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Genetic Basis of Yield and Nutritional Quality in Cherry Tomato: Insights from Half-Diallel Crosses in North East India

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ABSTRACT

Cherry tomato (*Solanum lycopersicum* var. cerasiforme) is regaining popularity in North East India for its nutritional value and adaptability to local agro-climatic conditions. To enhance its yield and nutritional properties, this study investigated the genetic basis of key traits through a half-diallel cross involving ten genetically diverse parental lines. A total of 45 F_1 hybrids were evaluated for 18 morphological, yield-related, and biochemical traits, including β-carotene, lycopene, and ascorbic acid content. The analysis of variance revealed significant differences among genotypes for most traits, with high genotypic and phenotypic coefficients of variation for yield per plant (YP), fruit weight (FW), and number of fruits per cluster (NFC). Combining ability analysis showed the predominance of non-additive gene action, suggesting the effectiveness of heterosis breeding. Hybrids such as CT 2 × CT 7 exhibited significantly better-parent heterosis and specific combining ability effects for yield and nutritional traits. The potence ratio analysis indicated a spectrum of dominance, including partial to over-dominance for some traits such as plant height and lycopene content. Parental lines CT 2, CT 4, CT 7, and CT 10 were identified as superior general combiners for yield and quality traits. The study highlights the potential of exploiting hybrid vigor for developing high-yielding, nutrient-rich cherry tomato cultivars suitable for commercial cultivation in the North East region. These findings provide a foundation for targeted hybrid development, although further validation across multiple seasons and environments is recommended to ensure the stability and adaptability of promising hybrids.

Keywords: North East India, Cherry tomato, half-diallel crosses, β-carotene, Lycopene, and Ascorbic acid.

Introduction

From a basket of a wide diversity of vegetables, cherry tomato (*Solanum lycopersicum* var. *Cerasiforme*, 2n = 2x = 24) is an important solanaceous vegetable crop that has the potential

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to alleviate the problem of hidden hunger in countries like India, particularly the north-eastern region of India. It is typically a day-neutral plant, can be grown in a wide range of soil and climatic conditions, and is tolerant to heat and drought (Vidyadhar et al. 2014). It is a rich source of total carbohydrates (6.0g), calcium (1.0%), protein (1.0g), dietary fibre, vitamin C, vitamin A, lycopene, and also an ample amount of vitamin E, β-Carotene, folate, phosphorus, copper, potassium, and manganese (Medina and Lobo 2001; Wang et al. 2022; Yin et al. 2024). One of cherry tomatoes' most famed eating benefits is its lycopene content. Lycopene is a strong antioxidant and, apart from its role in digestion, promotes gastric secretion, reducing heart diseases, regulating blood sugar, boosting immunity, and acting as a blood purifier (Bhowmik et al. 2012; Tufail et al. 2024; Shafe et al. 2024)). In *vitro* treatment of pre-existing cancer cell culture with lycopene is reported to prevent the continuous growth of cancer cells (Trejo-Solís et al. 2013; Koul et al. 2019).

Although with so many benefits mentioned above, attention to the improvement on yielding ability and other characters has been very limited in cherry tomato, which is reflected from the presence of very few varieties for commercial cultivation in the North-eastern region of India. Therefore, it is essential to evaluate the potentialities of the indigenous germplasm because the promise for a further improvement program depends on the genetic diversity of the crop. Subsequently, heterosis breeding is an efficient method of improving yield and other useful characters of the crop plants under study. For this, combining ability analysis helps in understanding the nature of gene action governing the expression of the character and thus helps in deciding breeding strategy. It also helps in choosing the best combiners, which can exhibit maximum hybrid vigour in the F_1. Many biometrical procedures have been used to obtain information on combining ability, and diallel analysis is one among them (Kaushik and Dhaliwal 2018), which is widely used to study the combining ability of the parents to be chosen for heterosis breeding. Cherry tomato offers much scope for improvement through heterosis breeding which can further be utilized for the development of desirable recombinants. Considering the potential of this crop and the need for improvement, the present investigation is being carried out to identify the best genotypes to be used as parents for the development of hybrids and to develop hybrids with better yield and nutritional qualities like higher Ascorbic acid (Vitamin C), β-Carotene (a precursor of vitamin A), and Lycopene, etc.

Materials and methods

The study was carried out between October 2019 and March 2021 (three seasons) in the research farm, Department of Vegetable Science, College of Horticulture and Forestry, Central Agricultural University (Imphal), Pasighat, Arunachal Pradesh, India, situated at 28.07°N latitude and 95.33°E longitude at a mean sea level of 155m.

Experimental material

Ten parental genotypes (Figure 1) designated as CT1 to CT10 were selected from a set of cherry tomato germplasm collected from different states of India based on their genetic divergence values (unpublished data). Self-pollinated seeds of ten selected genotypes were sown in pot-trays filled with soil and compost mixture (8:2 ratio) and covered with plastic sheets for germination. Necessary plant protection measures and cultural operations were performed carefully for the healthy growth of the seedling. One-month-old seedlings were transplanted in the crossing block during 1st week of September 2019 to obtain the F_1 generation. Parental genotypes were crossed in all possible combinations in a half-diallel mating design to estimate the relative heterosis % of the hybrid compared to the average and best parents and to identify suitable combiner(s) for quantitative traits, morphological traits, and biochemical parameters.

Evaluation of F_1 hybrids along with parental genotypes

Seedlings from seeds of forty-five hybrids, along with ten parents, were raised in a nursery following the method mentioned above. One-month old seedlings were transplanted in the main field during 1st week of September 2020. The hybrid and parental plants were arranged in a randomized complete block design (RCBD) with three replicates, with 60 cm between rows and 50 cm between the plants within rows. Standard cultural practices were performed carefully to ensure successful plant stands. Five randomly selected plants per replication in each genotype and hybrid were considered for recording observations on different parameters.

