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GENETIC DIVERSITY AND MORPHO-PHYSIOLOGICAL TRAITS IN CHERRY TOMATO GENOTYPES IN NORTH-WESTERN HIMALAYAS

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Abstract

The investigation conducted an analysis of 23 cherry tomato genotypes, examining 19 qualitative and quantitative traits related to plants, flowers, fruits, and seeds. A wide spectrum of variability was observed among the cherry tomato genotypes. The correlation coefficients unveiled significant positive and negative relationships between various traits, particularly emphasizing flowering time, fruit quality, and biochemical characteristics. The evaluation through path coefficient analysis pinpointed essential factors that affect fruit yield per plot, highlighting traits such as stem girth, number of fruits per cluster, pericarp thickness and shelf-life. PCA indicated that both quantitative and qualitative morphological parameters captured a substantial amount of variability. The hierarchical cluster analysis categorized the genotypes into groups, suggesting opportunities for breeding for different objectives. The dendrogram illustrated differences and similarities in traits among cherry tomato genotypes. Therefore, selection based on these traits could be effective for higher yield in cherry tomato genotypes.

Introduction

Tomato (*Solanum lycopersicum* L.), originating in South America, is extensively cultivated globally. The ancestor of cultivated tomato is cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) which thrives well in diverse climates and soils, particularly in tropical and subtropical regions of America, Asia, and Africa (Shiksha and Sharma 2018). These tomatoes are valued for their resilience against heat and drought, and their use in various culinary forms such as sauces, ketchups, and purees (Prema *et al.* 2011). They have indeterminate growth, robust branches, and clustered berry fruits, gaining popularity in India due to their high nutritional value, including elevated levels of ascorbic acid, lycopene, and beta-carotene, which provide numerous health benefits (Tsouvaltzis *et al.* 2023).

The rising demand for cherry tomatoes highlights the need to identify genotypes that can adapt to different environments for commercial cultivation (Pobiega *et al.* 2020). This study evaluated cherry tomato genotypes based on stability, growth, yield, and quality in regions like Himachal Pradesh (Flores *et al.* 2017). It employs path analysis to assess the direct and indirect effects of various traits, analyzing 19 characteristics among 23 genotypes. The study uses multivariate analysis, specifically PCA, to pinpoint the most important traits that help distinguish between different genotypes, particularly in the low-hill regions of Himachal Pradesh.

Materials and Methods

The study was conducted in the Department of Vegetable Science, College of Horticulture and Forestry, Neri, Hamirpur, Himachal Pradesh, India, using 23 semi-determinate to indeterminate tomato genotypes, including a check cultivar. The experiment was laid out in a

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randomized complete block design (RCBD) with three replications, with seedlings raised in a nursery and transplanted to the field at 90 × 30 cm spacing in 1.5 × 1.5 m² plots (10 plants per plot). Standard agronomic practices were followed (Anonymous 2022), and observations were recorded on morphological, physico-chemical, and biochemical traits. Morphological parameters included plant height, stem girth, days to 50% flowering, first fruiting node, flowers per cluster, and fruit set percentage. Fruit traits such as weight, dimensions, locules, pericarp thickness, shelf life, seeds per fruit, seeds per gram, and yield per plant were assessed. Biochemical traits were assessed using established protocols. Data were analyzed using SPSS (v20) to perform correlation and hierarchical clustering analyses were conducted using PAST (v4.11), and PCA was performed to reduce data dimensions and understand trait relationships. Results were visualized through scatter plots, and PCA biplots to provide insights into variability and associations among traits.

Results and Discussion

Analyzing quantitative data using a simple correlation coefficient method, a straightforward study of the correlation coefficient revealed the existence of strong positive and negative correlations among different attributes. The genotypic and phenotypic correlations were calculated to ascertain how the various traits are related to yield and with one another. The results of a correlation analysis showed that genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients, indicating the inherent association between various characters. The consequences of present study indicated that the genotypic and phenotypic correlation coefficients among different characters showed that fruit yield per plot had positive and significant correlation with days to 50% flowering, first fruiting node, stem girth, number of flowers per cluster, number of fruits per cluster, percentage of fruit set, average fruit weight, fruit length, number of locules per fruit, pericarp thickness, shelf life, total soluble solids, ascorbic acid, and number of seeds per fruit (Fig. 1). These results are similar to the findings of Meena and Bahadur (2014), Pujer *et al.* (2015), Naveen *et al.* (2017) and Jogi *et al.* (2018).

