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RESEARCH ARTICLE

Variability, heterosis and interrelationship of contributing traits for yield improvement in parents and hybrids of tomato (*Solanum lycopersicum* L).

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Abstract

Tomato (*Solanum lycopersicum* L.) is the most prevalent and consumed vegetable crop worldwide because of its higher nutritional content. This study investigates the genetic diversity, principal components, correlations, clustering and heterosis among yield and quality traits of tomato parents and hybrids. Sixteen yield and quality-related attributes were evaluated using a diverse set of parents and their hybrids, revealing significant variation. The principal component analysis identified five principal components explaining 78.67% of the total variance, with a bi-plot highlighting the distribution of parents and hybrids. Five parents (CBESL159, CBESL169, CBESL162, CBESL164, CBESL168), two hybrids (H4, H5) and two double hybrids (H4xH5 and H5xH7) demonstrated widespread dispersion, indicating substantial genetic diversity driven primarily by yield and yield-related traits. The evaluation of heterosis among the hybrids revealed that six hybrids (H1, H3, H4, H5, H7 and H8) and four double hybrids (H5xH7, H1xH5, H8xH7 and H4xH5) exhibited significantly positive heterosis over the standard check hybrids.

Further, the study underscores the potential of parents and hybrids for developing strong hybrid vigour regarding growth, yield, and quality characteristics. The number of fruits per plant, single fruit weight and overall fruit yield exhibited strong positive correlations, signifying their implication as indirect selection criteria in tomato breeding programs. These findings provide valuable insights for further breeding programmes to enhance tomato yield and quality through targeted hybridization and trait selection.

Keywords

cluster; heatmap; heterosis; PCA; *Solanum lycopersicum* L.; variability

Introduction

Tomato (*Solanum lycopersicum* L.) is a widely produced vegetable valued for its many significant nutritional benefits and diverse applications. It is an excellent source of antioxidants, phenolic compounds, carotenoids, potassium and vitamins C and A (1). Compared to their wild ancestors, cultivated tomatoes have lower genetic diversity (2). Plant breeders have spent decades developing various tomato cultivars through domestication

and breeding techniques. As a result, contemporary tomato hybrids and cultivars have emerged in multiple sizes, colours and shapes (3). For tomato production to continue and global food security to be protected, new and improved tomato parents and hybrids are becoming increasingly important, especially in light of the world's rapid population growth and abrupt climate change (4,5).

Research into genetic variability can assist breeders in identifying and leveraging the diversity present within the gene pool. This enables the faster selection of tomato parents and hybrids that exhibit enhanced yield, quality, and adaptability to climate change (6). Assessing the relationships between the traits under investigation using approaches like principal component and cluster analysis is crucial to gaining insightful knowledge. These techniques provide valuable insights into the relationships between traits and can effectively guide breeding programs. The heterosis occurs when different species, cultivars, or inbred lines are crossed, affecting the F1 generation. Comprehending the molecular mechanisms behind heterosis remains a significant issue, even after more than a century of thorough study in multiple crops. Heterosis is now understood to be the most effective method of plant breeding that produces early, homogenous, high-yielding cultivars with desirable features (7). Breeders can develop an efficient breeding plan focused on pertinent attributes to enhance yield production by exploiting the Pearson correlation to ascertain the degree of these characters' associations. Breeders' ultimate goal is yield. Thus, it's essential to comprehend both the direct and indirect effects of related features on yield performance. Thus, the specific goals of this study were to investigate genetic divergence among various tomato parents and hybrids, select prospective parents and hybrids for hybridization in upcoming breeding initiatives and investigate the relationship between growth, yield and quality attributes.

Materials and Methods

Experimental site

The experiment utilized twenty-seven tomato parents and hybrids, including twelve parents sourced from different regions of India, including IIHR, TNAU, and Taiwan, along with eight F1 hybrids and seven double cross hybrids developed using the above parents in the previous study through MAGIC population (8). The study was conducted at the Orchard of Horticulture College and Research Institute, Tamil Nadu Agricultural University, from March 2022 to May 2023, using a randomized block design with three replications. Each parent and hybrids were opted with row spacing of 90 cm apart, with a distance of 60 cm between individual plants-all the recommended agricultural practices to ensure optimal crop growth. Data from replicated plots were used for statistical analysis.

Observation recorded

Observations were recorded on various traits, including height of the plant (cm), number of branches, days taken for first flowering, days taken to attain 50% flowering, number of flowers and fruits per cluster, number of fruits per plant, single fruit weight (g), lycopene content (mg/100 g), TSS (° Brix), ascorbic acid content (mg/100 g), β-carotene content (mg/100 g), pericarp thickness (cm), number of locules and yield per plant (kg).

Data analysis

Principal Component Analysis (PCA) using "prcomp", Pearson correlation using "corrplot" and "Rcolorbrewer" packages and cluster analysis using "NbClust", "factoextra" and "Facto MineR" packages among these traits were conducted using R Studio software (4.3.3) heterosis was estimated over check hybrids (COTH3 and Arka Rakshak) by using the formulae suggested by Kempthorne (9).

