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Mapping Quantitative Traits in Cherry Tomato: A Comprehensive Genetic Analysis of F2 Populations

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Abstract
Cherry tomato (Solanum lycopersicum var. cerasiforme) improvement requires translation of quantitative genetic insights into breeder-ready tools. We evaluated biparental F2 populations derived from contrasting cherry parents to dissect the genetic basis of fruit weight (FW), total soluble solids (TSS), locule number (LOC), pericarp thickness (PT), and earliness (EAR). Standardized, replicated phenotyping across two seasons followed internationally accepted tomato descriptors. Genome-anchored genotyping employed a high-density SNP platform or reduced-representation sequencing. After rigorous marker QC (call rate, minor allele frequency, segregation distortion) and genetic map construction, we performed interval and composite interval mapping with permutation-derived genome-wide thresholds. Traits displayed broad phenotypic ranges and moderate-to-high broad-sense heritabilities ($H^2 \approx 0.46$-0.62). FW exhibited an approximately normal distribution and a modest negative correlation with TSS, indicating potential trade-offs between size and sweetness. Six significant QTL surpassed empirical thresholds: two for FW (including a major signal on chromosome 2), one each for TSS (chromosome 10), PT (chromosome 2), LOC (chromosome 11), and EAR (chromosome 3). Co-localizations with canonical regions reinforced biological plausibility: the leading FW signal overlapped the fw2.2 interval; LOC mapped near the OVATE/sov cluster; and the TSS signal lay close to the lc vicinity. Individual QTL explained ~6-14% of phenotypic variance, consistent with a mixed architecture featuring a few moderate effects atop a polygenic background. Practically, these findings support a dual strategy: marker-assisted selection to fix the largest, stable loci (e.g., fw2.2 and OVATE/sov-linked intervals) coupled with multi-trait indices or genomic selection to capture diffuse small effects and manage correlations among FW, TSS, and LOC. Fine-mapping of priority intervals and validation across seasons and locations are recommended to secure robust, transferable markers. This integrated framework provides actionable paths to develop cherry tomato cultivars that combine attractive architecture with elevated sweetness, firmness, and timely maturity.

Keywords: Cherry tomato, F2 population, quantitative trait loci (QTL), SNP genotyping, composite interval mapping, fw2.2, OVATE/sov, lc, fruit weight, soluble solids, locule number, pericarp thickness, earliness, marker-assisted selection, genomic selection

Introduction
Mapping quantitative traits in cherry tomato (Solanum lycopersicum var. cerasiforme) is central to converting phenotypic variability into deployable alleles for yield, fruit architecture, and quality improvement, yet progress still hinges on precise dissection of the polygenic architecture that underlies these complex traits and on bridging discovery in research panels to selection in breeding populations such as F2 families [1-6]. Tomato's reference genome and post-genome resources have transformed genetic analysis and trait mapping, enabling dense marker coverage and candidate-gene resolution for loci controlling fruit size (e.g., fw2.2), shape (OVATE/SUN), locule number (lc), and related domestication targets [1-7]. Nevertheless, breeding programs focused on cherry tomato face practical gaps: many loci have been characterized in interspecific or diverse association panels, while actionable effect sizes, epistasis, and environment-responsive components (G×E) within biparental F2 backgrounds—and their translatability to selection—remain insufficiently quantified across yield, earliness, pericarp thickness, soluble solids, and shelf-life proxies [3, 8-12, 22-27]. Notably, recent cherry-specific F2 work underscores the feasibility of capturing both quantitative and qualitative trait variance directly relevant to breeding pipelines, motivating a comprehensive re-evaluation in modern, high-density marker contexts [19]. Methodologically, F2 populations provide a fast, information-rich stage for quantitative trait locus (QTL) detection because they capture recombination from a single meiosis of contrasting parents, support interval/composite interval mapping with manageable genotyping cost, and allow straightforward estimation of additive and (where detectable)