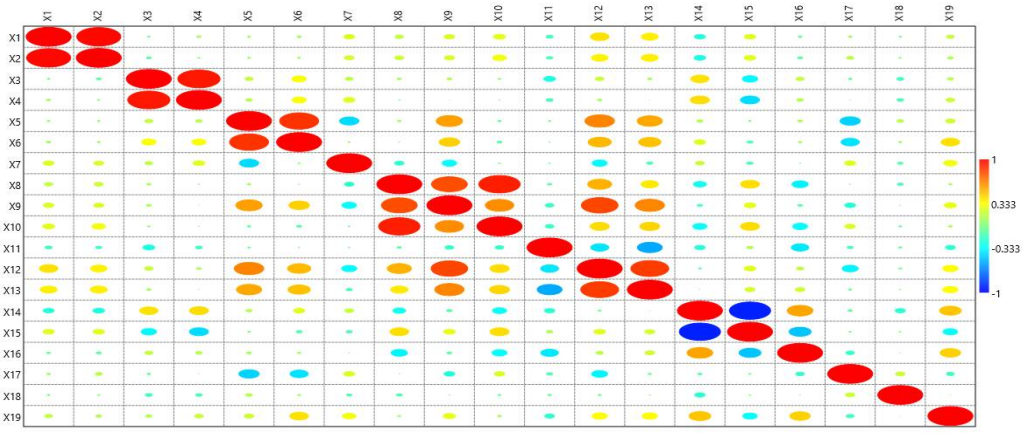

Fig. 1. Genotypic and phenotypic coefficients of correlation among different characters in cherry tomato. Abbreviations are similar as in Table 1.

Table 1 displays route coefficient estimates for the direct and indirect effects of horticultural features on fruit yield. Path coefficient analysis showed a high positive direct effect for fruit yield per plot and was most positively affected by stem girth (1.251), number of fruits per cluster

Table 1. Path coefficient analysis showing the direct and indirect effect of eighteen characters on marketable fruit yield genotypic at level.

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18	X19
X1	**-0.232**	0.064	-0.007	0.143	-0.099	0.120	-0.064	0.003	0.095	-0.549	-0.043	0.173	0.142	0.130	0.218	-0.050	0.019	0.015	0.079
X2	-0.231	**0.064**	-0.013	0.147	-0.087	0.083	-0.059	0.004	0.092	-0.637	-0.027	0.156	0.145	0.128	0.346	-0.064	0.037	-0.016	0.070
X3	0.014	-0.007	**0.123**	-0.039	-0.257	0.397	-0.044	0.002	0.044	-0.130	-0.120	0.081	0.038	-0.113	0.003	0.103	-0.019	0.043	-0.120
X4	-0.027	0.008	-0.004	**1.251**	0.940	-0.613	-0.139	0.009	0.007	-1.256	0.137	-0.076	-0.047	0.008	-0.081	-0.050	0.083	0.079	0.228
X5	-0.016	0.004	0.022	-0.828	**-1.421**	1.087	0.135	0.001	0.234	0.145	-0.074	0.273	0.216	-0.064	0.339	0.050	-0.105	-0.043	0.045
X6	-0.023	0.004	0.040	-0.627	-1.262	**1.224**	0.016	-0.001	0.185	0.226	-0.109	0.220	0.192	-0.099	0.216	0.045	-0.096	-0.018	0.131
X7	-0.053	0.014	0.019	0.620	0.683	-0.070	**0.282**	-0.003	-0.141	0.039	-0.087	-0.159	-0.070	-0.036	-0.185	-0.012	0.068	0.049	0.394
X8	-0.040	0.012	0.011	0.596	-0.096	-0.036	0.050	**0.019**	0.319	-1.886	0.150	0.218	0.144	0.108	0.476	-0.214	0.006	0.039	0.123
X9	-0.054	0.015	0.013	0.022	-0.825	0.559	0.099	0.015	**0.404**	-1.293	0.063	0.348	0.251	0.037	0.513	-0.060	-0.057	0.005	0.055
X10	-0.062	0.020	0.008	0.771	0.101	-0.136	0.005	0.018	0.256	**-2.038**	0.180	0.181	0.172	0.133	0.457	-0.192	0.056	0.019	-0.052
X11	0.028	-0.005	-0.041	0.479	0.295	-0.371	0.068	0.008	0.071	-1.024	**0.358**	0.043	0.069	0.116	-0.012	-0.065	0.020	0.012	0.051
X12	-0.096	0.024	0.024	-0.229	-0.931	0.644	0.107	0.010	0.337	-0.885	0.037	**0.417**	0.331	0.043	0.262	0.093	-0.084	0.018	0.123
X13	-0.085	0.024	0.012	-0.151	-0.795	0.608	0.051	0.007	0.263	-0.910	0.064	0.359	**0.386**	0.023	0.298	0.121	-0.017	-0.008	0.250
X14	0.085	-0.023	0.039	-0.027	-0.258	0.344	-0.028	-0.006	-0.042	0.768	-0.117	-0.051	-0.026	**-0.353**	-0.245	0.256	-0.029	0.057	0.343
X15	0.051	-0.022	0.000	0.102	0.485	-0.265	-0.052	-0.009	-0.208	0.937	0.004	-0.110	-0.116	-0.087	**-0.995**	0.239	-0.019	0.139	-0.073
X16	0.020	-0.007	0.022	-0.110	-0.123	0.095	0.006	-0.007	-0.042	0.683	-0.041	0.068	0.082	-0.158	-0.415	**0.573**	-0.046	0.003	0.605
X17	-0.019	0.010	-0.010	0.446	0.641	-0.501	-0.082	0.000	-0.099	-0.484	0.031	-0.151	-0.028	0.044	0.080	-0.112	**0.234**	-0.057	0.054
X18	0.013	0.004	-0.019	-0.360	-0.224	0.082	0.050	-0.003	-0.007	0.139	-0.016	-0.027	0.012	0.073	0.506	-0.007	0.049	**-0.273**	-0.010