Experimental data

Data on days to germination (DTF), days to first flowering (DFF), first flowering node (FFN), days to first fruit maturity (DFFM), days to first fruit harvest (DFFH), and plant height in cm (PH) were recorded on individual plants. Fruit weight (FW), fruit length (FL), fruit girth (FG), number of clusters/plant (NCP), number of fruits/cluster (NFC), number of locules/fruit (NLF), number of seeds/fruit (NSF), and yield/plant (YP) were recorded in five randomly selected

plants. The TSS content of fresh fruit was estimated using a refractometer expressed in ºBrix. Ascorbic acid (AA) content (mg/100g) of fresh fruit was estimated using the 2,6-dichlorophenol indophenol method (Sadasivam and Manikam 1987). The lycopene (L) content of the fruits was determined by weighing 5 g of cherry tomato pulp and extracting it following the method described by Ranganna (1976). The β-Carotene (βC) content (mg/100g) of cherry fruit tomato was estimated as per the method described by Sadasivam and Manikam (1987). Similarly, the observations on morphological traits were recorded as per IPGRI descriptors for Tomato such as fruit shape: flattened/slightly flattened/rounded/high rounded/heart shaped/cylindrical/pyriform/ellipsoid; Fruit colour: green/yellow / orange / pink/red; Plant growth type: dwarf/determinate/semi determinate / indeterminate were recorded when fruits were ripe and at marketable stage. Stem pubescence (SP): sparse / intermediate / dense; Stem internodal length (SIL): short / intermediate / long; and Foliage density (FD): sparse / intermediate / Dense.

Statistical analysis and estimation of genetic parameters

Data of all the traits mentioned above obtained from a randomized complete blocks design were analysed using different statistical methods and tools. Principal component analysis (PCA) was done using the data of the above-mentioned traits. Principal components (PC), attributing to a higher percentage of variation within the parental genotypes and correlation of traits with PC explaining high variation, were identified with the help of software Past version 4.03.

Similarly, the Mahalanobis D^2 statistic was used for assessing the genetic divergence of parental genotypes employing eighteen important yield and quality attributing traits (Raina et al. 2015; Spaldon and Kumar 2017). Mahalanobis D^2 value was estimated using DOSBox software version 0.74-3 and d2m.exe file downloaded from TNAUSTAT https://sites.google.com/site/tnaustat. Analysis of variance (ANOVA) for yield and quality attributing traits in parental genotypes and hybrids was estimated, and the values that are significant at 5% and 1% were identified, respectively. The genotype (G.C.V.) and phenotype (P.C.V.) coefficient of variation were calculated using the following formula given by Burton (1952).

Heritability in a broad sense (H) and the expected genetic advance (GA) was calculated as per the method described by Srinivasulu et al., (2024). Path coefficients were calculated to estimate the direct and indirect effects of the characters as per Dewey and Lu (1959) by considering

yield per plant as the dependent variable on 17 other traits as independent variables. The magnitude of heterosis was estimated in relation to better-parent as well as mid-parent values using a method described by Abu et al. (2019). Both mid and better parent heterosis values were calculated as percentage increase or decrease of F_1 s over the Better-Parent (BP) and Mid-Parent (MP) values using the formula; (a) Heterosis over mid-parent (H_1)={[(mean of F_1 – mean of mid parent)/mean of mid parent] x 100}; (b) Heterosis over better-parent (H_2)={[(mean of F_1 – mean of better parent)/mean of better parent] x 100}. The dominance estimates (D.E.), also referred to as "potence ratio," were computed using the formula as given by Smith (1952) as Potence ratio = F_1 - M.P / [0.5 (P2-P1)], where, F_1=mean value of hybrid, P1= mean of smaller parent, P2 = mean of greater parent, M.P. = mid parent value.

Combining ability variances and effects were worked out according to Griffing's (1956) approach. Method 2 and Model 1 were considered most appropriate for the materials under study. Method 2 was applicable to the present study as parents and one set of non-reciprocals F1s were included. Model 1 assumes that variety and block effects are constant, but the environmental effect is variable, and the experimental material is the population about which inferences are to be made. The additive and non-additive genetic variances were estimated from the combining ability using a method described by Verma and Srivastava (2004). Most of the statistical analysis were done using Windostat version 9.3 (Indostat Service Hyderabad), and the rest were done using Microsoft Excel.

