Zoo Botanica 03(3) 2025. 559-566

Zoo Botanica
ISSN: 3007-2050 (E), 3007-2042 (P)

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Research Article

Assessment of genetic variability and heritability of vegetative, floral and fruit traits in tomato (*Solanum lycopersicum* L.)

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ABSTRACT

Genetic diversity is crucial for tomato (*Solanum lycopersicum* L.) improvement. To assess this variability, a field experiment was conducted using eleven tomato varieties arranged in randomized complete block design with five replications. This study was designed to estimate genetic parameters for 19 vegetative and reproductive traits. Statistical analysis revealed significant differences among the genotypes for the majority of the traits, confirming the presence of substantial genetic diversity. The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were highest for pulp weight and leaf rachis length, indicating a strong inherent genetic potential for selection. Fruit length recorded the highest genotypic (85.88) and phenotypic (104.44) variances. Heritability estimates were high for most traits crucial for yield, with the maximum value observed for fruit length (0.82). The combination of a pronounced level of heritability and substantial expected genetic advance for these traits appears to suggest that their expression is primarily controlled by gene action. Therefore, future breeding programs should prioritize direct selection for characters such as fruit length, pulp weight, and leaf architecture to achieve rapid genetic gain and enhance tomato yield productivity.

Keywords: Tomato; genetic variability; heritability; morphological characterization; coefficient of variation.

OPEN ACCESS

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Article History
Received: November 20, 2025
Accepted: December 19, 2025
Published: December 31, 2025

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INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is a key vegetable crop valued for its versatility in fresh intake and processing into products like paste, sauce, and ketchup (Kaundal et al., 2024). Owing to its high content of lycopene, ascorbic acid, and β-carotene, its nutritional profile further underscores its importance in human diets (Tufail et al., 2024). In Pakistan, tomato yield remains critically low at approximately 19.6 tonnes per hectare, compared to a global average of 38 tonnes per hectare (Younas et al., 2024). This yield gap is largely attributed to factors such as the limited availability of quality seed, a narrow genetic base of available genotypes, and a lack of varieties resilient to local biotic and abiotic stresses (Zannat et al., 2023).

Cultivar selection is a primary genetic factor determining key agronomic traits, including yield potential, fruit quality, and stress tolerance (Fadhilah et al., 2022). Significant yield variations among tomato cultivars have been consistently demonstrated, highlighting the potential for genetic improvement (Zannat et al., 2023). The key to a successful breeding rests in the existence of substantial genetic variability within the available germplasm. For the genetic enhancement of diverse, quantitative traits like yield, it is essential to understand the magnitude and nature of this variability by partitioning the observed phenotypic variance into its heritable (genetic) and non-heritable (environmental) components. Parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and heritability (H^2) are fundamental for this purpose (Singh et al., 2022). High heritability estimates indicate that a trait is predominantly controlled by gene action, meaning that selection based on phenotypic performance is likely to be effective and result in significant genetic advance in subsequent generations (Shashikanth, 2008).

While molecular markers offer powerful tools for diversity analysis, morphological characterization remains a fundamental, accessible, and cost-effective first step for the classification and selection of germplasm, providing directly selectable traits for breeders (Kumar et al., 2024). Key morphological characters, including leaf architecture, flower morphology, and fruit dimensions, are highly discriminative and play a crucial role in breeding for improved cultivars (De Mori and Cipriani, 2023).

Research has demonstrated that yield-related traits in tomato, including fruit weight and fruit count per cluster expression is largely due to additive gene action, as evidenced by pronounced heritability and genetic advance. This confirms that selection for these traits is an effective strategy for yield improvement (Rasheed et al., 2023). Studies of vegetative (particularly leaves) and reproductive (flowers) architecture are of notable interest for researchers. Biologists have long formulated Goethe's hypothesis that leaves are considered the ancestral structures of floral organs. (Arber, 1950). Leaf area size and distribution govern light capture in the canopy, impacting photosynthesis and crop yield (Huang et al., 2016). In a study, Rowland et al. (2020) revealed that the morphology of leaves is indicative of fruit quality and overall cultivar performance in tomato. Leaf form, particularly rounder leaves, had a strong positive impact on both yield and fruit sugar content. In their study two tomato cultivars (Stupice and Glacier) which have round leaves, showed the best performance in yield and fruit sugar.