Residual effect 0.01650, Diagonal Figures represent the direct effect.

X1 = Days to 50% flowering, X2 = First flowering node, X3 = Plant height (cm), X4 = Stem girth (mm), X5 = Number of flowers per cluster, X6 = Number of fruits per cluster, X7 = Percentage of fruit set (%), X8 = Average fruit weight (gm), X9 = Fruit length (mm), X10 = Fruit width (mm), X11 = Number of locules per fruit, X12 = Pericarp thickness (mm), X13 = Shelf life (days), X14 = Total soluble solids (^{0}B), X15 = Titratable acidity (%),X16 = Ascorbic acid (mg/100g), X17 = Ascorbic acid (mg/100g), X18 = Number of seeds per fruit X19 = Fruit yield per plot (kg) .

(1.224), pericarp thickness (0.417), fruit length (0.404), shelf life (0.386), number of locules per fruit (0.358), percentage of fruit set (0.282), ascorbic acid (0.234), plant height (0.123), first flowering node (0.064), and average fruit weight (0.019). Path coefficient study showed that fruit width (-2.038), titrable acidity (-0.995), total soluble solids (-0.353), days to 50% blooming (-0.232), and quantity of seed per fruit had a high negative direct influence. This shows the necessity of direct selection for cherry tomato improvement. The indirect effects of most traits were moderate to strong, particularly for average fruit weight, fruit width, and the number of fruits per cluster. Rahman *et al.* (2015) revealed similar effects for the number of fruits per plant and average fruit weight. The residual effect (0.01650) on yield per plot was low, suggesting most of the yield components were included in this investigation. Overall, all these traits contributed to higher plant yield, which is consistent with findings by Thakur *et al.* (2022). Kumar *et al.* (2015) found that plant height, fruit weight, and fruit length directly affected fruit yield in tomatoes, similar results were found by Singh *et al.* (2018). Thus, factors like average fruit weight and number of fruits per plant positively correlated with yield and directly affected it. These features can be utilized as tomato selection indices to increase yield.

In the present study, the resulting dendrogram (Fig. 2) reveals numerous clusters of disparities and effectively portrays the full spectrum of variations among cherry tomatoes. The 23 cultivars were grouped into two major clusters (groups). One cluster contains ten cultivars, while the other cluster contains the remaining thirteen, and each cluster is further divided into 2 sub-clusters. Using the dendrogram as a basis, it is evident that the populations of cherry tomato genotypes used under trial exhibit significant phenotypic variability. While using multivariate analysis, in the present study, variability was observed in all 18 measured characteristics, suggesting the presence of a high degree of phenotypic polymorphism among the cultivars of cherry tomato. Similar results were found by Du *et al.* (2009) and Islam *et al.* (2019).