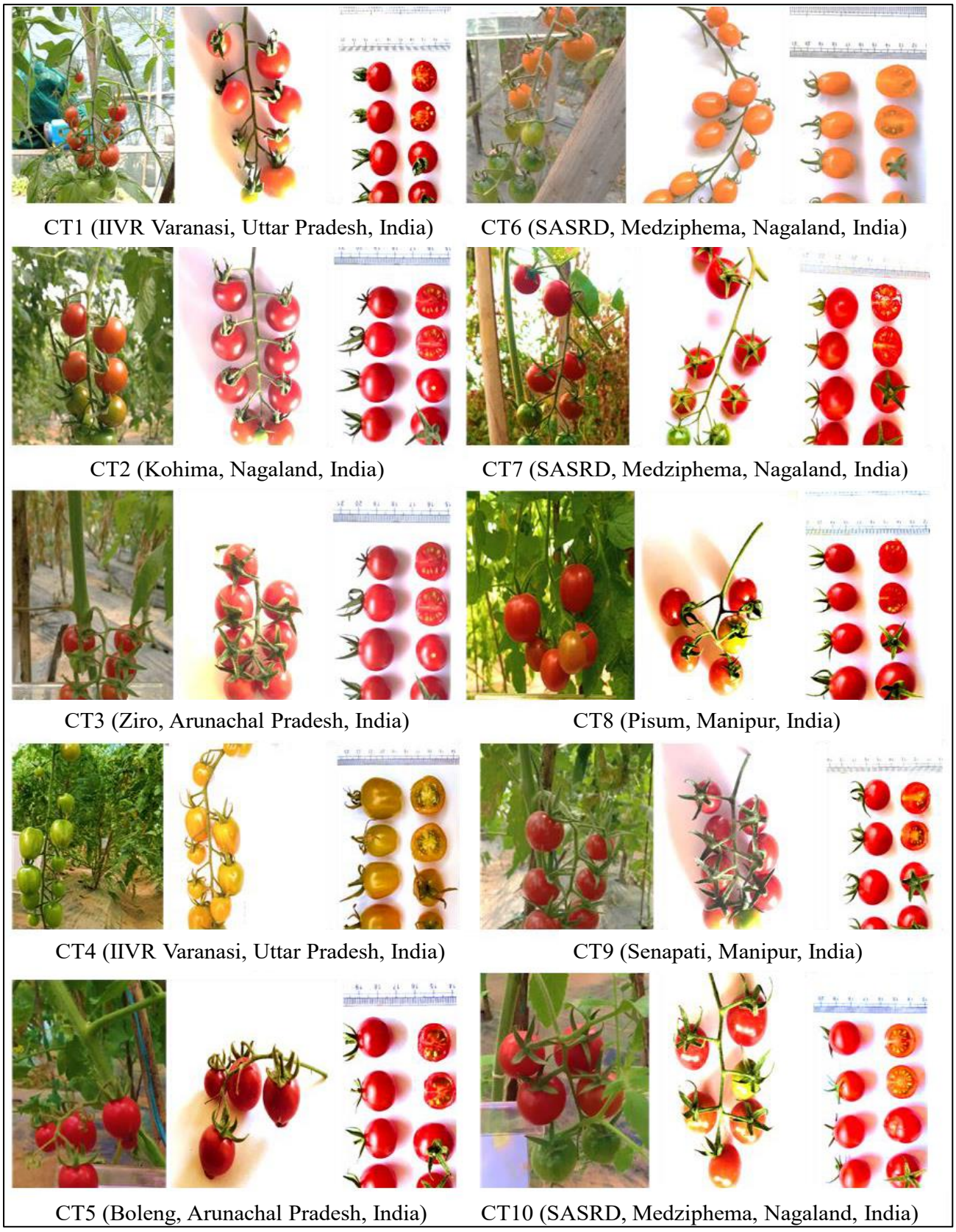

Figure 1. Fruits of cherry tomato genotypes designated as CT-1 to CT-10 (CT for Cherry tomato) were used in the present experiment as parental lines for the development of F_1 hybrids. IIVR: Indian Institute of Vegetable Research; SASRD: School of Agricultural Sciences and Rural Development.

Results and Discussion

Genetic Diversity and Trait Variability

The ten parental genotypes used in this study demonstrated significant genetic variation across morphological, physiological, and biochemical values of traits (Supplementary tables S1, S2, and Table 1). Cluster analysis and Mahalanobis D2 statistics (Figure 2A) also revealed high distances within and between groups, confirming the presence of large genetic divergence between genotypes, which is the prerequisite for effective hybridization and exploitation of heterosis (Raina et al. 2015). PCA revealed that PC1 alone explained over 97% of the total variation (Figure 2B), with yield per plant (YP), fruit weight (FW), and number of fruits per cluster (NFC) contributing most prominently to PC1 (Figure 2C). These findings align with similar observations in tomato by Williams and Anbuselvam 2023 and Prakash and Vijay 2017, emphasizing the importance of these traits in explaining genetic divergence.

ANOVA for yield and quality traits (Supplementary Table 3) showed significant differences among parental genotypes and hybrids, confirming the presence of considerable variability. The traits exhibited considerable variability among the genotypes, as reflected by the estimates of the GCV and PCV. The highest GCV (49.61%) and PCV (50.18%) were recorded for yield per plant, indicating a wide range of genetic variability for this trait (Table 1). This was followed by fruit weight and number of fruits per cluster, which also showed relatively high GCV and PCV values. The close correspondence between GCV and PCV values for these traits suggests that the observed variation is largely due to genetic factors with minimal environmental influence. Hence, these traits are likely to respond effectively to selection, as reported by Thakur et al. (2025), and can be considered important criteria for improving yield potential in cherry tomato breeding programs. High heritability estimates coupled with high genetic advance as a percentage of the mean were recorded for fruit length (99.1%), fruit weight (97.7%), and Yield per Plant (97.6%) (Table 1). Such combination of high heritability and high genetic advance indicates that these traits are predominantly governed by additive gene action, with minimal environmental influence (Hossain et al. 2021). This implies that the expression of these traits is largely heritable and that selection based on phenotypic performance would be highly effective (Hossain et al. 2021). Therefore, these characters can be reliably improved through simple and direct selection methods suggests the predominance of additive gene effects and confirms that these traits can be improved through simple selection methods

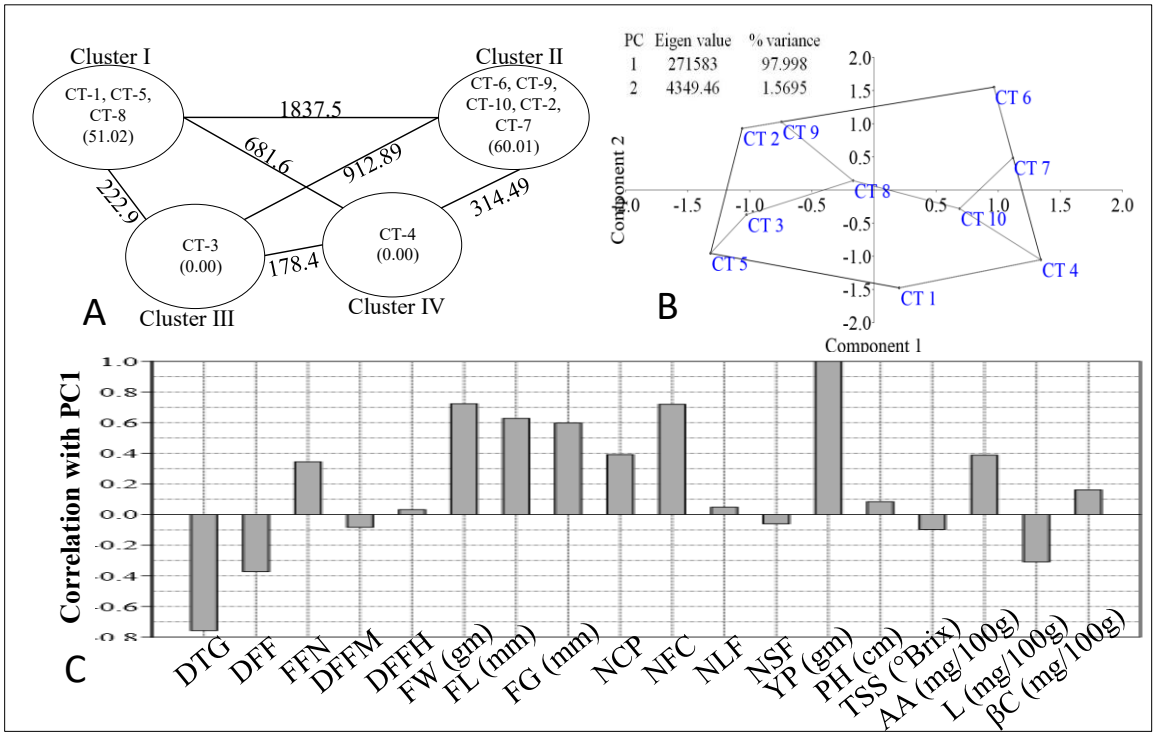

Figure 2. Analysis of parental genotypes diversity **(a)** Cluster diagram with inter and intra cluster distance, **(b)** Scatter plot showing the % variance explained by principal components (PC) 1 & 2. Eigenvalue score and % variance explained by PC1 & PC2 are mentioned at the bottom of the scatter plot, and **(c)** Correlation of different physiological, morphological, and biochemical traits with principal component 1 (PC1), which has explained more than 97% of variation present in the parental genotypes.