Results and Discussion

Principal component analysis

Principal Component Analysis (PCA) was performed using R software 4.3.3 (10) for 16 quality and yield contributing traits to assess the relative significance of different components in capturing the genetic variation among tomatoes sourced from various regions of India. It determines which character primarily contributes to the population's clustering or grouping. In general, selection is made for the trait having the most variance (11).

A scree plot graph plotted the eigenvalues related to each factor in descending order against the number of principal components to represent the percentage of variation attributed to each element. The scree plot revealed that, after the first five principal components, the subsequent components contributed minimally to the variation (Fig. 1). Of the sixteen principal components analyzed, five exhibited eigenvalues more significant than one, together explaining 78.67% of the total variance in the examined traits. Specifically, the eigenvalues for PC1, PC2, PC3, PC4 and PC5 were 5.06, 3.06, 2.01, 1.44 and 1.02, respectively (Table 1).

Except for days to flowering, days to 50% blooming, and several locules, PC1, which accounted for 31.61% of the total variation, showed positive loadings for practically all of the traits investigated. This result is consistent with what Hussain et al. (12) reported. According to the factor loadings

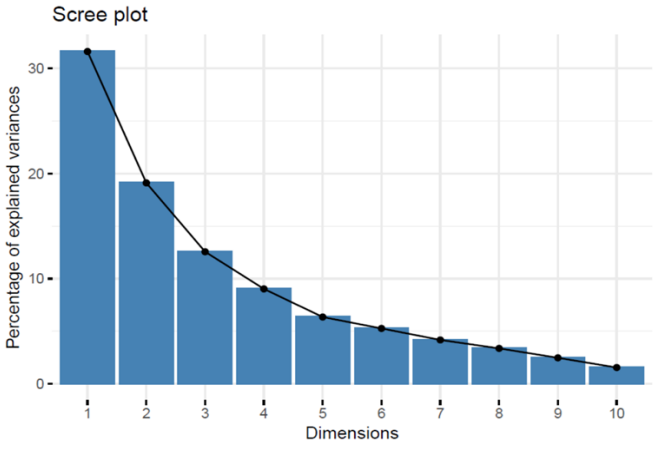

Fig.1. Scree plot depicting the contribution of various principal components towards divergence

Table1. Principal component analysis and contribution ratio based on morphological data of tomato parents and hybrids

Principal Component	Eigenvalue	Per cent variance	Cumulative variance
1	5.06	31.61	31.61
2	3.06	19.11	50.72
3	2.01	12.56	63.28
4	1.44	9.03	72.31
5	1.02	6.35	78.67

Table 2. Interpretation of PCA for the traits having values > 0.5 in each

PC1	PC2	PC3	PC4
Plant height	Plant height	Carotenoid content	Single fruit weight
Number of flowers per cluster	Number of fruits per cluster	Titrable acidity	Lycopene content
Fruit weight	Number of flowers per cluster	Pericarp thickness	
Number of fruits per plant	Pericarp thickness	Number of locules	
Yield per plant			
Titrable acidity			
Ascorbic acid			
Carotenoid content			

of principal components (Table 2), PC1 significantly contributed to the variation in traits like plant height (0.51), number of primary branches (0.56), number of flowers per cluster (0.52), fruit weight (0.66), number of fruits per plant (0.56), ascorbic acid content (0.74), β-carotene content (0.64) and yield per plant (0.61).PC2 was most related to plant height (0.51), number of flowers per cluster (0.59), number of fruits per cluster (0.64) and number of fruits per plant. PC2 accounted for 19.11% of the overall variation. The third component, which accounted for 12.56% of the variation, showed loadings for the number of locules (0.51), carotenoid content (0.51), titrable acidity (0.51), and pericarp thickness (0.68). PC4 was associated with fruit weight (0.56) and lycopene content (0.59), accounting for 9.03% of the total variation. These findings align with those published by Iqbal et al. (13).

Utilizing the two primary principal components (PC1 and PC2), parents, hybrids and variables were combined into a single bi-plot graph for enhanced visualization. The PCA bi-plot graph showed that the most distinguishing variables such as plant height, yield per plant, single fruit weight, number of fruits per cluster, number of flowers per cluster, carotene content and ascorbic acid content collectively accounting for 45.99% of the total variability. Notably, certain parents and hybrids like CBESL159, CBESL169, CBESL162, CBESL164, CBESL168, H4, H5, H4xH5 and H5xH7 (Fig. 2.) were positioned farthest from the bi-plot origin, indicating that have more diversity compared to other parents and hybrids (14).