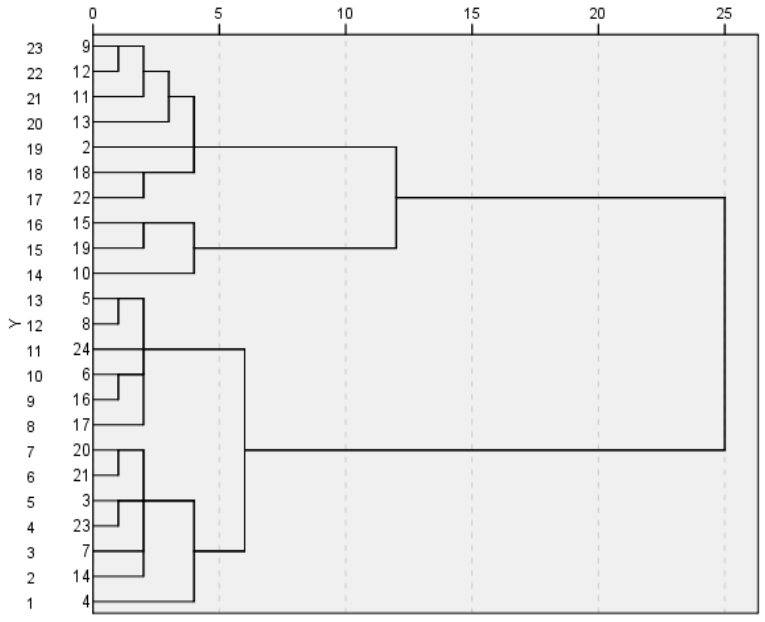

Fig. 2. Dendrogram visualization of 23 cherry tomato genotypes based on different qualitative and quantitative characters.

The PCA explained 82.24% of the total variation through six principal components (Table 2), highlighting significant genetic diversity in the cherry tomato population. PC1 (26.95%) contributed the highest variation, with positive associations for key traits such as fruit yield per plot and pericarp thickness, while traits like total soluble solids and number of locules per fruit exhibited negative correlations. PC2 (18.26%) accounted for a substantial portion of the variation, with fruit width showing a strong positive correlation, whereas plant height and titratable acidity had negative associations. PC3 (11.55%) emphasized reproductive and fruit quality traits, particularly shelf life, while negatively correlated with fruit weight and number of seeds per fruit. PC4 (10.66%) captured variations in pericarp thickness and fruit set percentage, which are crucial for fruit development and quality, whereas it showed negative associations with plant height and number of locules per fruit. PC5 (7.67%) primarily influenced biochemical traits such as ascorbic acid, which plays a vital role in fruit nutritional quality. PC6 (7.14%) contributed to morphological variation, with plant height and number of seeds per fruit being the most influential factors, while fruit length and titratable acidity had negative correlations.

Table 2. Principal Component Analysis of 23 cherry tomato genotypes based on different qualitative and quantitative characters.

	PC1	PC2	PC3	PC4	PC5	PC6
Eigen Value (Root)	5.121	3.470	2.195	2.025	1.458	1.357
% Var. Exp.	26.954	18.265	11.554	10.659	7.673	7.140
Cum. Var. Exp.	26.954	45.219	56.773	67.432	75.105	82.245
X1	0.370	0.477	0.430	-0.549	-0.135	-0.323
X2	0.375	0.519	0.358	-0.582	-0.045	-0.249
X3	0.767	-0.550	-0.092	-0.144	-0.042	0.017
X4	0.630	-0.543	0.192	-0.179	-0.105	0.189
X5	0.150	-0.262	0.398	0.075	-0.266	0.478
X6	-0.255	0.700	0.327	0.410	-0.031	0.208
X7	0.894	0.145	-0.004	0.252	-0.081	0.111
X8	0.484	0.741	-0.022	0.329	-0.029	0.234
X9	0.900	-0.009	0.193	0.115	0.004	-0.216
X10	0.088	0.471	-0.272	0.568	0.319	-0.241
X11	-0.412	0.263	0.647	-0.197	-0.076	0.319
X12	0.838	0.229	0.007	0.329	-0.181	0.030
X13	0.735	-0.135	0.046	0.043	0.417	0.045
X14	-0.161	-0.591	0.184	0.265	-0.104	0.340
X15	-0.585	-0.285	0.292	0.299	-0.137	-0.463
X16	-0.054	-0.445	0.530	0.197	0.492	-0.261
X17	-0.349	0.501	-0.042	-0.235	0.278	0.359
X18	0.112	-0.038	-0.393	-0.459	0.622	0.276
X19	0.043	-0.067	0.695	0.194	0.543	0.060