Combining Ability and Gene Action

Combining ability analysis using Griffing's Method 2, Model 1 revealed highly significant effects of general and specific combining abilities (GCA and SCA) for most of the studied traits (Table 2; Supplementary Table 1B), this indicates the contribution of both additive and non-additive gene actions to the inheritance of these traits. However, the GCA/SCA ratio was less than unity for almost all traits, indicating the predominance of non-additive gene action. This is consistent with earlier findings by Amin et al. (2017) and Gautam et al. (2018), who reported the importance of non-additive effects for yield and quality traits in tomato. Among the parental genotypes, CT10, CT7, and CT4 exhibited significant and positive GCA effects for multiple traits (Table 2). CT10 was a good general combiner for nine traits including yield per plant, fruit weight, TSS, ascorbic acid, and β-carotene, while CT 7 and CT 4 were good combiners for lycopene, ascorbic acid, and yield per plant as indicated as explained by Specific combining ability (SCA) effects of crosses (hybrids) for yield and quality attributing traits in cherry tomato (Table 3). These results corroborate the reports of Chattopadhyay et al. (2011), who emphasized the use of good combiners in hybrid development for quality and productivity.

Performance of Specific Crosses

The hybrid CT 2 x CT 7 was the most promising, showing superior SCA effects for yield per plant, fruit weight, number of fruits per cluster, and biochemical traits like the fruit content of ascorbic acid and β-carotene (Table 3). This hybrid combined one high GCA parent, CT 7, with another good combiner, CT 2, exemplifying complementary gene action. Other hybrids such as CT 3 x CT 4 and CT 1 x CT 10, also showed significant SCA for multiple traits, indicating their potential for hybrid development.

The analysis of different cross types (HxH; HxL; LxH and LxL) further confirmed the contribution of both additive and epistatic effects in trait expression. Hybrids from HxL or LxH crosses, such as CT 2 x CT 7 and CT 5 x CT 7, demonstrated superior performance for yield and quality traits, indicating the role of complementary gene action.

Heterosis and Potence Ratio

Significant heterosis over both mid and better parents was recorded for several traits, indicating the presence of substantial hybrid vigor among the evaluated crosses. A total of 19 hybrids exhibited positive and significant better-parent heterosis for yield per plant, while 20, 13 and 15 hybrids showed favourable better-parent heterosis for ascorbic acid content, lycopene content, and β-carotene content, respectively. The CT2 × CT7 hybrid showed the highest relative heterosis in yield per plant trait, outperforming its best parent (151.12%) and desirable heterosis for several other traits (Table 4). These results are supported by earlier studies (Yashavanthakumar, 2008; Santosh et al., 2011) that emphasized heterosis as an effective breeding strategy for improving yield and quality traits in cherry tomato. These results highlight the potential of specific hybrid combinations for simultaneous improvement of yield and nutritional quality through heterosis breeding.

Potence ratio analysis revealed a wide range of dominance effects among hybrids. Traits such as plant height and days to first fruit harvest exhibited over-dominance, while fruit weight and lycopene content showed partial to complete dominance (Figure 3A and 3B). These observations are consistent with the work of Kurian et al. (2001) and Kumar et al. (2014), who documented diverse gene actions for biochemical traits in tomato.

234 **Table 1.** Mean, range, variability, heritability, and genetic advance % of the mean yield and quality attributing traits of cherry tomato.

Traits	Mean	Range		Variability		Heritability	Genetic advance	Genetic advance as per cent of the mean
		Min	Max	GCV %	PCV %			
Days to germination	4.29	2.07	7.33	44.66	46.9	90.6	3.76	87.59
Days to first flowering	33.05	25.5	45.5	20.16	20.24	69.1	13.66	41.34
First flowering node	10.03	7	13.33	20.96	22.19	89.2	4.09	40.8
Days to first fruit maturity	29.2	24.5	35.5	11.42	11.92	91.8	6.58	22.53
Days to first fruit harvest	106.06	93.66	119	9.32	9.46	57.2	20.09	18.94
Fruit weight (gm)	6.16	2.45	10.5	38.19	48.63	97.7	4.79	77.76
Fruit length (mm)	22.2	17.04	31.34	20.18	20.28	99.1	9.19	41.39
Fruit girth (mm)	21.54	16.5	26.63	16.45	16.7	27	7.19	33.37
Number of clusters per plant	9.6	5.5	11.5	17.08	17.8	92	3.24	33.75
Number of fruits per cluster	10.01	6	19.5	45.36	46.01	97.2	9.23	92.15
Number of locules per fruit	2.26	2	2.87	11.77	14.27	68	0.45	19.99
Number of seeds per fruit	79.06	33.33	144	40.14	41.41	93.9	63.37	80.15
Yield per plant (gm)	1046.26	361	1746.66	49.61	50.18	97.6	77.12	101.03
Plant height (cm)	309	214	417	21.32	21.37	89.6	1.35	43.83
Total soluble solids (˚Brix)	7.34	4.43	8.84	18.64	18.96	96.7	2.77	37.78
Ascorbic acid (mg/100g of sample)	40.88	26.09	53.6	19.57	19.8	77.7	16.29	39.84
Lycopene (mg/100g of sample)	5.62	2.63	8.29	31.25	31.47	88.6	3.59	3.94
Beta-carotene(mg/100g).	9.2	7.07	16.67	9.58	35.75	72	0.48	5.29

