.14 | -0.14 | -0.01 | -0.65 | -0.53 | 0.07  |
| Pericarp thickness (cm)                    | 0.45  | -0.12 | 0.25  | 0.01  | 0.28  | -0.02 | -0.23 | -0.31 | 0.67  | 0.21  |
| Number of locules                          | 0.24  | 0.37  | -0.58 | -0.19 | -0.24 | 0.09  | 0.17  | -0.01 | 0.42  | -0.42 |
| Total soluble solids (°Brix)               | 0.26  | 0.24  | -0.24 | 0.31  | 0.77  | -0.04 | -0.05 | 0.21  | -0.23 | -0.16 |

differentiation of fruit structural and quality traits from vegetative vigour. Therefore, PC2 primarily represented a vegetative growth and plant architecture component. PC3 was characterized by strong negative loading for the number of locules (-0.579) and number of primary branches (-0.486), while fruit length (0.351) and pericarp thickness (0.254) showed positive associations. The correlation plot supported this differentiation by indicating moderate correlations of NL and NPB with PC3. This suggested that PC3 captures variation related to internal fruit structure and branching pattern, highlighting possible trade-offs between locule number and fruit elongation.

Days to first flowering (-0.522) and number of fruits inflorescence<sup>-1</sup> (-0.521) showed strong negative loadings in PC4, whereas plant height (0.493) and total soluble solids (0.314) contributed positively. The correlation plot similarly demonstrated significant associations of DFPF with PC4. This dimension differentiated genotypes based on flowering time and reproductive efficiency. The negative loading of DFPF indicated that early flowering lines were distinctly positioned along this component. PC5 was overwhelmingly dominated by total soluble solids (0.770), which exhibited the highest loading among all traits across components. The correlation plot confirmed the strong positive association of TSS with PC5. The minimal contribution of major yield traits to PC5 indicated that fruit quality (sweetness) varied relatively independently of fruit size and productivity traits. This separation was advantageous in breeding programs aiming to improve quality without compromising yield. The separation of yield, vegetative, and quality traits into different principal components highlighted the multidimensional nature of variability in the triple cross F<sub>1</sub> population. The strong positive association among fruit size traits suggested that selection for one major yield parameter could simultaneously improve related characters. These findings were similar to the reports of Iqbal et al. (2014).

#### 4. CONCLUSION

Fruit size attributes were the major contributors to overall variation, while fruit quality and plant growth formed independent components. Among all, TCH-55 exhibited greater divergence (positioned away from the origin), indicating its potential as a promising parent for forwarding to next generation. The results demonstrated the effectiveness of multivariate analysis in identifying superior and diverse genotypes for strategic tomato breeding programs.

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