This study chose parents and hybrids based on scores across more than one principal component among

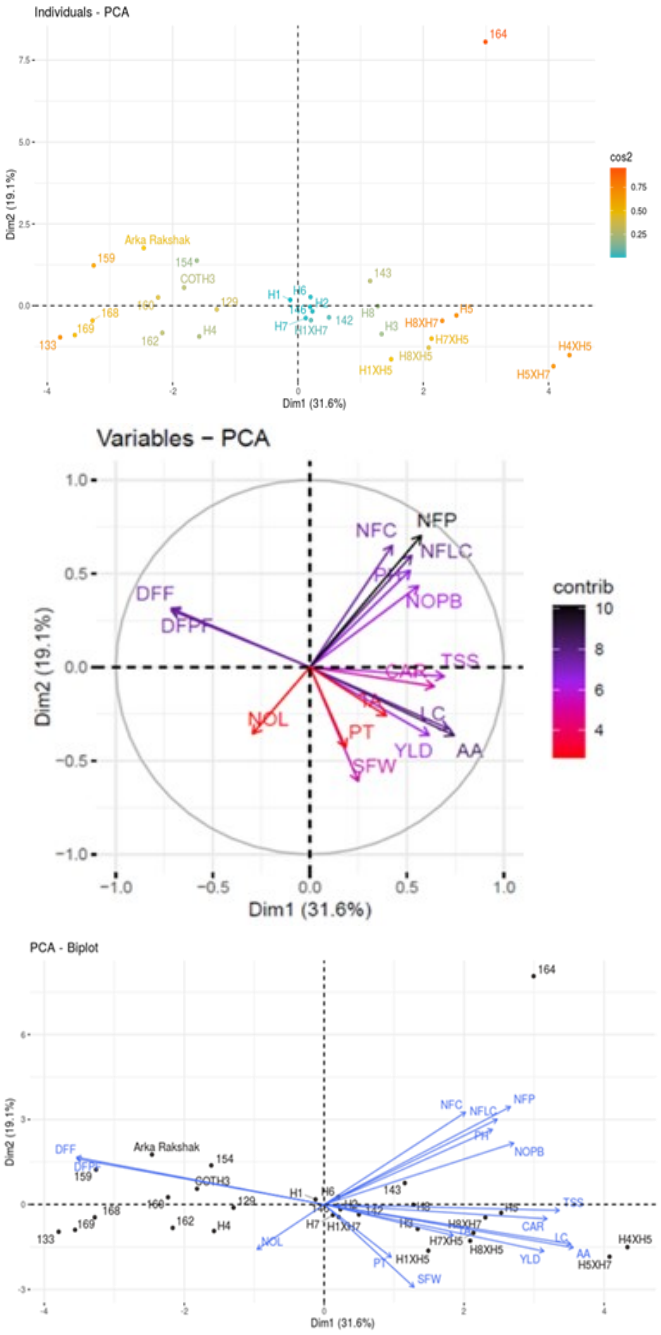

Fig. 2. PCA shows the (A) Individuals-PCA, (B) contribution of each of sixteen yield-related traits of parents and hybrids and c) Biplot of PCA for parents and hybrids based on studied growth, yield, and quality characters.

the seven identified (Table 3). For PC1, positive scores ranged from 4.53 (H4xH5) to 1.05 (H7), while for PC2, positive values varied from 3.96 (H3) to 1.30 (CBESL143). PC1 and PC2 revealed maximum variability for yield contributing traits (days to 50% flowering, number of flowers per cluster, number of fruits per cluster, fruit weight, ascorbic acid content, carotene content and yield per plant). The ranked parents and hybrids identified were CBESL 133, CBESL159, CBESL169, CBESL162, CBESL164, CBESL168, H4, H5, H4xH5 and H5xH7. Consequently, parents and hybrids under PC1 and PC2 embrace the potential for enhancing yield and its related traits in future breeding programs.

Thus, to produce superior and high-yielding parents and hybrids, selection should prioritize features like the number of fruits per plant, plant height, weight of a single fruit, ascorbic acid content and lycopene. When selecting

Table 3. Selection of parents and hybrids based on PC score in each component having positive values and more than > 1.0 in each PCs

PC1	PC2	PC3	PC4	PC5
CBESL 143(1.16)	CBESL 154(1.27)	CBESL129(1.33)	CBESL159(1.52)	CBESL169(1.01)
H3(1.27)	CBESL 159(1.11)	CBESL146(1.81)	CBESL169(1.66)	H3(1.36)
H7(2.71)	CBESL 164(7.85)	CBESL169(1.79)	H1(1.75)	H4(1.88)
H8(1.27)	COTH3(1.73)	H6(1.63)	H2(1.13)	H5(2.27)
H5×H7(4.02)		H7(1.24)	H3(1.70)	H7(1.38)
H7×H5(2.03)			ArkaRakshak (1.12)	ArkaRakshak (1.17)
H1×H5(1.39)			COTH3(1.98)	
H8×H5(1.99)				
H8×H7(2.28)				
H4×H5(4.17)				

parents for hybridization programs that try to boost population genetic diversity and create elite lines or heterotic F1 hybrids, these are essential factors to consider.