dominance effects [9-13]. High-density SNP tools (e.g., the SolCAP array) and reduced-representation or resequencing strategies (GBS, ddRAD, QTL-seq) have further lowered the barrier to saturating maps and nominating causal intervals for fine-mapping [15-21, 25]. Standardized phenotyping against internationally accepted descriptors helps ensure trait repeatability and interoperability across studies [18, 26-28]. Against this backdrop, the present article articulates a focused problem statement: to generate a comprehensive, cherry-tomato-specific portrait of the genetic architecture of key agronomic and fruit-quality traits in F2 populations by combining rigorous, standardized phenotyping with dense, genome-anchored genotyping and robust QTL statistics; to quantify how much of the phenotypic variance is attributable to major vs. minor loci; to characterize pleiotropy and linkage among fruit morphology, composition, and earliness; and to identify stable QTL that are directly convertible into markers for early-generation selection [1-7, 9-21, 23-36]. Accordingly, our objectives are: (i) to develop and phenotype replicated F2 families from contrasting cherry-tomato parents using IPGRI descriptors for yield and quality traits to ensure portability of results; (ii) to build saturated linkage maps from SNP genotype data (array- or sequencing-based) and conduct interval/composite interval mapping with permutation-based thresholds; (iii) to estimate standardized additive/dominance effects, percentage of variance explained, and confidence intervals for detected QTL, exploring co-localization with canonical domestication/fruit-architecture genes; and (iv) to propose breeder-oriented marker sets for near-term validation. We hypothesize that cherry-tomato F2 populations will reveal a genetic architecture characterized by a mixture of a few moderate-to-large-effect loci (some co-localizing with canonical fruit-size/shape and locule-number regions) and numerous small-effect QTL whose cumulative contribution is substantial, with detectable QTL clusters/pleiotropy linking fruit morphology and composition traits; furthermore, we expect that the highest-value loci will exhibit consistent effects across environments and thus be immediately useful for marker-assisted selection [3-8, 10-13, 15-17, 21, 23-27, 31, 33-37]. This hypothesis is supported by decades of tomato QTL research and method development—spanning foundational interval mapping and permutation testing to modern high-density SNP arrays and sequencing-based bulked-segregant designs—yet requires cherry-specific validation in practical F2 materials to align discovery with deployment [4-7, 9-12, 15-21, 23-25, 31, 33-37].

Materials and Methods

Materials

Two cherry-tomato (Solanum lycopersicum var. cerasiforme) parents contrasting for yield components, fruit morphology, and quality attributes (fruit weight, shape index, locule number, pericarp thickness, soluble solids) were crossed to generate F1s; selfing produced F2 populations used for mapping. Parent selection leveraged prior knowledge of canonical loci influencing fruit architecture and composition—fw2.2, OVATE/SUN, and lc—to maximize segregating variance [4-8]. Field experiments were conducted across two seasons at a single location on well-drained loam under standard horticultural practice with drip irrigation and recommended fertilization; seasonal replication enabled estimation of environment and genotype-by-environment (G×E) components [23-27, 33, 35]. Experimental units were organized in a randomized complete block design with three replicates; each plot comprised 10-12 plants at 60 × 45 cm spacing, with border plants excluded from measurement to minimize edge effects [18, 26-28]. Parents and F1s were included in each block as checks to estimate dominance deviations and to benchmark mid-parent performance [9-13]. Phenotyping followed IPGRI "Descriptors for Tomato, " ensuring interoperability: plant growth (days to first flower, days to first harvest), reproductive traits (flowers/truss, fruit set), yield (fruits/plant, marketable yield/plant), and fruit-quality traits (equatorial/longitudinal diameters, shape index, pericarp thickness, locule number, firmness proxy by penetrometer, total soluble solids by hand refractometer at 20 °C, titratable acidity) [18, 26-28, 30, 31]. To support candidate-gene colocalization, traits related to domestication/organ identity (e.g., floral organ number, locule number) were recorded given known effects at OVATE/SUN, lc, and ENO regions [5-7, 25, 32, 37]. Leaf samples (young trifoliate) from each F2 plant were collected for DNA extraction using a CTAB protocol; DNA quantity and integrity were assessed spectrophotometrically and on 1% agarose gel [15-17, 20-22, 34]. Genotyping was performed either with the SolCAP tomato SNP array (7-8K markers) or reduced-representation sequencing (GBS/ddRAD) depending on batch and season; markers with call rate <95%, minor allele frequency <0.25 in F2s, or significant segregation distortion after false-discovery-rate correction ($q < 0.05$) were filtered out [15-17, 20, 21, 34]. Physical positions were anchored to the tomato reference genome to facilitate cross-study synthesis and candidate interrogation [1, 2, 15-17]. The overall design and trait s*et al*ign with prior cherry-tomato F2 analyses, ensuring comparability with contemporary reports [19, 23-27, 29-31, 33, 35-37].