However, comprehensive studies on the genetic variability and heritability of a wide range of vegetative and reproductive morphological traits in local Pakistani tomato germplasm are limited. Therefore, the research sought to estimate the genetic variability, heritability, and expected genetic advance for 19 morphological traits across eleven tomato genotypes. The heritability estimates obtained will enable the prediction of selection progress and facilitate the identification of parents possessing desirable agronomic characteristics. This research ultimately aims to provide a scientific basis for formulating effective breeding strategies to enhance yield and quality in tomato. This study uniquely integrates vegetative, floral, and fruit traits to identify reliable selection indices for Pakistani tomato germplasm.

MATERIALS AND METHODS

The study was carried out at the vegetable research area, Institute of Horticultural Sciences, University of Agriculture, Faisalabad, Pakistan. Eleven tomato varieties (Nagina, Riogrande, Money Maker, Pakit, 88572, Picdeneto, Roma, Lyallpur, CC Haus, Tibrido, and Naqeeb) were evaluated. Seed was sourced from the National Agricultural Research Centre (NARC), Pakistan. Seedlings were raised in a controlled environment and transplanted to the field following standard nursery practices. The nursery plants were transplanted in the field after 35 days on both sides of raised beds at a distance of "50 × 150 cm". Each genotype was represented by four plants in five replications under a randomized complete block design. Standard agronomic and plant protection practices were followed.

Data on leaf, flower, and fruit morphological characteristics were recorded at the appropriate plant growth stages.

Leaf morphological parameters

To ensure comparison at a similar developmental stage, two leaves (the 9th and 11th from the base) were sampled from each replication for the evaluation. The assessed traits included the lateral leaflet number (LFN), defined as the count of leaflets with an area greater than 0.5 cm^2; the maximum leaflet length (LFL) and width (LFW), measured in centimeters; two calculated leaf shape indices—the LR index (LFLR, the ratio of total width to total length) and the DLR index (LFDLR, the ratio of the distance from the leaflet base to the point of maximum width to the total leaflet length); the Petiolule length (PLL); and the leaf rachis length.

Flower morphological parameters

Two flowers per replication were sampled to evaluate the following traits: sepal number (SEN) and petal number (PEN) were counted directly. Linear measurements included sepal length (SEL) and petal length (PEL), as well as sepal width (SEW) and petal width (PEW), the latter measured at the point of petal fusion. From these measurements, two shape indices were derived: the sepal length-to-width ratio (SELR) and the petal length-to-width ratio (PELR) (deVicente and Tanksley, 1993; Wu, 2000).