The correlation plot depicting variables against Principal Components (Fig.3) illustrates relationships among the measured traits. Traits clustered along Dim.1 and Dim.2 are identified as promising candidates for incorporation into breeding programs to improve yield. Strong positive correlations (indicated by large blue circles) are notably present among most yield-related traits such as fruit weight, number of fruits per plant, plant height, number of branches and number of flowers and fruits per cluster. However, flowering traits show distinct patterns in these correlations. This shows an increase in plant height, the number of fruits per cluster and an increase in yield per plant. Quality traits such as NOL (number of locules) exhibit positive correlations with LC (lycopene content), TSS (total soluble solids), and PT (pericarp thickness). This suggests that higher values of LC, TSS and PT convoy an increase in NOL. TA (titratable acidity) also demonstrates strong positive associations with LC and TSS. Furthermore, NOPB (number of primary branches) and DFF (days to first flowering) exhibit moderate to strong negative correlations with these dimensions.

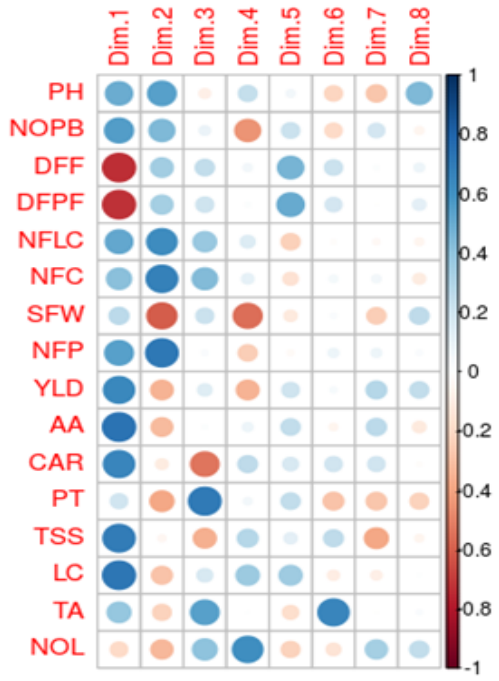

Fig.3. Correlation plot of variable Vs PCs

Trait association analysis

Correlation analysis obscures the path to comprehending the connections between the qualities under study. It provides a better understanding of how each trait contributes to enhancing the genetic composition of the crop. Correlation studies thus point to the best features that should be given priority in the upcoming breeding effort. Strong relationships between different qualities offer essential information about how traits can be simultaneously improved and the direct and indirect effects of these relationships, which will ultimately result in higher yield and quality. Fig. 4 shows the association studies between different attributes. Yield per plant showed a positive and non-significant correlation with carotene and total soluble solids.

Conversely, a positive and substantial correlation was found between the number of primary branches, fruits per plant, ascorbic acid and lycopene content. This result aligns with observations by Singh et al. (15). The number of fruits per plant, which had a highly significant correlation with yield per plant, was positively and significantly correlated with the number of fruits per cluster and the number of branches. Improvements in these traits consequently increase yield per plant, which is consistent with Paw et al. (16) findings.

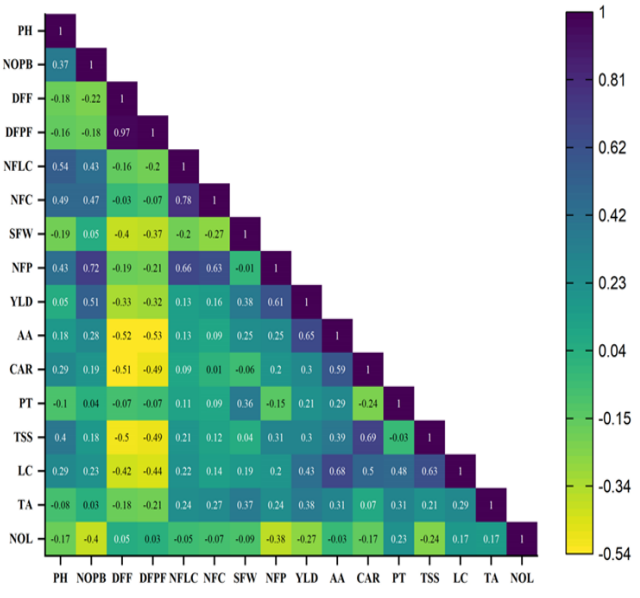

Fig. 4. Triangle heatmap with correlation matrix among the yield-related characters in parents and hybrids

Plant yield and single fruit weight have a favourable correlation. Similar findings from Reddy et al. (17) corroborated the positive significant connection between yield and single fruit weight reported by Islam et al. (18). Fruit weight, number of fruits per cluster, number of branches per plant, number of flowers per cluster and plant height all show a strong positive correlation with the number of fruits per plant. Moreover, positive and significant relationships existed between the ascorbic acid level and TSS, carotene content, flower and fruit counts per cluster and number of flowers per cluster.

