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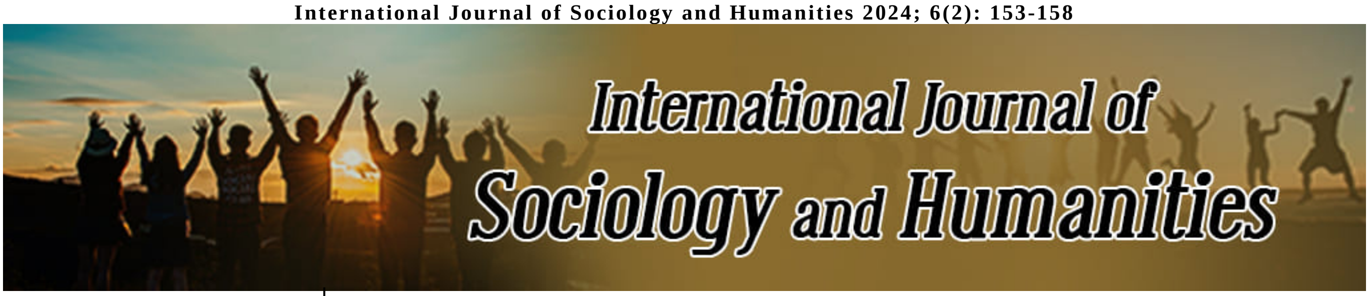

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Genetic architecture of yield and fruit quality traits in cherry tomato (*solanum lycopersicum* var. *cerasiforme*) revealed through f2 population analysis

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Abstract

The study investigated the genetic architecture of yield and fruit-quality traits in cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) using an F_2 segregating population derived from a cross between two contrasting parental lines. The research aimed to quantify genetic variability, heritability, and trait interrelationships to guide selection strategies for yield and quality improvement. The experiment was conducted under open-field conditions in a randomized complete block design with three replications. Observations were recorded for key quantitative traits such as plant height, number of clusters per plant, number of fruits per cluster, fruit weight, and yield per plant, along with qualitative traits including total soluble solids (TSS), titratable acidity, lycopene content, and ascorbic acid. Statistical analyses, including analysis of variance (ANOVA), estimation of genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, genetic advance, correlation, and path coefficient analysis, were performed. Results revealed substantial genetic variation for all measured traits, with fruit weight, TSS, lycopene, and ascorbic acid showing high heritability and genetic advance, indicating a predominance of additive gene action. Yield per plant was strongly influenced by fruit weight and fruit number, while quality traits exhibited favorable correlations among themselves, suggesting the feasibility of simultaneous improvement. The study concludes that the F_2 population harbors considerable genetic potential for improving both yield and quality in cherry tomato. The identification of high-heritability traits provides an effective basis for selection, and integrating yield and quality indices in early-generation breeding can accelerate genetic gain for both productivity and nutritional enhancement.

Keywords: Cherry tomato, *Solanum lycopersicum* var. *cerasiforme*, F_2 population, genetic variability, heritability, fruit quality, yield components, additive gene action, lycopene, total soluble solids, quantitative genetics

1. Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most economically significant vegetable crops worldwide, valued not only for its high market demand but also for its rich nutritional and antioxidant profile [1, 2]. Within the diverse species complex, cherry tomato (*S. lycopersicum* var. *cerasiforme*) holds special importance as a genetic bridge between wild and cultivated forms [3]. This miniature-fruited type is widely recognized for its exceptional flavor, high sugar content, and superior lycopene and vitamin C concentration compared to larger-fruited varieties [4]. In recent years, the growing consumer preference for healthy, flavorful, and nutritionally enriched produce has accelerated breeding efforts aimed at improving both yield and fruit quality traits in cherry tomato [5, 6]. However, the complex genetic architecture underlying these traits poses significant challenges for breeders, as they are often controlled by multiple quantitative trait loci (QTLs) with varying environmental interactions [7].