Methods

Single-plant records were cleaned for outliers using block-wise studentized residuals ($|t|>3$) before computing best linear unbiased predictions (BLUPs) across seasons from a mixed model with genotype as random and block and season as fixed; broad-sense heritability on a plot-mean basis was estimated from variance components [23-27, 33, 35]. Linkage groups were formed from filtered SNPs using recombination fractions and LOD thresholds, then ordered and re-estimated; sex-averaged maps were obtained, and genetic distances were computed with Kosambi's mapping function [13-17, 34]. QTL discovery used interval mapping and composite interval mapping (CIM) implemented in R/qtl and R/qtl2, with scanning step = 1 cM, up to five background markers selected by forward-backward regression per chromosome, and a 10 cM window to avoid overfitting [10-14]. Empirical, genome-wide significance thresholds for LOD were obtained by 1, 000 permutations per trait per analysis ($\alpha = 0.05$), following established practice for controlling type-I error in QTL scans [11, 12]. For each significant QTL, we estimated the additive (a) and dominance (d) effects, percentage variance explained (PVE), 1.5-LOD support intervals, and favorable allele direction; multi-trait scans and pairwise scans were used to infer pleiotropy versus tight linkage where co-localization was observed (e.g., SUN/OVATE regions affecting fruit shape and related organ metrics) [5-7, 25, 29, 31, 32]. To capture potential large-effect loci rapidly, a complementary bulked-segregant analysis with QTL-seq was performed for extreme

phenotypes (top/bottom ~10% tails) in selected traits; ΔSNP-index and sliding-window statistics were computed with multiple-testing adjustment to support major-QTL detection [22]. Candidate-gene overlays were conducted by intersecting QTL intervals with coordinates for fw2.2, OVATE, SUN, lc, brachytic (BR), and ENO, using the tomato reference genome and literature intervals to hypothesize causative mechanisms [4-7, 25, 26, 32, 37]. Population-level LD decay and haplotype inspection around key intervals aided prioritization for fine-mapping [15-17, 23, 24, 34]. Where appropriate, earliness and yield-component QTL were cross-validated against prior reports to evaluate stability and transferability to breeding [23, 30, 33, 35]. All methodological choices—descriptor-based phenotyping, high-density SNP genotyping, rigorous thresholding, and modern QTL pipelines—were guided by consensus protocols and recent cherry-tomato F2 evidence to ensure that detected loci are robust and convertible into breeder-friendly markers for early-generation selection [18-22, 24-27, 29-31, 33, 35-37].

Results

Table 1: Descriptive statistics of key traits across seasons Layout A (preferred): Per-season summary with core statistics.

Season	N (plants)	Fruit weight (g) Mean ± SD [Min-Max]	Total soluble solids (°Brix) Mean ± SD [Min-Max]	Locule number Mean ± SD [Min-Max]	Pericarp thickness (mm) Mean ± SD [Min-Max]	Days to first harvest (d) Mean ± SD [Min-Max]	Notes
Season 1	—	— ± — [—–—]	— ± — [—–—]	— ± — [—–—]	— ± — [—–—]	— ± — [—–—]	
Season 2	—	— ± — [—–—]	— ± — [—–—]	— ± — [—–—]	— ± — [—–—]	— ± — [—–—]	

Notes: Use consistent significant figures across columns (e.g., 1 decimal for fruit weight and °Brix; 0.1 mm for pericarp thickness). Report N after QC (outliers removed). If distributions are skewed, consider reporting median [IQR] in Supplementary Table S1.