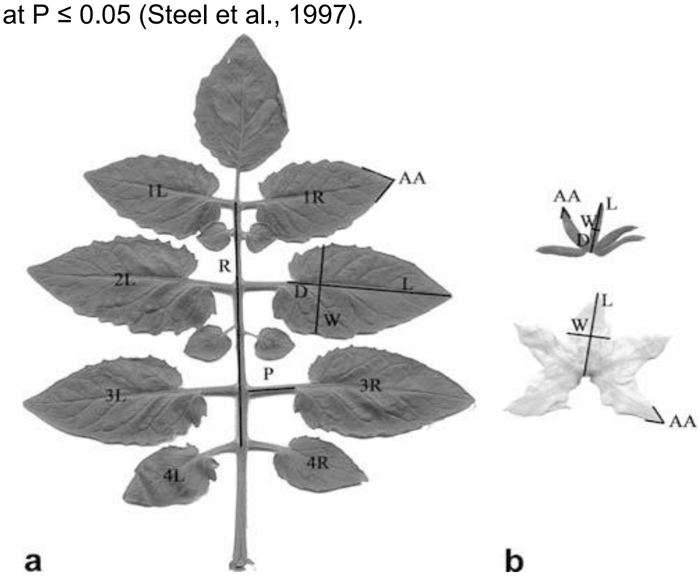
Fruit morphological parameters

Fifteen fruits per variety (three from each replication) were harvested at maturity for evaluation. Linear measurements of fruit length (from top to bottom) and maximum fruit width were taken using a Vernier caliper. Five fruit shape indices were calculated: 1) stem-end blockiness (ratio of width 10% below the top to width at the midpoint); 2) blossom-end blockiness (ratio of width at the midpoint to width 10% above the bottom); 3) heart shape (ratio of width 10% below the top to width 10% above the bottom); 4) elongation index (ratio of length to maximum width); and 5) bumpiness (ratio of measured circumference to calculated circumference × 10) (van der Knaap & Tanksley, 2003). Additional parameters included locule number (counted from horizontal cross-sections), pulp-to-jelly ratio (determined by separation and weighing), and individual fruit weight with derived pulp weight.

Estimation of genetic parameters

Genetic parameters were estimated to quantify the variability and heritability of the measured traits. Phenotypic ($\sigma^2 p$) and genotypic ($\sigma^2 g$) variances were used to calculate the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) as percentages, according to the Kwon and Torrie (1964) method, using the formulas: $GCV = (\sqrt{\sigma^2 g} / \bar{X}) \times 100$ and $PCV = (\sqrt{\sigma^2 p} / \bar{X}) \times 100$, where $\bar{X}$ is the grand mean of the trait. Broad-sense heritability (H^2) was estimated as the ratio of genotypic variance to phenotypic variance ($H^2 = \sigma^2 g / \sigma^2 p$) (Falconer and Mackay, 1996).

Analysis of variance (ANOVA) was conducted according to a randomized complete block design (RCBD), with treatment means separated at $P \leq 0.05$ (Steel et al., 1997).



Figures: a and b. Representative leaf and flower.

RESULTS AND DISCUSSION

This study assessed genetic variability and heritability for key morphological traits across eleven tomato varieties (*Solanum lycopersicum* L.). The analysis encompassed vegetative characters (leaflet number, dimensions, and rachis length), reproductive floral parts (sepal and petal number, length, and width), and fruit attributes (length, width, and weight). The results of this investigation are presented and discussed below.

Leaf parameters

With the exception of Petiolule length, all traits related to leaf morphology exhibited significant differences among the genotypes (Table 1 & 4). The highest estimates of genotypic variance (3.06) and phenotypic variance (6.09) were recorded leaf rachis length, respectively. The GCV and PCV were also highest for leaf rachis length (24.83% and 86.50%, respectively), while the lowest values were observed for the LR index (6.78%) and DLR index (0.68%) for leaflet. Broad sense heritability was highest for the total number of leaflets (0.65) and lowest for Petiolule length (0.17). The high heritability estimates observed for traits e.g. total number of leaflets length and width of leaflets suggest a predominant genetic component, reflecting their potential utility for effective phenotypic use in breeding programs.

Flower parameters

Analysis of floral traits revealed distinct genetic potential for selection (Table 2 & 4). Sepal number (SEN) and petal number (PEN) showed no significant genetic differences among varieties, with high environmental coefficients of variation (18.90 and 23.64, respectively) and low heritability ($H^2 \leq 0.11$), indicating strong environmental control.

Table 1. Mean performance of eleven tomato genotypes for various leaf morphology related traits.