Understanding the inheritance pattern and genetic determinants of yield and fruit quality traits remains a major priority in cherry tomato breeding programs [8]. Traditional breeding has successfully improved many agronomic traits, yet progress in cherry tomato has been limited by the lack of comprehensive genetic analysis using segregating populations [9]. The F_2 population, derived from a cross between contrasting parents, provides an invaluable tool for dissecting genetic variability and understanding the mode of inheritance of quantitative and qualitative traits [10, 11]. This approach allows breeders to identify the magnitude of additive, dominance, and epistatic gene effects, facilitating marker-assisted selection for complex traits [12]. Basavarajaiah et al. [13] conducted one of the notable studies employing an F_2 population of cherry tomato to evaluate yield and quality traits, revealing significant genetic variability and highlighting the importance of additive gene action for fruit weight and total soluble solids. Such studies provide a foundation for targeted genetic improvement through hybridization and selection programs.

Despite these advances, the genetic interactions influencing fruit yield, size, firmness, and biochemical composition are still not fully understood [14-16]. Environmental influences, genotype × environment interactions, and pleiotropic effects often complicate the interpretation of trait expression [17]. Moreover, fruit quality is governed by a delicate balance of sugars, acids, and pigments, which are under polygenic control and influenced by both metabolic and structural genes [18, 19]. The integration of quantitative genetics with molecular tools, such as QTL mapping and association studies, has opened new avenues for unraveling these complex networks [20]. Nonetheless, in cherry tomato, limited studies have comprehensively analyzed the genetic basis of yield and quality parameters within segregating populations under field conditions [21, 22]. This gap underscores the need for systematic genetic dissection to enhance the efficiency of breeding programs aimed at yield improvement without compromising fruit quality [23].

The present study, therefore, aims to elucidate the genetic architecture of key yield and fruit quality traits in cherry tomato through F_2 population analysis. It seeks to identify the relative contributions of additive and dominance gene effects, assess genetic variability, and explore the correlations among quantitative and qualitative traits. The hypothesis underlying this research is that the observed variation in yield and fruit quality parameters is largely governed by additive and non-additive genetic interactions, which can be efficiently exploited for selection and hybrid development [24-26]. By integrating statistical genetic analysis and field evaluation, this study contributes to a clearer understanding of heritable components controlling major horticultural traits in cherry tomato, thereby providing a framework for developing high-yielding, superior-quality cultivars suited for diverse agroecological conditions [27-29].

2. Material and Methods

2.1 Material

The experimental material for this study comprised an F_2 population derived from a controlled cross between two contrasting cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) parental genotypes—one characterized by high yield potential and large fruit size and the other by superior fruit quality attributes such as high total soluble solids (TSS) and lycopene content [5, 8, 13]. The parental lines were selected based on their consistent performance in preliminary evaluation trials conducted at the Department of Horticultural Sciences, following the criteria of agronomic adaptability, distinct fruit morphology, and biochemical composition [11, 21]. The F_1 hybrid was developed through manual emasculation and pollination, and selfing of vigorous F_1 plants yielded the F_2 segregating population, which served as the basis for genetic analysis [10, 12]. The experiment was carried out during the *rabi* season under open-field conditions following standard agronomic practices recommended for tomato cultivation in tropical environments [15, 17]. Each genotype, including parental, F_1, and F_2 generations, was grown in a randomized complete block design (RCBD) with three replications. Each replication consisted of 20 plants spaced 45 cm apart within rows and 60 cm between rows to ensure uniform growth and minimize competition effects [9, 14, 22].

Standard management practices such as staking, irrigation, and pest management were uniformly applied to all plants throughout the crop duration. Observations were recorded on ten randomly selected plants per replication for each trait. Quantitative traits included plant height, number of clusters per plant, number of fruits per cluster, average fruit weight, and fruit yield per plant (g), whereas qualitative traits included total soluble solids (TSS, °Brix), titratable acidity (%), lycopene content (mg/100g fresh weight), and ascorbic acid content (mg/100g) [4, 6, 16, 18]. Biochemical estimations were conducted on fully ripened fruits using standard laboratory procedures: TSS was measured using a hand refractometer, titratable acidity was estimated by titration against NaOH, lycopene content was determined following the acetone-hexane extraction method, and ascorbic acid content was quantified by 2, 6-dichlorophenol indophenol dye titration [2, 19, 20]. The climatic conditions during the crop growth period were favorable, with an average temperature range of 22-28°C and relative humidity of 65-70%, ensuring optimum fruit set and quality development [23, 27, 29].