Abbreviations are similar as in Table 1

The results suggest that the substantial variation among genotypes is primarily driven by a combination of yield-related, morphological, and biochemical traits, emphasizing the complexity of genetic diversity within cherry tomatoes. The strong contributions of traits such as pericarp thickness, fruit yield per plot, and shelf life indicate their potential importance in breeding programs aimed at improving both productivity and post-harvest quality. The findings of this study align with previous studies of Rai *et al.* (2017), Saputra *et al*. (2017), Hussain *et al.* (2018) and Jogi *et al*. (2018), further supporting the effectiveness of PCA in characterizing morphological

and biochemical diversity in cherry tomatoes. In addition, the relationship among the 23 cherry tomato genotypes was illustrated by scatter plots and PCA biplots based on the first two PCs (Fig. 3), which almost explained 45.21% of the total variation.

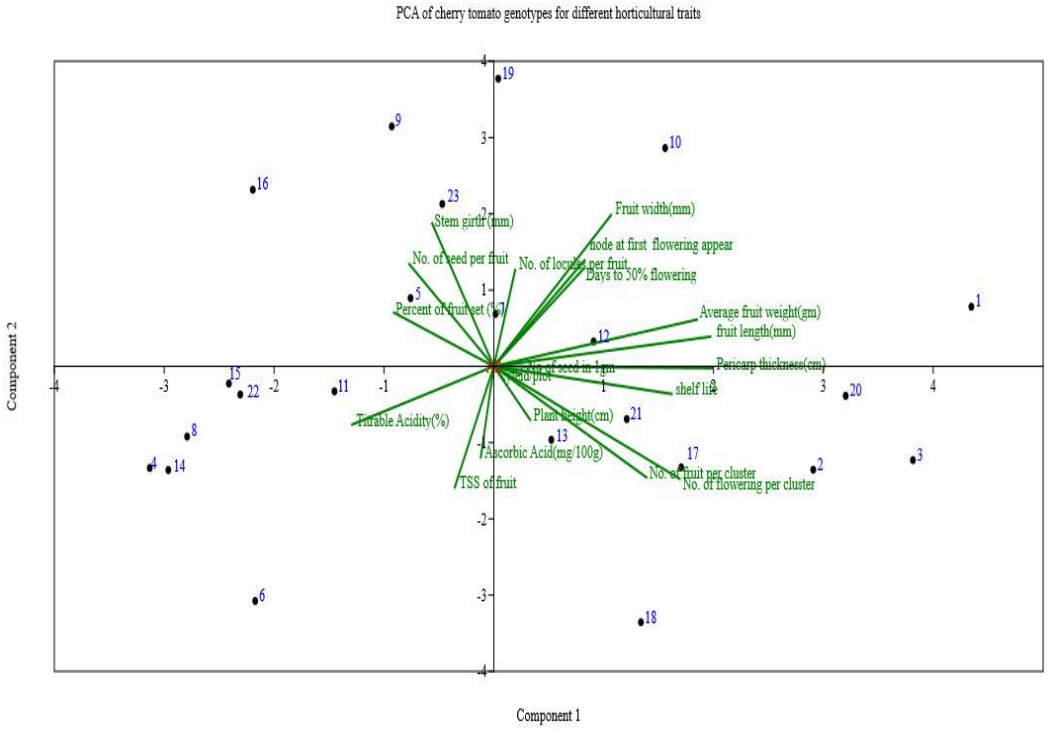

Fig. 3. Principal Component Analysis (PCA) of the cherry tomato genotypes for different traits illustrated by bi-plot.

The cherry tomato genotypes tested showed significant variation in qualitative and quantitative traits, which can improve cultivation. Substantial statistical variations among traits help choose genotypes with better physical and chemical properties. Additionally, PCA and cluster analysis reveal critical traits in cherry tomato genotype characterization. Understanding the genotypes' growth patterns, flowering behavior, and fruit quality may help to select germplasm for low-hill Himachal Pradesh farming. Cherry tomatoes, as potential progenitors, can play a pivotal role in tomato breeding initiatives by being key contributors to the development of new cultivars, specifically tailored to local conditions, combining superior fruit quality with enhanced adaptability.

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