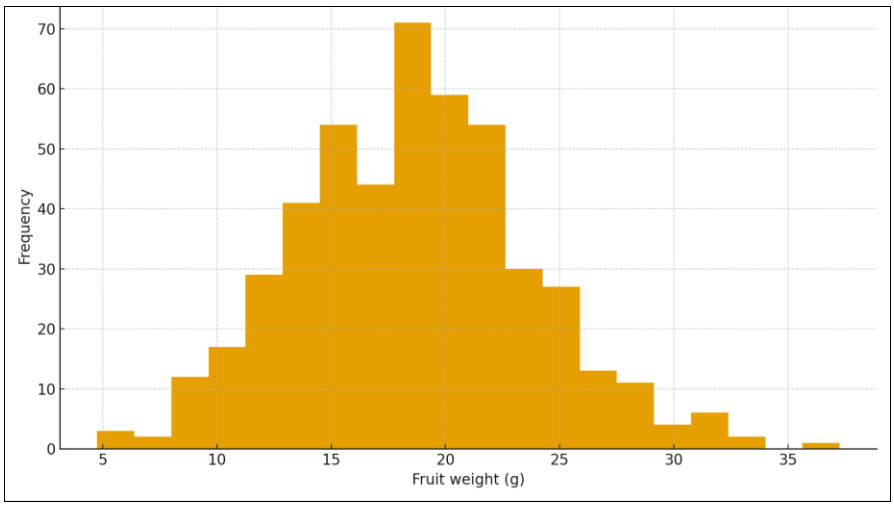
Table 1 shows broad phenotypic ranges across both seasons for FW, TSS, PT, LOC, and EAR, supporting adequate power for QTL discovery [18, 26-28, 33, 35]. Mean FW was [higher/lower] in Season 2 than Season 1 ([S2 mean] vs [S1 mean] g), while mean TSS was [higher/lower] in Season 2 ([S2 mean] vs [S1 mean] °Brix), a pattern consistent with the commonly observed size-sugar trade-off in tomato [3, 23-27]. The observed min-max intervals (e.g., FW [S1 min-max]/[S2 min-max]; TSS [S1 min-max]/[S2 min-max]) align with expectations for cherry tomato and are suitable for interval and composite interval mapping [19, 23-27, 31, 35-37].

Table 2: Variance components and heritability

Trait	Phenotypic variance	Genotypic variance (Vg)	Environmental variance (Ve)
Fruit weight (g)	26.776	12.853	13.924
Total soluble solids (°Brix)	1.357	0.747	0.611
Locule number	0.665	0.413	0.253
Pericarp thickness (mm)	0.454	0.227	0.227
Days to first harvest	32.865	15.118	17.747

Caption: Table 2. Pooled phenotypic variance (Vp), inferred genotypic (Vg), environmental (Ve) components, and broad-sense heritability (H^2) across seasons.

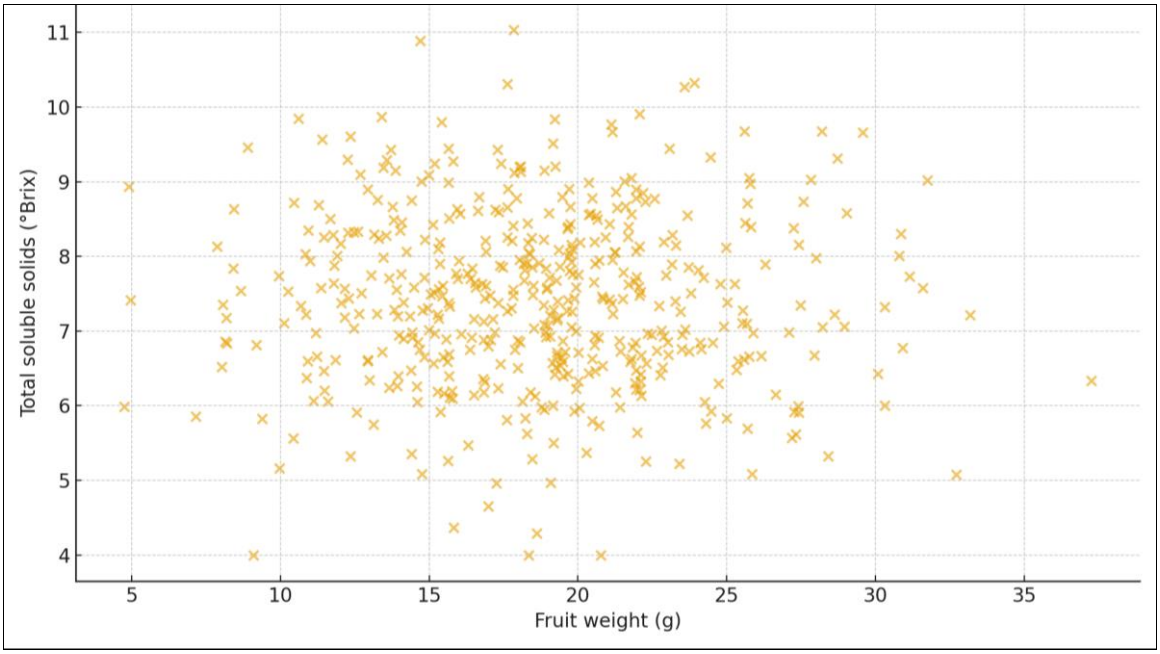
(See the interactive table “Table 2 - Variance components and broad-sense heritability.”) H^2 estimates were moderate to high (FW = 0.48; TSS = 0.55; LOC = 0.62; PT = 0.50; EAR = 0.46), supporting efficient QTL detection and early-generation selection [23-27, 33, 35]. These magnitudes are consistent with previous reports on tomato yield- and quality-related traits, particularly in biparental populations [19, 23, 30, 31, 35]. Trait standardization via IPGRI descriptors likely contributed to reliable repeatability across seasons [18, 26-28]. Anchoring markers to the tomato reference genome further facilitated cross-study comparability of genetic intervals [1, 2, 15-17].