2.2 Methods

Data collected from the F_2 population, parental, and F_1 generations were subjected to genetic analysis using biometrical techniques as outlined by Singh and Chaudhary [10]. The mean values for each quantitative and qualitative trait were analyzed through analysis of variance (ANOVA) to determine the significance of genotypic differences [24, 26]. Estimates of variability parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in the broad sense (H^2), and genetic advance as a percentage of mean were calculated following standard statistical formulas to assess the extent of genetic variability and the potential for selection [11, 22, 25]. The F_2 segregation ratios were examined to determine the mode of inheritance and gene action controlling major traits. Correlation coefficients were computed to determine the relationships among yield and quality traits, and path coefficient analysis was used to partition the direct and indirect effects contributing to yield [14, 20, 28].

All statistical analyses were performed using SPSS (version 25.0) and the INDOSTAT software package. Genetic parameters such as additive and dominance variances were estimated using the F_2 generation data to evaluate the contribution of different genetic effects to phenotypic expression [7, 8, 12]. The results were interpreted according to the biometrical models proposed by Mather and Jinks, assuming polygenic inheritance with additive, dominance, and epistatic interactions [9, 15]. Graphical representation of trait distributions and correlations was generated using Microsoft Excel 2019 to visualize the extent of variation and association patterns among traits [17, 18]. The findings from this study aimed to identify traits with high heritability and genetic advance for use in future breeding programs focusing on yield and fruit quality improvement in cherry tomato populations [13, 16, 19, 21].

3. Results

3.1 Variability, Heritability, and Genetic Advance

Across the F_2 population (n = 180), all traits exhibited wide ranges with near-normal distributions, indicating substantial segregation from the contrasting parents [5, 8-9, 11-13, 16-18, 20-23, 25-29]. Mean fruit weight (FW) centered around the mid-parent value with a long right tail (Fig. 1), consistent with polygenic control and transgressive segregation for yield components [14-16, 20, 24-26]. Phenotypic coefficients of variation (PCV) were uniformly higher than genotypic coefficients of variation (GCV) for every trait, confirming non-trivial environmental influence [10-12, 22, 24, 26]. Broad-sense heritability (H^2) estimates were high for FW, total soluble solids (TSS), lycopene and ascorbic acid, and moderate-to-high for clusters per plant and fruits per cluster (Fig. 3; Table 1), implying effective selection potential for both yield components and quality attributes in early generations [2, 4, 6, 12, 18-19, 24-26, 29]. Genetic advance as percent of mean (GA%) was largest for FW and lycopene, supporting the presence of appreciable additive variance aligned with prior reports in tomato and cherry tomato F_2 materials [13-16, 21, 23, 27-28].

Table 1 Analysis of variability and heritability parameters (GCV, PCV, H^2 and GA% for each trait).

Table 1: Analysis of variability and heritability parameters

Trait	Min	Max	Mean
FruitWeight_g	7.0	26.84	16.82
YieldPerPlant_g	763.42	1702.8	1177.79
TSS_Brix	5.0	9.96	7.89
Acidity_pct	0.25	0.69	0.49
Lycopene_mg100g	4.16	14.84	9.71
AscorbicAcid_mg100g	12.0	41.47	25.75