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Traits\Parents	CT-1	CT-2	CT-3	CT-4	CT-5	CT-6	CT-7	CT-8	CT-9	CT-10	CD at 5%
Days to germination	0.12	0.05	0.77	-0.49	1.1	-0.81	-0.77	0.1	0.26	-0.33	0.3
Days to first flowering	1.6	0.02	0.52	1.72	3.31	-0.77	-2.86	-0.07	-3.36	-0.11	0.26
First flowering node	-0.77	-0.56	0.12	-0.45	-0.11	0.1	0.56	0.23	0.8	0.09	0.29
Days to first fruit maturity	-0.54	0.91	-0.11	0.45	-0.05	-0.04	-1.08	0.74	-0.64	0.36	0.34
Days to first fruit harvest	3.82	0.85	3.94	1.7	1.49	1.24	-3.11	-1.37	-1.83	-6.71	0.66
Fruit weight (gm)	-0.96	0.46	-1.82	0.46	-1.18	-0.6	1.15	0.31	0.27	1.96	0.13
Fruit length (mm)	-1.41	-1.02	-2.12	2.22	-0.66	1.94	-0.06	1.66	-1.04	0.5	0.59
Fruit girth (mm)	-0.89	-0.46	-3.1	0.72	-2.81	-0.14	2.28	1.66	0.11	2.62	0.17
Number of clusters per plant	-0.27	0.81	-0.65	-0.4	-0.77	0.72	-0.11	0.31	0.18	0.18	0.17
Number of fruits per cluster	-0.19	-1.02	-1.46	1.98	-1.48	2.94	0.44	-1.19	-0.76	0.76	0.26
Number of locules per fruit	0.11	0.12	0.11	-0.02	-0.17	0.05	0.02	-0.07	-0.01	-0.15	0.1
Number of seeds per fruit	9.53	15.25	-17.5	-12.1	-19.4	-6.42	10.50	-3.33	-7.81	31.36	2.94
Yield per plant (gm)	6.19	-117	-481	166.3	-375	32.52	393.9	21.16	161.7	192.2	67.38
Plant height (cm)	-0.33	0.21	-0.21	-0.25	-0.07	0.37	-0.06	0.04	0.12	0.19	0.5
Total soluble solids (˚Brix)	-0.4	0.45	-0.48	-0.04	0.64	0.06	0.35	-0.43	-0.37	0.22	0.09
Ascorbic acid (mg/100g of sample)	-7.04	0.69	-5	0.88	-0.59	5.12	3.26	1.28	2.38	-0.97	0.48
Lycopene (mg/100g of sample)	0.04	-0.23	-0.26	-0.8	1.01	-0.94	0.9	-0.29	-0.26	0.83	0.12
Beta-carotene(mg/100g).	-1.45	-1.28	0.09	1.1	0.37	0.84	0.1	-0.15	-0.18	0.56	0.07
Blue shaded values are significant at 5% and orange shaded values are significant at 1%, respectively											

Table 2. General combining ability (GCA) effects of parents (Genotypes) for yield and quality attributing traits in cherry tomato.

248 **Table 3.** Specific combining ability (SCA) effects of crosses (hybrids) for yield and quality attributing traits in cherry tomato.

S. N.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	C. D at 5%
Cross / Traits	G1× G2	G1× G3	G1× G4	G1× G5	G1× G6	G1× G7	G1× G8	G1× G9	G1 × G10	G2 × G3	G2 × G4	G2 × G5	G2 × G6	G2 × G7	G2 × G8	G2 × G9	G2 x 10	G3 x G4	G3 x G5	G3 x G6	G3 x G7	G3 x G8	G3 x G9	
DTG	0.62	-1.5	3.71	-0.8	-0.2	0.33	0.45	-1.7	-2.1	0.53	0.45	-3.1	2.44	0.9	-1.1	-1.4	4.13	-1.42	0.65	-2.3	-1.3	2.15	-2.1	0.91
DFF	10.1	-0.4	-2.6	-7.2	3.42	3.50	-3.8	-6.9	-1.2	6.21	0.01	-5.6	-1.5	-4.4	-4.2	1.08	6.84	-1.99	-6.1	-2.5	0.08	-0.2	-1.2	0.78
FFN	-.04	0.62	0.85	1.50	-1.4	-.16	-1.6	0.94	-3.1	-0.6	0.98	3.96	-1.9	-.04	-.04	-1.6	1.77	0.3	-0.8	-0.6	1.28	0.61	-3	0.87
DFFM	5.01	-1.6	-0.7	-3.1	-0.2	2.83	3.51	-2.6	-3.6	-7.7	-3.6	-2.1	-2.6	1.39	1.07	-.05	1.95	-1.12	-1.6	-0.6	1.40	1.58	-3.6	1.02
DFFH	5.04	-2.5	-1.3	4.91	-13	4.5	-13	5.23	7.6	-7.5	-3.8	2.88	-5.3	-14	8.74	10.2	8.57	-0.93	0.78	-7.4	6.38	-1.86	8.6	1.98
FW	-2	-0.2	-2.8	0.98	-0.9	-2.4	-3.1	1.49	4.15	2.2	1.67	-.01	-1.2	3.43	0.2	-0.2	2.53	4.76	-0.7	-0.9	-2.8	-0.82	4.15	0.39
FL	1.76	0.66	-1.9	-0.1	-1.5	2.04	1.82	2.52	-9.8	1.01	-2.3	1.57	-1.9	6.32	-3.3	-5.1	2.68	-4.16	-.05	-1.9	-3.6	-0.34	-9.8	1.76
FG	1.88	1.52	0.19	-2.8	-0.4	1.14	-0.2	-6.6	-2.2	-2.9	2.26	6.30	-0.8	-.12	-1.4	2.43	-2.5	0	-0.5	-4.1	0.55	1.163	-2.2	0.5
NCP	-0.8	1.67	-1.6	1.79	-0.7	0.13	-2.3	-1.6	0.83	-1.4	0.34	3.71	-1.7	1.04	-1.3	3.25	-3.2	2.29	-1.3	0.67	-2.5	1.09	0.83	0.51
NFC	-1.8	4.12	-3.9	1.64	-4.3	-1.9	1.34	1.7	1.07	-.55	-1.5	0.96	-0.9	2.04	0.84	1.41	0.56	1.78	0.41	-.01	-2.5	-0.38	1.07	0.77
NLF	-0.3	0.46	0.32	-0.4	0.38	0.31	-.25	0.02	0.04	-0.6	0.44	1.11	-.03	-0.5	0.86	0.12	0.13	0.15	0.09	0.85	0.41	0.06	1.04	0.29
NSF	49.7	-6.1	30.4	6.76	-45	-32	0.02	13.2	29.9	-30	28.	6.04	-9.6	28.8	-43	-28	31.6	66.22	1.85	-1.5	-2	-4.9	29.9	8.8
YP	-216	-449	-353	533	-705	-397	748	304	552	-0.1	144	128	-419	1035	-98	460	-191	943.8	222	-469	43.3	-445	552	201.9
PH	0.20	0.76	-0.3	1.35	0.02	-1.1	-0.8	0.50	0.60	-0.5	1.24	0.05	0.07	-0.6	-0.3	-.01	0.18	0.23	-0.2	-0.5	-0.8	0.58	0.60	0.15
TSS	-1	1.06	-0.3	1.50	0.59	1.33	1.08	0.48	0.68	0.73	1.36	0.09	-1.1	-.88	-1.2	0.87	1.62	1.53	-2.4	-1.1	0.01	-0.65	0.68	0.2
AA	-8.1	-2.3	-4.1	8.58	0.84	-13	13.9	1.39	6.69	3.62	-7.6	4.05	-4.9	10.1	-5.6	13.3	-0.3	3.10	-10	1.44	7.61	-7.07	6.69	1.38
L	-1.6	-.01	-.07	-0.3	0.88	0.44	-0.7	-0.3	0.98	1.39	2.34	-0.5	0.18	0.36	-0.3	-1.7	-0.4	2.06	-0.8	-2.2	-0.5	-0.9	0.98	0.35
βC	1.78	-1.5	-3.7	-0.2	-2.2	-2.5	0.06	1.85	6.43	2.47	-2.7	0.80	-4.7	-0.3	2.02	-2.3	-1.1	2.35	4.01	-0.8	3.31	-0.06	6.43	0.2