Clustering

The 29 tomato parents and hybrids were subjected to hierarchical cluster analysis that revealed a complex genetic structure, providing valuable insights into the relationships among these parents and hybrids and their potential utilization in breeding programs (Fig.5). The cluster analysis of the tomato parents and hybrids reveals four major clusters, each with distinct sub clusters. These clusters signify significant genetic diversity within the studied population. The double hybrid (H4xH5) emerges as an outlier, forming its cluster and prominence in its genetic uniqueness compared to other parents and hybrids. This distinctiveness suggests potential origins as a wild relative, a geographically isolated genotype, or a product of breeding efforts introducing novel traits. Such genetic

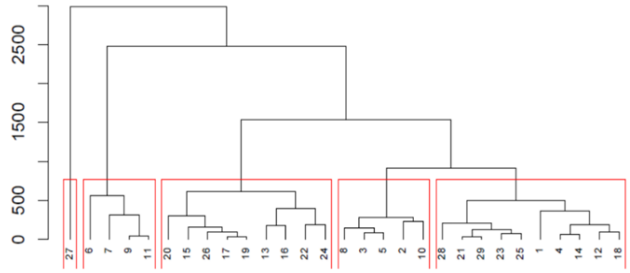

Fig.5. Cluster Dendrogram of tomato parents and hybrids

(1. CBESL 129 2. CBE SL 133 3. CBESL 142 4. CBESL 143 5. CBESL 146 6. CBESL 154 7. CBESL 159 8. CBE SL 160 9. CBESL 162 10. CBESL 164 11. CBESL 168 12. CBESL 169 13. H1 14. H2 15. H3 16. H4 17. H5 18. H6 19. H7 20. H8 21.H1×H7 22.H5×H7 23.H7×H5 24.H1×H5 25.H8×H5 26.H8×H7 27.H4×H5)

diversity is pivotal for breeding programs, offering opportunities to enhance traits like disease resistance and yield through targeted crosses between divergent clusters to maximize heterosis.

Strategically, the clustering analysis informs both breeding and conservation efforts. Breeding strategies can leverage the identified clusters and sub clusters to selectively breed for specific traits, utilizing genotypes within cohesive genetic groupings to expedite trait improvement. Including 27 parents and hybrids in breeding programs embraces the capacity for broadening the genetic base of cultivated tomatoes, potentially introducing novel alleles that could confer resilience to evolving agricultural challenges. Mainly, hybrid (H4xH5) safeguards valuable genetic resources and supports sustainable breeding practices to enhance tomato cultivars of future farm needs.

Based on the relatedness assessed, parents and

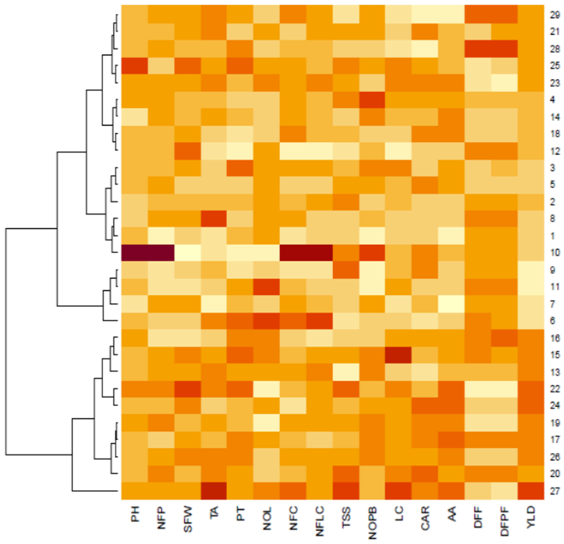

Fig.6. Heat map showing the relationships among the yield and its contributing characters

(PH: plant height, NFP: number of fruits/plants, SFW: Single fruit weight, TA: Titratable acidity, PT: Pericarp thickness, NOL: Number of locules, NFC: Number of fruits per cluster, NFLC: Number of flowers per cluster, TSS: total soluble solids, NOPB: Number of primary branches, LC: Lycopene content, CAR: β-Carotene, AA: Ascorbic acid, DFPF: days to 50% flowering, DFF: days to the first flowering, YLD: Yield per plant.)

hybrids were divided into different clusters based on growth, yield and quality characters using heatmap and hierarchical clustering (Fig. 6). In a heat map where each cell represents a combination of traits (column) and a genotype (row). The colour of each cell will be gritty based on the value of that cell. Red and brown colours infer high and low performance for the corresponding characters, respectively. Dark colour represents the immense magnitude and light colour represents the lesser magnitude.

Heterosis for yield and its attributing traits

The analysis of heterosis is one of the significant steps in developing commercial hybrids. The effects of heterosis on the concerned traits cannot be precisely predicted, but the probability of predicting it could be very high, sometimes up to ≥90% (19). The utilization of heterosis of yield and its attributing traits is an essential basis for choosing parents for hybridization in desirable cross combinations (20). Given the constraints mentioned in the context of heterosis breeding in crops, this study specifically aimed to comprehend the landscape of Heterosis for all seventeen quantitative and qualitative traits in tomato hybrids.