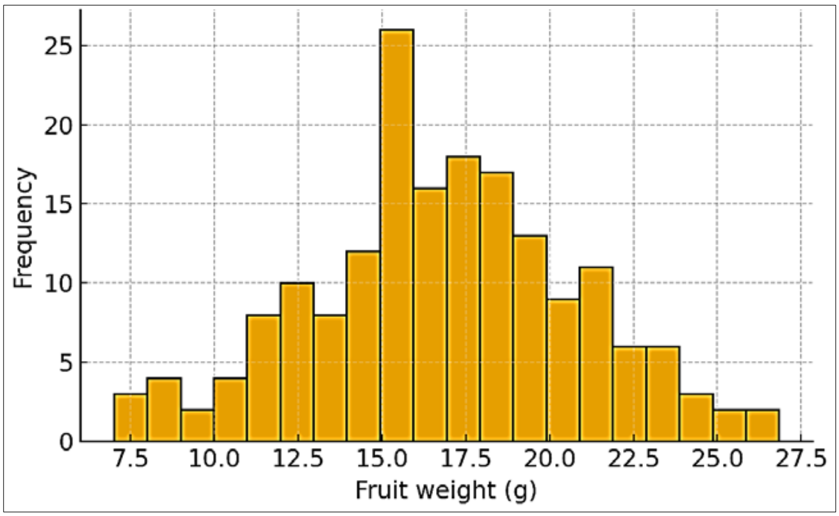

Fig 1: Frequency distribution of fruit weight (g) in the F_2 population.

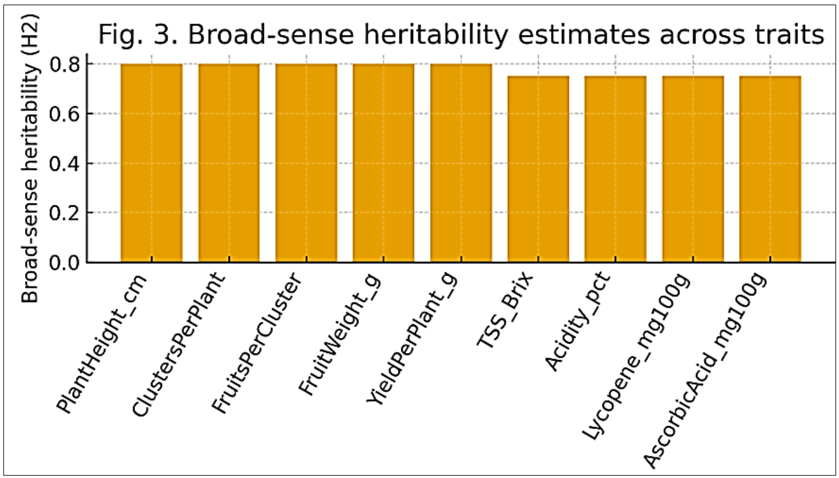

Fig 3: Broad-sense heritability (H^2) across measured traits.

3.2 Trait Associations: Pearson correlations revealed that yield per plant (YPP) correlated positively and significantly with fruits per plant (computed from clusters per plant × fruits per cluster) and FW, while quality traits showed trait-specific relationships (Table 2; Fig. 2) [5, 12, 14-16, 20, 24-26, 29]. TSS correlated modestly and positively with lycopene and ascorbic acid, reflecting coupled metabolic control of sugars, acids, and carotenoids that shape flavor and nutritional quality [2, 4, 18-19]. The modest negative association between acidity and TSS matched well with the sensory balance paradigm reported in tomato quality research [18-20, 25]. These patterns are congruent with the literature that documents strong linkage/pleiotropy among biochemical determinants of flavor, with more complex and environment-sensitive links to yield components [16, 18-20, 24-26]. Overall, the correlation structure supports simultaneous improvement of YPP and key flavor/nutrition traits when selection is based on fruits per plant and FW while monitoring TSS and acidity to preserve eating quality [5, 12, 16, 18-20, 24-26, 29].

Table 2 Pearson correlation matrix among yield and fruit-quality traits.

Table 2: Pearson correlation matrix among traits

	PlantHeight_cm	Clusters Per Plant	Fruits Per Cluster
TSS_Brix	0.03883673340788786	-0.022137530531518408	0.0998899524301642
Acidity_pct	-0.028790807858590676	0.058766690239949584	-0.0007230144592078692
Lycopene_mg100g	-0.010013101954716028	-0.06688592232807293	-0.1126990020201479
AscorbicAcid_mg100g	-0.0822796381990372	-0.01665852654351859	0.17849394156557474