Values significant at the 5% and 1% levels are highlighted with blue and orange shades, respectively

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250 S.N: Serial number of the crosses. DTG: Days to germination; DFF: Days to first flowering; FFN: First flowering node; DFFM: Days to first fruit maturity; DFFH: Days to
251 first fruit harvest, FW: Fruit weight (gm); FL: Fruit length (mm); FG: Fruit girth (mm); NCP: Number of clusters per plant; NFC: Number of fruits per cluster, NLF- Number
252 of locules per fruit, NSF-Number of seeds per fruit, YP-Yield per plant (gm), PH-Plant height (cm); TSS: Total soluble solids (˚Brix); AA: Ascorbic acid (mg/100g of sample);
253 L: Lycopene (mg/100g of sample),βC: Beta-carotene(mg/100g).

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Traits	Better parent heterosis range (%)	Mid-parent heterosis range (%)	Best hybrid
Days to germination	-69 to 165	-56.6 to 178.95	CT 9 x CT 10
Days to first flowering	-36 to 39.68	-25.88 to 47.9	CT 1 x CT 9
First flowering node	-43.75 to 62.5	-40 to 69.57	CT 1 x CT 10
Days to first fruit maturity	-34.27 to 25.49	-29.82 to 31.43	CT 2 x CT 3
Days to first fruit harvest	-16.88 to 21.76	-12.36 to 23.58	CT 1 x CT 8
Fruit weight (gm)	-66.65 to 80.42	-59.17 to 140.56	CT 2 x CT 3
Fruit length (mm)	-44.7 to 57.7	-38.4 to 59.84	CT 1 x CT 10
Fruit girth (mm)	-41.77 to 23.08	-39.33 to 31.84	CT 2 x CT 5
Number of clusters per plant	-34.78 to 38.1	-31.82 to 58.83	CT 6 x CT 10
Number of fruits per cluster	-30.31 to 63.56	-26.61 to 65.95	CT 2 x CT 5
Number of locules per fruit	-56.25 to 129.61	-33.86 to 194.62	CT 3 x CT 4
Number of seeds per fruit	-66.67 to 48	-53.29 to 72.09	CT 8 x CT 9
Yield per plant (gm)	-85.17 to 151.12	-77.7 to 153.81	CT 2 x CT 7
Plant height (cm)	-43.43 to 83.22	-30.06 to 93.15	CT 1 x CT 5
Total soluble solids (˚Brix)	-30.61 to 42.44	-27.66 to 60.66	CT 1 x CT 8
Ascorbic acid (mg/100g of sample)	-46.62 to 41.88	-40.85 to 54.24	CT 2 x CT 9
Lycopene (mg/100g of sample)	-68.79 to 81.96	-58.78 to 96.11	CT 6 x CT 9
Beta-carotene(mg/100g).	-77.2 to 96.25	-69.92 to 120.31	CT 5 x CT 9

Table 4. Relative heterosis % of the best hybrids compared to the mean of their respective parents and to the best parents for all studied traits.