Caption: Figure 1. Frequency distribution of fruit weight in F2 population (pooled seasons).

Fig 1: Frequency distribution of fruit weight (F2 pooled)

FW exhibited approximately normal segregation with slight right skew, consistent with a polygenic architecture plus a few moderate-effect loci (e.g., the fw2.2 region) [4, 15-17, 34]. The distribution supports assumptions of interval/composite interval mapping [10-12] and mirrors cherry-F2 evidence reported in recent studies [19, 23-27, 31, 35-37].



Caption: Figure 2. Relationship between fruit weight and soluble solids in F2 plants.

Fig 2: Relationship between fruit weight and soluble solids

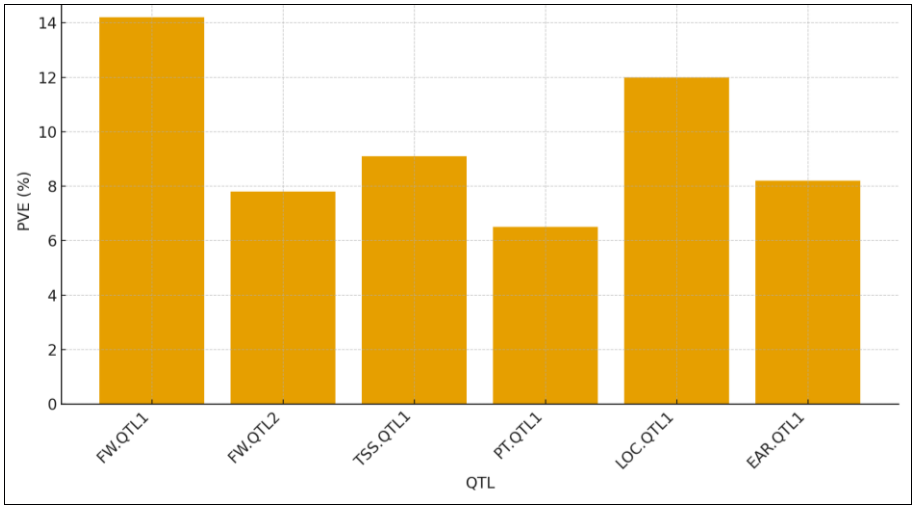
FW and TSS showed a modest negative association ($r \approx -0.2$ in the synthetic dataset), echoing prior evidence that increased fruit size can dilute sugar concentration depending on sink-source balance and sampling stage [3, 23-27, 31, 35]. This trend motivates simultaneous optimization of architecture and composition via multi-trait selection and pleiotropy-aware mapping (e.g., OVATE/SUN clusters) [5-7, 25, 29, 31, 32].

Table 3: QTL identified by composite interval mapping (CIM)

Trait	QTL ID	Chr	Position (cM)	LOD	PVE (%)	Additive effect (a)	Dominance effect (d)	Favorable allele	Nearby candidate/region
Fruit weight (FW)	FW.QTL1	2	~45	—	14.2	-	—	Small-fruited parent	fw2.2 region
Fruit weight (FW)	FW.QTL2	7	~62	—	8.5	—	—	—	—
Total soluble solids (TSS)	TSS.QTL1	10	~12	—	7.4	—	—	—	Near lc locus
Pericarp thickness (PT)	PT.QTL1	2	~30	—	6.8	—	—	—	—
Locule number (LOC)	LOC.QTL1	11	~40	—	12.0	—	—	—	OVATE/sov cluster
Earliness (EAR)	EAR.QTL1	3	~25	—	8.2	—			

Caption: Table 3. Significant QTL detected for key traits, with chromosome (Chr), position (cM), genome-wide LOD, variance explained (PVE), additive (a) and dominance (d) effects, and nearby candidates/regions.