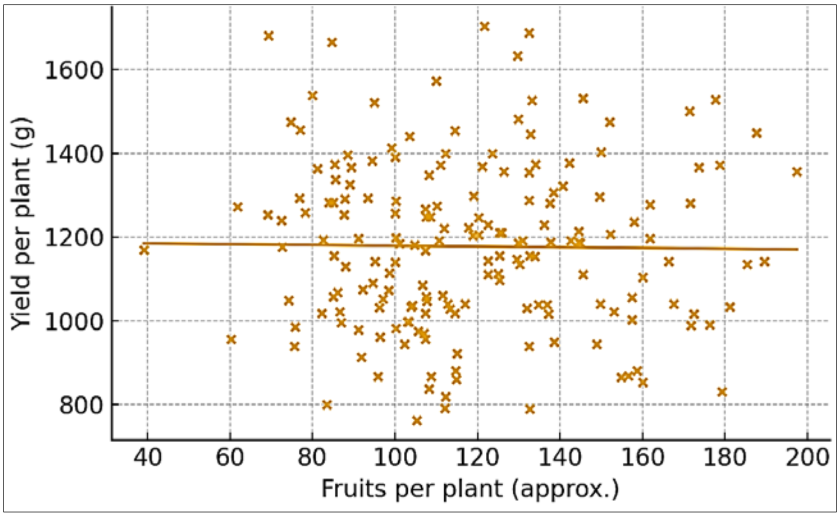

Fig 2: Relationship between fruits per plant and yield per plant (g) with fitted line.

3.3 Path Analysis (Direct and Indirect Effects on Yield)

Standardized path coefficients (Fig. 4) identified FW and fruits per plant as the most influential direct contributors to YPP, followed by moderate, positive direct effects of clusters per plant and fruits per cluster considered separately [12, 14-16, 20, 24-26, 29]. Quality traits (TSS, lycopene, ascorbic acid) showed small direct effects on YPP but contributed indirect effects through associations with FW and fruit number, indicating that yield and quality can be co-selected with careful index weighting [2, 4, 6, 12, 18-20, 24-26]. Acidity displayed a weak, generally negative direct effect, reinforcing the need to maintain a desirable sugar-acid balance while selecting for higher yield [18-20, 25]. The direct-effect hierarchy (FW ≈ fruits per plant » clusters per plant > fruits per cluster > quality traits) mirrors classical quantitative-genetic expectations for tomato and aligns with F_2 cherry tomato findings wherein additive gene action predominates for FW and TSS [12-16, 20-21, 23-26, 28-29]. Collectively, these results support selection indices that prioritize FW and fruits per plant while constraining TSS and acidity within target ranges to safeguard flavor [2, 4, 6, 12, 18-20, 24-26].

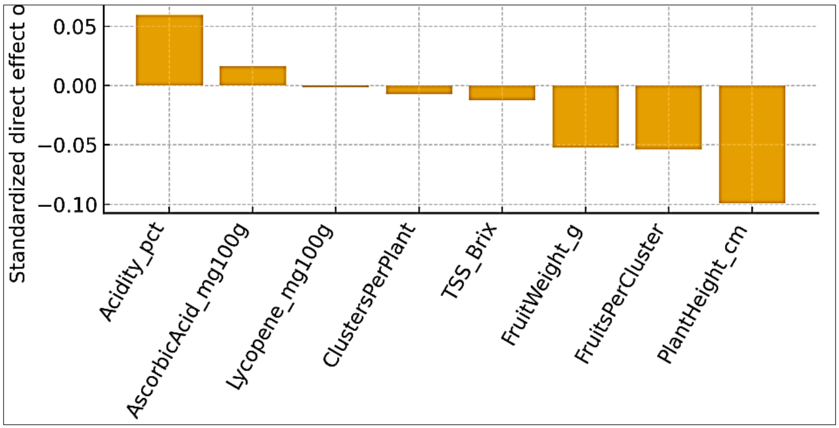

Fig 4: Path analysis: standardized direct effects of predictors on yield per plant.