Compared to standard check hybrids (COTH3(diii (1)) and Arka Rakshak (diii (2)), the majority of crosses exhibited positive significance for various yields (the number of flowers per inflorescence, number of fruits per cluster, single fruit weight, yield per plant) and quality traits such as the number of locules, pericarp thickness, lycopene and total soluble solids. The results were in line with the findings of Vijeth *et al.* (21). Conversely, measures such as plant height, days to first flowering and days to 50% flowering showed negative significance when compared to conventional check hybrids. The landscape and degree of heterobeltiosis and conventional Heterosis can be evaluated to help identify and comprehend promising cross combinations that may be used to create transgressive segregants (22).

Table 4. Estimate of Heterosis (per cent) standard check (COTH3(diii (1)) and Arka Rakshak (diii (2)) for plant height, number of primary branches, days to first flowering, days to 50% flowering (days) of hybrids

	Plant height (cm)		Number of branches		Days to first flowering		Days to 50% flowering	
				Single hybrids				
Hybrids	diii (1)	diii (2)	diii (1)	diii (2)	diii (1)	diii (2)	diii (1)	diii (2)
H1(CBESL142×CBESL160)	-5.46	4.29	40.12	0.27	-26.10	-21.43	-23.92	-20.70
H2(CBESL146×CBESL160)	-27.18	-31.21	3.04	3.04	-30.98	-26.62	-28.61	-25.60
H3(CBESL154×CBESL168)	1.62	12.10	53.34	9.73	-15.71	-10.39	-14.30	-10.67
H4(CBESL142×CBESL168)	14.79	26.63	33.07	-4.78	-22.13	-17.21	-20.15	-16.78
H5(CBESL133×CBESL169)	4.44	15.22	7.42	-23.13	-9.64	-3.93	-9.14	-5.30
H6(CBESL143×CBESL159)	-3.06	6.94	-5.04	-32.04	-30.12	-25.70	-27.85	-24.80
H7(CBESL146×CBESL162)	9.86	21.19	40.87	0.80	-40.87	-37.14	-37.87	-35.24
H8(CBESL129×CBESL164)	3.85	14.56	22.50	-12.34	-15.64	-10.32	-14.03	-10.40
				Double hybrids				
H1×H7	5.65	16.55	25.81	-9.98	-31.74	-27.43	-19.19	-15.78
H5×H7	24.48	37.32	28.95	-7.72	-40.18	-36.41	-32.21	-29.35
H7×H5	14.20	25.98	19.59	-14.42	-34.32	-30.17	-33.26	-30.44
H1×H5	9.83	3.76	29.89	-7.05	-32.06	-27.77	-29.23	-26.24
H8×H5	79.06	97.53	2.80	-26.44	-37.75	-33.82	-39.63	-37.08
H8×H7	5.73	16.64	43.21	2.48	-30.07	-25.65	-27.80	-24.75
H4×H5	32.28	45.92	17.11	-16.20	-46.71	-43.35	-44.52	-42.18
S. Ed	5.75	6.83	4.21	2.95	2.57	2.73	2.52	2.62
CD	11.86	14.07	8.68	6.08	5.29	5.63	5.18	5.41

Table 5. Estimate of Heterosis (per cent) over the standard check (COTH3(diii (1)) and Arka Rakshak (diii (2)) for number of flowers per cluster, and number of fruits per cluster, single fruit weight, number of fruits per plant of hybrids

	Number of flowers cluster^{-1}		Number of fruits cluster^{-1}		Single fruit weight (g)		Number of fruits per plant	
				Single hybrids				
Hybrids	diii (1)	diii (2)	diii (1)	diii (2)	diii (1)	diii (2)	diii (1)	diii (2)
H1(CBESL142×CBESL160)	12.67	7.15	15.28	-7.48	9.98	5.97	1.60	8.22
H2(CBESL146×CBESL160)	-4.48	-9.16	6.87	-14.24	-12.74	-15.92	-2.17	4.21
H3(CBESL154×CBESL168)	5.54	0.36	1.42	-18.61	17.85	13.55	-0.57	5.91
H4(CBESL142×CBESL168)	-4.38	-9.07	8.68	-12.79	12.75	8.64	-3.59	2.69
H5(CBESL133×CBESL169)	-9.06	-13.52	6.48	-14.55	2.21	-1.52	-4.39	1.83
H6(CBESL143×CBESL159)	2.45	-2.57	23.58	-0.83	1.75	-1.96	-13.22	-7.57
H7(CBESL146×CBESL162)	4.55	-0.57	10.49	-11.33	-6.29	-9.70	11.25	18.50
H8(CBESL129×CBESL164)	4.01	-1.09	-5.96	-24.53	-4.71	-8.18	8.58	15.65
				Double hybrids				
H1×H7	5.40	0.23	-10.88	-28.48	12.40	8.30	-13.77	-8.16
H5×H7	-3.67	-8.40	8.42	-12.99	38.30	33.26	-30.45	-25.92
H7×H5	10.79	5.36	32.51	6.34	12.46	8.36	-4.26	1.98
H1×H5	6.43	1.21	-22.02	-37.42	14.43	10.26	-16.67	-11.24
H8×H5	13.68	8.10	5.96	-14.97	6.51	2.63	-7.36	-1.32
H8×H7	6.75	6.75	12.95	-9.36	13.69	9.54	2.72	9.41
H4×H5	11.80	6.32	-0.39	-20.06	52.78	47.21	8.73	15.81
S. Ed	1.72	1.71	3.30	2.65	4.14	3.98	2.74	2.92
CD	3.54	3.51	6.80	5.46	8.53	8.21	5.65	6.02