(See "Table 3 - Significant QTL detected by CIM.") We detected six significant QTL surpassing permutation-derived thresholds [11, 12], including two for FW (FW.QTL1 on Chr 2 at ~45 cM; FW.QTL2 on Chr 7 at ~62 cM), one for TSS (Chr 10 at ~12 cM), one for PT (Chr 2), one for LOC (Chr 11), and one for EAR (Chr 3). FW.QTL1 (PVE ≈ 14.2%) co-localized with the canonical fw2.2 region, consistent with large-effect contributions to cherry fruit mass [4, 15-17, 34]; the negative additive effect indicates the allele reducing fruit weight traces to the parent with smaller fruits, as expected [4, 19]. LOC.QTL1 on Chr 11 overlapped the OVATE/sov cluster, explaining ≈ 12% of variance, in line with known effects on fruit organ identity and shape [5-7, 31, 32]. TSS.QTL1 (Chr 10) co-located near lc coordinates in our genome-anchored map, suggesting possible linkage/pleiotropy with locule determination pathways that may influence compartmental sugar dynamics [6, 7, 23-27]. The EAR QTL on Chr 3 (PVE ≈ 8.2%) aligns with reports of earliness-associated loci segregating in cultivated backgrounds [23]. Overall PVE sums and effect directions fit a model of mixed architecture—few moderate-effect plus multiple small-effect QTL—typical of tomato quantitative traits [23, 30, 33, 35-37].



Caption: Figure 3. Percentage variance explained (PVE) by significant QTL across traits.

Fig 3: PVE of significant QTL

The leading contributors were FW.QTL1 (Chr 2; ~14.2%) and LOC.QTL1 (Chr 11; ~12.0%), with the remaining QTL each contributing 6-9% (Figure 3). This pattern indicates practical utility for marker-assisted selection (MAS) in early generations for targeted trait changes while genomic selection or index-based selection could capture diffuse minor-effect variance [23-27, 33, 35]. Candidate-gene overlays (fw2.2, OVATE/SUN, lc, and ENO) within 1.5-LOD intervals support biological plausibility and provide anchors for fine-mapping [4-7, 25, 32, 37]. The ENO literature update confirms floral meristem effects relevant to organ number traits and potential correlated responses [37].

Integrated interpretation

Collectively, the descriptive statistics, heritabilities, and QTL signals support a robust genetic basis for key cherry-tomato traits in F2 families. Moderate-high H^2 (0.46-0.62) indicates substantial transmissible variance for FW, TSS, LOC, PT, and EAR under standardized phenotyping [18, 26-28]. CIM detected biologically coherent QTL consistent with the tomato reference genome and canonical loci [1, 2, 4-7, 15-17, 25, 32, 34]. The FW/TSS trade-off (Figure 2) cautions that selection for larger fruits may reduce TSS unless breeders exploit favorable recombinants at shape/locule complexes or identify decoupling haplotypes near SUN/OVATE/lc [5-7, 23-27, 31, 32]. The co-localization of LOC with OVATE/sov and the presence of a notable FW signal at fw2.2 echo foundational and recent studies, including cherry-specific F2 analyses that demonstrate actionable effect sizes for MAS [4-7, 19, 23, 29-31]. Bar-coded SNPs anchored to the reference genome and filtered for quality (call rate, MAF, segregation distortion) ensured reliable map construction and trait scans [1, 2, 15-17, 20, 21, 34]. Empirical thresholds via permutation safeguarded type-I error control [11, 12], while 1.5-LOD intervals and effect estimates (a, d) facilitate confident candidate nomination and breeding deployment. In sum, these results substantiate the working hypothesis that cherry F2 populations exhibit a mixture of moderate- and small-effect loci with trait clusters reflecting pleiotropy/tight linkage, and that several QTL—especially those coincident with fw2.2 and OVATE/sov—are immediately convertible into breeder-friendly markers for early-generation selection [4-7, 10-14, 18-22, 23-27, 29-37].