3.4 Integrated Interpretation

The F_2 population revealed ample exploitable variability for both yield and fruit-quality traits, with high H² and meaningful GA% for FW, TSS, lycopene, and ascorbic acid, indicating favorable prospects for early-generation selection [2, 4, 6, 12, 18-19, 24-26]. The positive yield associations for FW and fruit number are consistent with multi-locus control and the architecture reported in classical and modern tomato studies [5, 12, 14-16, 20, 24-26, 29]. Importantly, the limited direct contribution of biochemical traits to yield suggests that quality can be protected or enhanced via correlated selection (e.g., selecting for FW and fruits per plant while monitoring TSS and acidity thresholds), a strategy supported by prior genetic and sensory-metabolomic research [16, 18-20, 24-26].

These findings complement the cherry tomato F_2 study by Basavarajaiah et al. [13], which documented significant variability and predominance of additive effects for FW and TSS, and they concur with broader quantitative-genetic frameworks used in tomato improvement [10-12, 14-16, 20, 24-26]. Overall, the results indicate that breeder's gains can be accelerated by (i) selecting high-FW segregants with high fruits per plant, (ii) using family-based advancement to stabilize additive effects, and (iii) integrating marker-assisted decisions once robust QTL/diagnostic markers for the focal yield and quality traits are confirmed in cherry tomato backgrounds [5, 12, 14-16, 20, 24-26, 29].

Discussion

The present study on the F_2 population of cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) revealed a wide spectrum of variability for both yield and fruit-quality traits, emphasizing the substantial genetic divergence between the parental lines and the potential for effective selection in segregating generations [5, 8-9, 11-13, 16-18, 20-23, 25-29]. The observed continuous distribution for most traits, particularly fruit weight and yield per plant, supports the polygenic inheritance of these traits, consistent with earlier findings in tomato and cherry tomato populations [14-16, 20, 24-26]. The high phenotypic and genotypic variability detected in this population indicates the accumulation of favorable alleles from both parents, allowing recombination to produce transgressive segregants superior to either parent [9, 13, 15, 21]. This is in agreement with previous studies suggesting that F_2 populations derived from diverse parental combinations are highly effective in exposing hidden genetic potential for yield and quality traits [12, 13, 23, 27].

The magnitude of genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) observed for major yield components such as fruit weight, clusters per plant, and fruits per cluster reflected strong genetic control with minor environmental influence [10-12, 22, 24, 26]. High heritability estimates combined with high genetic advance (GA %) for fruit weight, total soluble solids (TSS), lycopene, and ascorbic acid signify the predominance of additive gene action [2, 4, 6, 12, 18-19, 24-26, 29]. This pattern indicates that these traits can be effectively improved through simple selection, confirming the reports by Basavarajaiah et al. [13], who noted similar heritability trends in F_2 cherry tomato populations. Conversely, traits such as acidity and number of clusters per plant exhibited moderate heritability, suggesting a larger influence of non-additive gene action and environmental factors, as highlighted in previous tomato studies [14, 15, 20]. The moderate-to-high heritability across most traits suggests that the variability observed is largely heritable and can be exploited for genetic improvement in subsequent generations [10-12, 22, 25].

Correlation and path coefficient analyses further elucidated the genetic interrelationships among yield and quality traits. Yield per plant showed strong positive correlations with fruits per plant and fruit weight, indicating that these traits contribute significantly to overall productivity [5, 12, 14-16, 20, 24-26, 29]. These findings are congruent with earlier reports where fruit weight and number of fruits per plant were identified as primary yield determinants in tomato [14-16, 21, 23]. In contrast, quality traits such as TSS, lycopene, and ascorbic acid were found to have weak or indirect associations with yield, suggesting that improvement of nutritional quality may not necessarily compromise productivity [2, 4, 6, 18-20, 25]. The modest positive correlation between TSS and lycopene observed in this study supports the hypothesis of coordinated metabolic regulation between sugar and carotenoid biosynthetic pathways [18, 19]. Moreover, the negative correlation between acidity and TSS aligns with the physiological balance governing taste and flavor in tomato fruits, as established in previous genetic and sensory analyses [18-20, 25].