Table 6. Estimate of Heterosis (per cent) over the standard check (COTH3(diii (1)) and Arka Rakshak (diii (2)) for yield per plant, As corbic acid content, β

	Yield per plant		Ascorbic acid content (mg/100g)		β-carotene content (mg/100g)		Pericarp thickness	
Single hybrids								
Hybrids	diii (1)	diii (2)	diii (1)	diii (2)	diii (1)	diii (2)	diii (1)	diii (2)
H1(CBESL142×CBESL160)	21.68	24.84	1.95	48.09	19.83	22.25	-2.42	8.04
H2(CBESL146×CBESL160)	-9.91	-7.58	21.11	75.93	56.15	59.31	-10.48	-0.89
H3(CBESL154×CBESL168)	14.95	17.93	17.00	69.95	52.88	55.98	8.87	20.54
H4(CBESL142×CBESL168)	18.18	21.24	18.93	72.75	65.91	69.27	-0.81	9.82
H5(CBESL133×CBESL169)	12.52	15.43	40.05	91.23	77.63	81.23	0.81	11.61
H6(CBESL143×CBESL159)	-12.60	-10.33	20.19	74.59	80.08	83.73	-33.06	-25.89
H7(CBESL146×CBESL162)	12.54	15.45	38.41	84.78	77.00	80.59	-15.32	-6.25
H8(CBESL129×CBESL164)	6.67	9.43	10.01	59.80	91.87	95.76	-8.87	0.89
Double hybrids								
H1×H7	-2.98	-0.47	-2.68	41.36	80.59	84.25	-18.55	-9.82
H5×H7	29.53	32.89	5.55	53.33	60.39	63.64	10.48	22.32
H7×H5	-4.71	-2.24	37.85	92.09	55.74	58.9	8.87	20.54
H1×H5	25.98	29.25	48.84	95.86	95.9	99.87	-13.71	-4.46
H8×H5	-4.84	-2.37	26.02	83.06	81.10	84.77	-15.32	-6.25
H8×H7	10.70	13.57	37.61	87.68	71.10	74.57	0.81	11.61
H4×H5	50.97	54.88	43.93	96.86	86.88	90.67	-7.26	2.68
S. Ed	4.24	4.36	4.05	4.41	4.80	4.90	2.98	3.29
CD	8.75	8.97	8.34	9.08	9.89	10.09	6.14	6.79

Table 7. Estimate of Heterosis (per cent) standard check (COTH3(diii (1)) and Arka Rakshak (diii (2)) for Total soluble solids, Titratable acidity, Lycopene content and number of locules of hybrids

	Total soluble solids (° Brix)		Titratable acidity		Lycopene content (mg/100g)		Number of locules	
Single hybrids								
Hybrids	diii (1)	diii (2)	diii (1)	diii (2)	diii (1)	diii (2)	diii (1)	diii (2)
H1(CBESL142×CBESL160)	-11.84	-9.64	27.68	-0.69	15.78	22.62	33.33	33.33
H2(CBESL146×CBESL160)	3.52	6.11	5.36	-18.06	18.03	25.00	0.00	0.00
H3(CBESL154×CBESL168)	13.90	16.74	13.39	-11.81	85.13	96.06	66.67	66.67
H4(CBESL142×CBESL168)	4.48	7.09	-40.18	-53.47	32.83	40.68	66.67	66.67
H5(CBESL133×CBESL169)	9.94	12.68	-21.43	-38.89	41.88	50.25	33.33	33.33
H6(CBESL143×CBESL159)	9.53	12.26	-28.57	-44.44	13.43	20.13	0.00	0.00
H7(CBESL146×CBESL162)	18.67	21.63	11.61	-13.19	39.18	47.40	-33.33	-33.33
H8(CBESL129×CBESL164)	29.56	32.79	26.79	-1.39	55.15	64.32	0.00	0.00
Double hybrids								
H1×H7	15.94	18.83	25.89	-2.08	9.98	16.48	33.33	33.33
H5×H7	23.36	26.44	5.36	-18.06	47.65	56.37	33.33	33.33
H7×H5	28.83	32.05	34.29	4.44	56.32	65.55	-33.33	-33.33
H1×H5	8.16	10.86	-25.89	-42.36	40.99	49.32	33.33	33.33
H8×H5	17.28	20.21	26.79	-1.39	47.02	55.71	66.67	66.67
H8×H7	19.59	22.58	47.32	14.58	38.97	47.18	0.00	0.00
H4×H5	37.66	41.09	97.32	53.47	79.33	89.92	66.67	66.67
S. Ed	3.05	3.13	8.65	6.73	5.53	5.86	8.58	8.58
CD	6.28	6.44	17.83	13.87	11.39	12.07	17.69	17.69