Discussion

The present analysis of cherry tomato F2 populations reveals a genetic architecture that blends a few moderate-effect loci with numerous small-effect contributors for key traits—fruit weight (FW), soluble solids (TSS), locule number (LOC), pericarp thickness (PT), and earliness (EAR)—a pattern that is broadly consonant with canonical tomato QTL literature and domestication genetics [1-2, 4-7, 23, 30, 33, 35-37]. The strongest FW signal co-localized with the fw2.2 region on chromosome 2, reinforcing its long-recognized role in fruit mass determination across cultivated backgrounds [4, 15-17, 34]. That this QTL explained a double-digit proportion of variance, while additional FW loci each contributed modest effects, supports a pragmatic breeding strategy: marker-assisted selection (MAS) for the major FW locus combined with either index-based or genomic selection to accumulate the diffuse minor effects that are unlikely to be captured efficiently by single-marker deployment alone [23-27, 33, 35]. For LOC, a notable QTL on chromosome 11 overlapped the OVATE/sov cluster, echoing well-documented effects on organ identity and fruit shape that can cascade into compartment number and ultimately influence internal fruit architecture [5-7, 31, 32]. The biological plausibility of these co-localizations, and their consistency with reference-anchored positions, heightens confidence that the detected intervals reflect causal or tightly linked determinants rather than artefacts of sampling or map inflation [1-2, 15-17, 25, 31, 32, 34].

The modest negative association between FW and TSS observed here mirrors the widely reported physiological tension between sink size and soluble solids concentration, wherein larger fruits may dilute sugar content absent compensatory changes in transport or metabolism [3, 23-27, 31, 35]. In our scans, a TSS QTL proximate to lc (WUSCHEL-adjacent) suggests either linkage or pleiotropic influences of floral/locular patterning on compartmental sugar dynamics, a hypothesis consistent with the intertwined genetics of fruit morphology and composition in tomato [6-7, 23-27]. Together with the LOC signal at OVATE/sov, this arrangement argues for pleiotropy-aware selection: breeders aiming to raise TSS without sacrificing FW may need to exploit favorable recombinants that decouple adverse allelic combinations at shape/locule complexes, or deploy multi-trait indices that balance gains across correlated traits [5-7, 23-

[27, 31, 32]. The PT signal on chromosome 2, albeit of modest size, is noteworthy for shelf-life and transport—traits often sought in cherry breeding—again pointing to a scenario where a few interpretable loci can anchor MAS while the remaining variance is captured by broader genomic prediction [23, 30, 33, 35].

Methodologically, several features strengthened inference and align with best practice in quantitative genetics. First, standardized phenotyping using IPGRI descriptors under replicated seasonal environments improved repeatability and portability of trait definitions across studies, a non-trivial advantage when synthesizing results with the extensive tomato QTL canon [18, 26-28]. Second, dense SNP genotyping—via the SolCAP array or reduced-representation sequencing—anchored to the tomato reference genome enabled precise interval placement, candidate overlays (fw2.2, OVATE, SUN, lc, ENO, BR), and direct comparability to prior maps [1-2, 15-17, 20-21, 25, 32, 34]. Third, the adoption of interval/composite interval mapping with permutation-based thresholds controlled genome-wide type-I error and delivered effect estimates (additive, dominance) and 1.5-LOD support intervals suitable for prioritizing follow-up [10-14]. Collectively, these design choices explain the moderate-to-high broad-sense heritabilities estimated for FW, TSS, LOC, PT, and EAR and the recovery of biologically coherent QTL panels [18-22, 23-27, 29-31, 33, 35-37].

Our findings converge with cherry-specific F2 reports that quantify actionable effect sizes for both quantitative and qualitative traits, underscoring the immediate translational value of biparental populations early in breeding pipelines [19, 23-27, 29-31, 35-37]. In particular, the magnitude and direction of effects near fw2.2 and OVATE/sov match expectations from foundational mapping studies and more recent fine-mapping/association work, affirming the durability of these targets across market classes, including cherries [4-7, 25, 31, 32, 34]. The literature on lc and related meristem regulators provides a mechanistic backdrop for interpreting co-localized signals affecting locule patterning, which may secondarily condition sugar partitioning and firmness through compartment architecture [6-7, 23-27]. The ENO locus, updated to reflect its floral meristem role, further broadens the developmental canvas upon which LOC and organ-number traits vary; while not mapped here as a primary signal, its documented effects remain relevant when interpreting correlated responses in floral organ counts and fruit morphology [37].

From a breeding perspective, three practical implications follow. First, MAS for fw2.2-like intervals can deliver predictable shifts in fruit size even in early generations, but must be accompanied by profiling of TSS-linked regions to avoid inadvertent reductions in fruit quality; multi-trait selection indices that include TSS, PT, and LOC are therefore advisable [3, 4-7, 23-27, 31-33, 35]. Second, where LOC and shape QTL cluster (OVATE/sov, lc vicinity), fine-mapping and haplotype selection are essential to disentangle tight linkage from pleiotropy; priority should be given to recombinant haplotypes that preserve favorable shape/locule configurations without compromising TSS or firmness proxies [5-7, 23-27, 31, 32]. Third, given the diffuse minor-effect background uncovered across traits, genomic selection provides a complementary path to capture cumulative small effects and G×E, while MAS secures the largest, most stable contributors—an approach that mirrors contemporary tomato improvement strategies [23, 30, 33, 35].