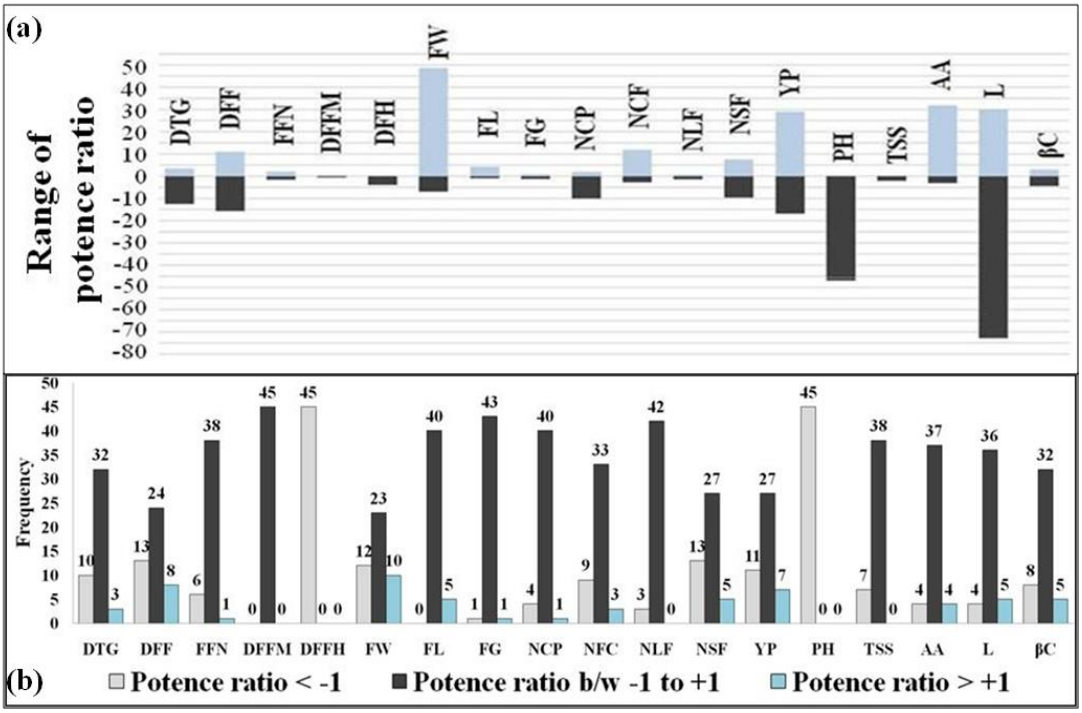

Figure 3. Potence ratio (Dominance effect) of the studied traits estimated from 45 hybrids**(a)** Range of potence ratio in hybrids, potence ratio ranging towards negative and positive values are highlighted with light & dark colour bars, respectively, and (**b)** Frequency of potence ratio in 45 hybrids. The frequency distribution is divided into three categories, *i.e.*, less than -1, -1 to +1, and more than +1. Values exceeding ±1 indicate over dominance, value within ±1 indicates partial dominance, and value of ±1 indicates complete dominance.

Correlation and Path Coefficient Analysis

The correlation analysis among yield and quality attributing traits in cherry tomato (Table 5) revealed that the genotypic correlation coefficients were generally higher than the corresponding phenotypic correlations, suggesting a strong inherent genetic association among these traits with minimal environmental influence. Fruit yield per plant exhibited highly significant and positive correlations with fruit weight, fruit length and number of fruits per cluster, indicating that improvement in these traits would directly enhance overall yield. Positive associations were also recorded with ascorbic acid and lycopene content, implying that selection for yield may simultaneously improve nutritional quality. Conversely, traits such as days to germination, days to first flowering and days to fruit maturity showed significant negative correlations with yield per plant, indicating that early flowering and fruiting genotypes tend to be higher yielders. Similar observations have been reported by Kumar et al. (2013); Akhter and Najnine (2022), who found that earliness traits generally exhibit negative associations with yield but are desirable for developing early, high-yielding hybrids in tomato. The path coefficient analysis (Table 6) provided further insights into the nature of direct and indirect effects of various traits on yield per plant. The residual effect (1.0106) indicated that

the selected traits collectively explained a substantial proportion of the variation in yield. Among all characters, fruit weight exhibited the highest positive direct effect on yield, followed by number of clusters per plant and ascorbic acid content, confirming their importance as the major yield-contributing traits. Traits such as fruit length and number of fruits per cluster exerted high indirect effects on yield through fruit weight, emphasizing their supportive role in yield improvement. On the contrary, traits like days to flowering, plant height and number of seeds per fruits showed negligible or negative direct effects, suggesting their limited or inverse contribution to yield. Similar results were reported by Hazra et al. (2011), Singh et al. (2018) and Nevani and Sridevi (2021), who emphasized that fruit weight, number of clusters per plant, and fruit size traits are the most critical yield determinants in tomato breeding and selection for these traits could indirectly improve yield,

Overall, the correlation and path analyses highlight that fruit weight, number of clusters per plant and ascorbic acid content are the key traits contributing directly to yield in cherry tomato. The strong positive association of these traits with yield, along with favourable correlations with nutritional parameters such as lycopene and β-carotene, underscores the potential for simultaneous improvement of both productivity and nutritional quality through selection.

These findings can guide breeders in formulating efficient selection strategies for developing high-yielding, nutritionally rich cherry tomato hybrids suitable for diverse growing environments

300 **Table 5.** Genotypic and phenotypic correlation among yield and quality attributing traits in cherry tomato.

Traits	DFF	FFN	DFFM	DFFH	FW	FL	FG	NCP	NFC	NLF	NSF	PH	TSS	AA	L	βC	Yield per plant	G/P
DTG	0.51	-0.12	-0.34	-0.05	-0.48	-0.47	-0.31	-0.59	-0.55	0.30	-0.13	-0.33	-0.38	-0.73	0.30	0.16	-0.77	G
	0.48	-0.15	-0.29	-0.05	-0.45	-0.45	-0.27	-0.54	-0.50	0.23	-0.10	-0.31	-0.36	-0.69	0.29	0.11	-0.72	P
DFF		-0.34	-0.12	0.18	-0.24	0.12	-0.02	-0.47	-0.24	-0.25	-0.13	-0.54	-0.35	-0.26	0.38	-0.22	-0.37	G
		-0.32	-0.09	0.17	-0.24	0.12	-0.02	-0.45	-0.23	-0.20	-0.13	-0.52	-0.34	-0.25	0.38	-0.06	-0.36	P
FFN			0.45	-0.48	0.50	-0.05	-0.02	0.20	-0.10	0.18	0.04	0.58	-0.15	0.09	0.14	0.08	0.35	G
			-0.39	-0.44	0.46	-0.03	-0.02	0.18	-0.12	0.12	0.04	0.55	-0.14	0.08	0.11	-0.10	0.33	P
DFFM				0.51	-0.18	-0.20	-0.45	0.34	0.23	0.18	0.34	0.12	0.42	0.17	-0.21	0.74	-0.08	G
				0.50	-0.18	-0.18	-0.40	0.31	0.22	0.14	0.31	0.12	0.39	0.16	-0.19	0.18	-0.08	P
DFFH					-0.49	0.13	-0.23	0.16	0.45	0.19	-0.34	-0.32	-0.07	-0.03	-0.56	-0.17	0.01	G
					-0.48	0.12	-0.22	0.15	0.43	0.15	-0.32	-0.31	-0.07	-0.02	-0.55	-0.07	0.02	P
FW						0.20	0.63	0.32	0.17	-0.25	0.50	0.06	-0.19	0.13	0.30	-1.03	0.73	G
						0.20	0.62	0.29	0.16	-0.20	0.49	0.06	-0.19	0.12	0.29	-0.07	0.70	P
FL							0.55	0.01	0.73	0.17	-0.52	-0.02	0.23	0.71	-0.47	-0.29	0.63	G
							0.55	0.02	0.72	0.14	-0.51	-0.02	0.21	0.70	-0.46	-0.21	0.61	P
FG								0.21	0.30	-0.09	0.13	-0.36	-0.37	0.05	-0.03	-1.21	0.60	G
								0.19	0.29	-0.07	0.13	-0.35	-0.36	0.04	-0.02	-0.10	0.58	P
NCP									0.21	0.05	-0.42	0.44	-0.21	0.07	-0.38	0.69	0.40	G
									0.21	0.04	-0.34	0.42	-0.20	0.06	-0.35	-0.27	0.37	P
NFC										0.47	-0.44	0.06	0.35	0.63	-0.76	-0.19	0.63	G
										0.41	-0.42	0.07	0.35	0.61	-0.73	0.06	0.70	P
NLF											-0.56	0.35	0.07	0.03	-0.74	0.98	0.07	G
											-0.46	0.29	0.06	0.01	-0.61	-0.04	0.01	P
NSF												0.04	-0.26	-0.39	0.55	-0.09	-0.05	G
												0.03	-0.26	-0.37	0.53	0.20	-0.06	P
PH													0.43	0.45	-0.28	1.67	0.08	G
													0.42	0.44	-0.28	0.01	0.08	P
TSS														0.76	-0.28	0.86	0.04	G
														0.75	-0.27	0.4	0.05	P
AA															-0.41	0.43	0.53	G
															-0.40	0.28	0.52	P
L																-0.65	-0.32	G
																0.11	-0.31	P
βC																	-1.09	G
																	-0.23	P