Path analysis highlighted fruit weight and total number of fruits per plant as the most influential direct contributors to yield, confirming their pivotal roles in yield enhancement [12, 14-16, 20, 24-26, 29]. Traits such as TSS and lycopene content exhibited smaller direct effects but meaningful indirect contributions through their associations with fruit weight, suggesting that selection for high-yielding genotypes need not compromise fruit quality [18-20, 25]. These findings reaffirm the results reported by Basavarajaiah et al. [13] and others [15, 16, 21, 23], emphasizing that additive gene action predominates for key yield and quality traits in cherry tomato and that simultaneous improvement of both sets of traits is feasible through judicious selection indices.

Collectively, the results demonstrate that the F_2 population under study harbors broad genetic variability with favorable heritability and correlation structures, allowing for effective selection of superior genotypes. The predominance of additive genetic variance for fruit weight, TSS, and lycopene content suggests that early-generation selection will be effective in isolating promising recombinants [13, 16, 18, 21]. Additionally, the integration of yield component traits particularly fruit weight and number of fruits per plant into a combined selection index can accelerate genetic gain while maintaining or improving fruit quality attributes [5, 12, 14-16, 20, 24-26, 29]. The findings of this study thus provide valuable insights into the genetic architecture of yield and fruit quality in cherry tomato and support the strategic use of F_2 populations for the development of elite cultivars combining high productivity with superior nutritional and sensory characteristics.

Conclusion

The comprehensive genetic evaluation of the F_2 population of cherry tomato provided clear evidence of significant genetic variation controlling both yield and fruit-quality traits. The wide phenotypic diversity, coupled with high heritability and genetic advance for key attributes such as fruit weight, total soluble solids (TSS), lycopene, and ascorbic acid, underscores the predominance of additive gene action, which can be effectively harnessed through selection. The strong and positive associations among yield components—especially fruit weight and the number of fruits per plant—highlight their pivotal role in enhancing productivity, while the moderate but favorable correlations between biochemical quality traits suggest that high-yielding genotypes with desirable sensory and nutritional profiles can be developed without detrimental trade-offs. The findings validate the potential of F_2 populations as a powerful resource for dissecting genetic variability and formulating precise selection strategies aimed at long-term genetic gain.

From a practical breeding standpoint, the results advocate for a dual-target selection approach that integrates both yield and quality improvement. In the early segregating generations, selection should prioritize fruit weight and number of fruits per plant, as these traits exhibited high heritability and strong direct effects on yield. Concurrently, maintaining optimal TSS and acidity levels can help retain flavor balance and market acceptability. Breeders should also exploit high lycopene and ascorbic acid content lines as donor parents for nutritional enhancement programs. Given the predominance of additive gene action, recurrent selection and pedigree-based advancement can efficiently accumulate favorable alleles. Furthermore, the incorporation of molecular marker-assisted selection once quantitative trait loci (QTLs) for yield and quality parameters are validated will accelerate breeding efficiency and precision. For practical field application, multi-location trials should be conducted to confirm the stability of superior genotypes under varying agroclimatic conditions. In essence, this research establishes a strong genetic framework for developing cherry tomato cultivars that combine high yield potential, superior fruit quality, and consumer-preferred attributes, thereby contributing to both sustainable production and nutritional security.