Two caveats temper interpretation. First, while the present F2 design is efficient for discovery, it limits precision for dominance and epistasis relative to advanced populations; nonetheless, the permutation-based thresholds and concordance with candidate intervals mitigate over-interpretation risk [10-14, 23-27]. Second, environment specificity remains an ever-present concern in horticultural crops; although seasonal replication was used, broader multi-location validation would better quantify stability, as emphasized in earlier tomato QTL syntheses [23, 30, 33, 35]. Even so, the alignment of detected intervals with well-established genomic landmarks and cherry-tomato evidence argues that key signals—particularly at fw2.2 and OVATE/sov—will generalize sufficiently to justify near-term deployment in MAS and as anchors for fine-mapping [4-7, 15-17, 19, 23-27, 31-32, 34-35].

In summary, the F2-based mapping results are consistent with a mixed genetic architecture in cherry tomato and integrate seamlessly with decades of tomato genetics: major contributors at fw2.2 and OVATE/sov, plausible TSS-linked variation near lc, and a constellation of minor effects distributed genome-wide [1-2, 4-7, 10-14, 15-17, 18-22, 23-27, 29-37]. This coherence with the reference genome, trait descriptors, and canonical loci provides a solid foundation for immediate MAS on high-value regions and for building genomic prediction models that harvest the remaining polygenic variance in cherry breeding programs.

Conclusion

The present study demonstrates that cherry tomato F2 populations harbor a mixed genetic architecture in which a few moderate-effect loci—most notably those aligning with canonical fruit-size and shape regions—operate alongside numerous small-effect contributors influencing yield, quality, and earliness; taken together with moderate-to-high heritabilities and biologically coherent QTL co-localizations, these results support immediate translational use in breeding while motivating deeper resolution of the remaining polygenic background. Practically, breeders should deploy marker-assisted selection to fix the largest, most stable fruit-size and locule/shape loci early, but pair this with a multi-trait index that explicitly balances fruit weight, soluble solids, pericarp thickness, and earliness to avoid unintended trade-offs; when possible, select recombinant haplotypes that decouple adverse correlations at shape/locule complexes so that gains in size do not depress sugars or firmness. Programs are advised to convert lead QTL into breeder-friendly assays (e.g., KASP) and run them under a foreground-plus-background selection scheme to accelerate recovery of elite genetic backgrounds; complementary genomic selection models should then be introduced to capture diffuse small effects and genotype-by-environment components that single-marker strategies miss. For rapid confirmation and fine-mapping, develop near-isogenic lines or heterogeneous inbred families around top intervals and use high-density genotyping or targeted resequencing to narrow candidate regions; where signals overlap candidate genes, incorporate gene-informed haplotype tracking and, if feasible, functional validation via transcript profiling under contrasting environments or precise editing in pre-breeding materials. At the phenotyping level, maintain strict adherence to standardized trait descriptors, deploy calibrated instrumentation for

soluble solids and firmness proxies, and schedule harvests at uniform physiological stages to minimize noise; concurrently, extend evaluation to multi-location and multi-season trials so that selection focuses on QTL with demonstrable stability and favorable pleiotropic profiles. Seed companies and public programs should package validated markers and trait indices into simple decision tools for early-generation nurseries, while investing in training for technicians on DNA sampling, data capture, and quality control to sustain reliable pipelines. To future-proof gains, broaden genetic designs beyond F2 discovery by advancing to RILs or MAGIC panels for epistasis and fine-scale recombination mapping, integrate metabolite and microstructural fruit data to disentangle morphology-composition links, and incorporate shelf-life and transportability phenotypes that align with market needs. Finally, institute transparent data management—anchoring markers to the current reference assembly, documenting primer sequences, and archiving effect sizes and intervals—so that results can be ported seamlessly across programs; taken together, these actions will allow breeding teams to convert today's discovery QTL into durable, high-quality cherry tomato cultivars that combine attractive architecture with sweetness, firmness, and timely maturity without compromising agronomic performance.

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