Values significant at the 5% and 1% levels are highlighted with blue and orange shades. G: Genotypic correlation; P: Phenotypic correlation.

Table 6. Genotypic path coefficient showing direct (diagonal blue shades) and indirect effects of seventeen traits on fruit yield per plant in cherry tomato (Residual effect: 1.0106).

Traits	DTG	DFF	FFN	DFFM	DFFH	FW	FL	FG	NCP	NFC	NLF	NSF	PH	TSS	AA	L	βC
DTG	**0.01**	0.24	-0.06	-0.16	-0.02	-0.23	-0.22	-0.15	-0.28	-0.26	0.14	-0.06	-0.16	-0.18	-0.35	0.14	0.08
DFF	0.17	**0.33**	-0.11	-0.04	0.06	-0.08	0.04	-0.01	-0.16	-0.08	-0.08	-0.04	-0.17	-0.12	-0.08	0.13	-0.07
FFN	-0.04	-0.11	**0.32**	-0.15	-0.16	0.17	-0.02	0.00	0.07	-0.03	0.06	0.02	0.19	-0.05	0.03	0.05	0.03
DFFM	0.05	0.02	0.07	**-0.14**	-0.07	0.03	0.03	0.07	-0.05	-0.03	0.03	-0.05	-0.02	-0.06	-0.03	0.03	-0.11
DFFH	-0.03	0.01	-0.03	0.04	**0.07**	-0.04	0.01	-0.02	0.01	0.03	0.01	-0.02	-0.02	-0.01	0.00	-0.04	-0.01
FW	-0.30	-0.15	0.32	-0.12	-0.31	**0.63**	0.13	0.40	0.20	0.11	-0.16	0.32	0.04	-0.12	0.09	0.19	-0.65
FL	0.56	-0.15	0.06	0.24	-0.16	-0.24	**-1.19**	-0.66	-0.02	-0.87	-0.21	0.62	0.03	-0.25	-0.84	0.56	0.35
FG	-0.14	-0.01	0.00	-0.21	-0.11	0.29	0.26	**0.47**	0.10	0.14	-0.05	0.06	-0.17	-0.18	0.03	-0.01	-0.57
NCP	-0.22	-0.18	0.08	0.13	0.06	0.12	0.01	0.08	**0.37**	0.08	0.02	0.16	0.16	-0.08	0.03	-0.14	0.26
NFC	-0.22	-0.10	-0.04	0.10	0.19	0.07	0.30	0.12	0.09	**0.41**	0.20	-0.18	0.02	0.15	0.26	-0.32	-0.08
NLF	-0.03	0.03	-0.02	0.02	-0.02	0.03	-0.02	0.01	-0.01	-0.05	**-0.11**	0.06	-0.04	-0.01	0.00	0.08	-0.11
NSF	0.05	0.06	-0.02	-0.15	0.15	-0.22	0.23	-0.06	-0.19	0.19	0.25	**-0.44**	0.00	0.12	0.17	-0.24	0.04
PH	0.16	0.26	-0.29	-0.06	0.16	-0.03	0.01	0.18	-0.22	-0.03	-0.18	0.00	**-0.50**	-0.22	-0.23	0.14	-0.84
TSS	-0.01	-0.01	-0.01	0.02	0.00	-0.01	0.01	-0.01	-0.01	0.01	0.00	-0.01	0.02	**0.04**	0.03	-0.01	0.03
AA	0.69	-0.24	0.09	0.17	-0.03	0.13	0.68	0.05	0.07	0.60	0.03	-0.37	0.43	0.73	**0.55**	-0.39	0.40
L	-0.09	-0.13	-0.05	0.07	0.19	-0.10	0.16	0.01	0.13	0.25	0.25	-0.18	0.09	0.09	0.14	**-0.33**	0.21
βC	0.01	0.00	0.00	0.01	0.00	-0.02	0.00	-0.02	0.01	0.00	0.01	0.00	0.03	0.01	0.01	-0.01	**0.01**

DTG: Days to germination; DFF: Days to first flowering; FFN: First flowering node; DFFM: Days to first fruit maturity; DFFH: Days to first fruit harvest, FW: Fruit weight (gm); FL: Fruit length (mm); FG: Fruit girth (mm); NCP: Number of clusters per plant; NFC: Number of fruits per cluster, NLF- Number of locules per fruit, NSF-Number of seeds per fruit, YP-Yield per plant (gm), PH-Plant height (cm); TSS: Total soluble solids (˚Brix); AA: Ascorbic acid (mg/100g of sample); L: Lycopene (mg/100g of sample),βC: Beta-carotene(mg/100g).

Conclusions

The present study demonstrates the effectiveness of heterosis breeding in enhancing both yield and nutritional quality in cherry tomato using genetically diverse parental genotypes. Among the evaluated hybrids, the CT2 × CT7 hybrid emerged as the most promising, exhibiting superior performance for fruit yield, β-carotene, and ascorbic acid content. The predominance of non-additive gene action in most traits highlights the potential of hybrid breeding strategies in this crop. Additionally, parental lines such as CT 2, CT 4, CT 7, and CT 10 were identified as excellent general combiners, offering valuable genetic resources for future improvement programs. Likewise, the study indentifies fruit weight, number of clusters per plant, and ascorbic acid content as key determinants of yield and nutritional quality, offering valuable targets for breeding high-yielding, nutrient-rich cherry tomato cultivars.

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