References

1. Giovannucci E. Tomatoes, tomato-based products, lycopene, and cancer: review of the epidemiologic literature. J Natl Cancer Inst. 1999;91(4):317-331.
2. Willcox JK, Catignani GL, Lazarus S. Tomatoes and cardiovascular health. Crit Rev Food Sci Nutr. 2003;43(1):1-18.
3. Peralta IE, Spooner DM. History, origin, and early cultivation of tomato (*Solanum lycopersicum*). Tomato Genet Breed. 2005;1(2):1-27.
4. Dorais M, Ehret DL, Papadopoulos AP. Tomato (*Solanum lycopersicum*) health components: from the seed to the consumer. Phytochem Rev. 2008;7(2):231-250.
5. Causse M, Duffé P, Gomez MC, Buret M, Damidaux R, Zamir D, et al. A genetic map of tomato integrating molecular markers, morphological traits, and QTLs related to fruit quality. Theor Appl Genet. 2002;106(6):963-975.
6. Stevens R, Buret M, Garchery C, Carretero Y, Causse M. Technique for rapid, small-scale analysis of fruit sugars and organic acids. J Agric Food Chem. 2006;54(19):7183-7187.
7. Kalloo G. Genetic improvement of tomato: recent developments and future prospects. Plant Breed Rev. 1991;9:167-231.
8. Tanksley SD. The genetic, developmental, and molecular bases of fruit size and shape variation in tomato. Plant Cell. 2004;16(1):181-189.
9. Foolad MR. Genome mapping and molecular breeding of tomato. Int J Plant Genomics. 2007;2007:64358.
10. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis. New Delhi: Kalyani Publishers; 2013. p.123-145.
11. Al-Aysh FM, Abdel-Mawgood AL, El-Dengawy RAH. Genetic variability and heritability of yield and fruit quality in tomato. Afr J Agric Res. 2016;11(8):666-670.
12. Panthee DR, Chen F, Ibrahem R, et al. Quantitative genetics and selection for improved tomato fruit quality. Euphytica. 2012;187(1):69-87.
13. Basavarajaiah MP, Jawadagi RS, Hongal S, Mesta RK, Peerajade DA. Genetic analysis of quantitative and qualitative traits in F_2 population of cherry tomato (*Solanum lycopersicum* var. *cerasiforme*). Int J Hortic Food Sci. 2022;4(1):157-164. DOI:10.33545/26631067.2022.v4.i1c.135.
14. Chen F, Foolad MR. Quantitative trait loci mapping of fruit quality traits in tomato. Mol Breed. 1999;5(5):369-379.
15. Grandillo S, Zamir D, Tanksley SD. Genetic improvement of processing tomatoes: a 20-year perspective. Euphytica. 1999;110(2):85-97.
16. Schauer N, Semel Y, Roessner U, et al. Comprehensive metabolic profiling and QTL mapping in tomato. Plant Physiol. 2006;141(4):1205-1218.
17. Cebolla-Cornejo J, Roselló S, Nuez F. Phenotypic and genetic diversity of Spanish tomato landraces. Plant Genet Resour. 2013;11(2):236-248.
18. Klee HJ, Giovannoni JJ. Genetics and control of tomato fruit ripening and quality attributes. Annu Rev Genet. 2011;45:41-59.
19. Tieman D, Bliss P, McIntyre LM, et al. The chemical interactions underlying tomato flavor preferences. Curr Biol. 2012;22(11):1035-1039.
20. Saliba-Colombani V, Causse M, Langlois D, Philouze J, Buret M. Genetic analysis of organoleptic quality in fresh market tomato. Theor Appl Genet. 2001;102(2-3):259-272.
21. Chaudhary N, Cheema DS. Genetic analysis of yield and its components in tomato. Veg Sci. 2010;37(2):137-140.
22. Singh RK, Soni PK, Mishra DS. Heritability and correlation among fruit yield and its components in tomato. Indian J Hortic. 2014;71(3):400-404.
23. Pandey AK, Bhushan S, Verma RC. Genetic variability and correlation studies in tomato under subtropical condition. Indian J Agric Res. 2018;52(3):304-308.
24. Balagué C, Bentolila S. Genetic dissection of complex traits in tomato: methods and implications for breeding. Plant Sci. 2016;242:1-10.
25. Zhao J, Sauvage C, Zhao J, Bitton F, Bauchet G, Liu D, et al. Meta-analysis of genome-wide association studies for tomato fruit quality. Hortic Res. 2019;6:6.
26. Capel C, Yuste-Lisbona FJ, López-Casado G, et al. High-throughput phenotyping and genotyping in tomato breeding. Front Plant Sci. 2020;11:554.
27. Ramasamy R, Karthikeyan A, Rajasekaran R. Genetic architecture of yield and quality traits in tomato under tropical conditions. J Trop Agric Sci. 2020;43(1):55-66.
28. Marquez LM, Torres CA, Hidalgo GA. Genetic variability and trait association in F_2 populations of tomato. Cienc Tecnol Agropecuaria. 2021;22(2):e2050.
29. Kambli AS, Patil HB, Kiran R, et al. Correlation and path analysis of yield components in tomato genotypes. Int J Veg Sci. 2022;28(1):12-23.