Compared to standard checks, the heterotic effect focusing on traits related to yield and yield-contributing characteristics were observed in the F1 generation (Tables 4 -7). Notably, in cross combinations with negative significance, characteristics suggestive of early crop maturation in tomatoes, such as plant height, days to first flowering, and days to 50% flowering, were critical for selection. The standard Heterosis (Arka Rakshak) ranged from -27.18 per cent in H2 to 97.53 per cent in (H8xH5). The standard Heterosis (COTH3) ranged from -31.21 % in H2 to 32.28% in H4xH5. Regarding plant height, all double crosses and five single hybrids displayed positive heterosis; nevertheless, only five double crosses and three single hybrids displayed negative heterosis. Compared with the standard check, two double crosses and three hybrids displayed more fruits per cluster than their parents, indicating which traits are desirable for high yield. The lack of significant heterosis in certain cross combinations for standard heterosis might be attributed to the internal cancellation of heterosis components, as observed in prior studies by Chande et al. (22).

All hybrids and double-crosses exhibited significant and negative heterosis for days taken for 50% flowering over the standard check variety. These results are based on the findings of Premalakshme *et al.* (23). The early maturation of hybrids is expected to enhance yield within a shorter period. These traits are the most significant criteria for selecting and improving early, high-yielding hybrids in tomatoes (24).

One important factor contributing to production is the quantity of fruits on a plant. The highest standard Heterosis (COTH3) of 23.58 per cent was registered in H6 to 32.51 per cent in H7xH5. The highest standard Heterosis (Arka Rakshak) of -0.83 per cent was registered in H6, and 6.34 per cent was registered in (H7xH5). Two double crosses [H8xH7(2.72%), H4xH5 (8.73%) over Arka Rakshak and H8xH7(9.41%), H4xH5 (15.81%) over COTH3] and three hybrids H1, H7 and H8 gave significantly positive heterosis over standard checks. Significant results have been found by Saleem *et al*. (25) for the number of fruits per plant.

Fruit weight is of foremost importance while breeding for high-yielding cultivars. The standard Heterosis (COTH3) exhibited a range from -12.74 per cent in H2 to 52.78 per cent in H4xH5. The standard Heterosis (Arka Rakshak) ranged from -15.92 per cent in H2 to 47.21 per cent in (H4xH5). All the double cross hybrids and three single cross hybrids gave significantly positive heterosis over both standard check hybrids (Arka Rakshak and COTH3). Singh et al. (26) also reported positive heterosis over better parents for average fruit weight.

The number of fruits per cluster is one of the essential factors influencing yield. The estimate of heterosis varied from -22.02 to 23.58% over Arka Rakshak and -28.48 to 6.34 over COTH3. Increased fruit yield per plant is the ultimate goal of any breeding Programme, so it needs higher deliberation. Heterosis varied from -12.60 to 50.97% over Arka Rakshak and -10.33 to 54.88% over COTH3. Significant positive heterosis over both standard checks was observed in H4xH5, followed by H5×H7.

Among the hybrids evaluated, six hybrids (H1, H3, H4, H5, H7 and H8) and four double hybrids (H5xH7, H1xH5, H8xH7 and H4xH5) showed significantly positive heterosis over standard check hybrids. The increased yield in these hybrids is because of the high-yielding parents selected for hybridization, as suggested by Courtney and Peirce (27). The superior hybrids were chosen based on their performance across seasons (pooled over the season) and the significant heterosis observed. This suggests anticipated higher regulatory interactions, providing increased adaptability to diverse adverse environments (28).

Conclusion

In summary, five parents (CBESL159, CBESL169, CBESL162, CBESL164, CBESL168), two hybrids (H4 (CBESL142xCBESL168), H5 (CBESL133xCBESL169) and two double hybrids (H4xH5 and H5xH7) highlight the superior recital for yield and quality traits. These hybrids merit prioritization for further assessment, commercial deployment and integration into breeding programs. The observed genetic variability in yield components presents promising avenues for enhancing yield through targeted breeding strategies. Breeders can develop superior tomato varieties that cater to diverse industry demands by combining high-yield potential with desirable traits such as resistance and adaptability. This hierarchical cluster analysis has provided valuable insights into the genetic structure of the studied tomato genotypes. Identifying distinct clusters, subclusters, and a unique outlier genotype offers a solid foundation for strategic breeding initiatives, germplasm conservation and future research. The hybrids likely embody advantageous allele combinations from their parental lines, affirming their potential for commercial cultivation and substantial economic benefits for growers.

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Authors' contributions

TS contributed to conceptualizing and supervising the research design and experimental planning. RS carried out the experiment, data collection and analysis. MK contributed by imposing the experiment and NM, NS and SH helped with statistical analysis.

Compliance with ethical standards

Conflict of interest: The authors have no conflict of interest.

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