Varieties	Total number of leaflets	Length of leaflets (cm)	Width of leaflets (cm)	LR index of leaflets	DLR index of leaflets	Petiolule length of leaflets (cm)	Leaf rachis length (cm)
Money Maker	5.8^{b}	3.65^{f}	2.04^{e}	0.82^{a}	0.43^{abc}	1.09^{abc}	5.55^{de}
Tibrido	6^{b}	4.48^{bcde}	2.77^{abc}	0.80^{ab}	0.46^{ab}	1.02^{abc}	6.03^{cde}
Lyallpur	6.2^{b}	3.99^{def}	2.63^{bcd}	0.58^{c}	0.38^{cd}	1.04^{abc}	4.92^{e}
Riogrande	6.3^{b}	5.04^{ab}	2.74^{abc}	0.73^{ab}	0.39^{bcd}	1.48^{a}	7.82^{bcd}
CC Haus	6.3^{b}	3.92^{ef}	2.30^{de}	0.76^{ab}	0.41^{abcd}	0.73^{c}	4.88^{e}
Roma	6.4^{b}	4.41^{bcde}	2.59^{bcd}	0.70^{abc}	0.37^{cd}	0.89^{bc}	5.79^{cde}
Picdeneto	6.4^{b}	4.29^{cdef}	4.29^{cd}	0.75^{ab}	0.41^{abc}	1.08^{abc}	6.39^{cde}
88572	6.4^{b}	5.52^{a}	2.66^{bcd}	0.70^{abc}	0.37^{abc}	1.26^{ab}	8.28^{bc}
Nagina	8.8^{a}	4.66^{bcd}	2.59^{bcd}	0.75^{ab}	0.35^{d}	1.18^{abc}	7.64^{bcd}
Pakit	9^{a}	4.82^{bc}	2.90^{ab}	0.77^{ab}	0.40^{abcd}	1.33^{ab}	9.21^{ab}
Naqeeb	9.7^{a}	5.57^{a}	3.07^{a}	0.66^{bc}	0.47^{a}	1.33^{ab}	5.55^{de}

Table 2. Mean performance of eleven tomato genotypes for various flower morphology related traits.

Varieties	Sepal number	Petal number	Sepal length (cm)	Petal length (cm)	Sepal width (mm)	Petal width (mm)	LR index for the sepal	LR index for the Petal
Money Maker	6.4^{a}	6.0^{a}	8.03^{bc}	7.86^{d}	3.06^{abc}	2.60^{cd}	0.38^{bc}	0.33^{ab}
Tibrido	6.2^{a}	5.4^{a}	8.13^{bc}	10.93^{a}	2.88^{bc}	4.06^{a}	0.35^{c}	0.37^{ab}
Lyallpur	6.0^{a}	5.4^{a}	6.93^{c}	10.59^{ab}	2.98^{bc}	3.59^{ab}	0.43^{b}	0.34^{ab}
Riogrande	5.0^{b}	5.2^{a}	9.83^{a}	10.13^{abc}	3.51^{ab}	2.93^{bcd}	0.35^{c}	0.28^{b}
CC Haus	6.4^{a}	6.2^{a}	7.26^{c}	7.80^{d}	2.96^{bc}	2.53^{d}	0.41^{bc}	00.33^{ab}
Roma	5.2^{ab}	5.0^{a}	9.07^{ab}	9.46^{bc}	3.32^{abc}	3.40^{abc}	0.36^{c}	0.36^{ab}
Picdeneto	5.8^{ab}	6.4^{a}	7.66^{bc}	9.73^{abc}	3.36^{abc}	4.00^{a}	0.44^{b}	0.41^{a}
88572	5.8^{ab}	5.4^{a}	6.66^{c}	9.73^{abc}	2.81^{c}	4.06^{a}	0.42^{bc}	0.41^{a}
Nagina	4.4^{b}	5.0^{a}	7.1^{c}	7.60^{d}	3.65^{a}	2.53^{d}	0.51^{a}	0.33^{ab}
Pakit	5.8^{ab}	5.8^{a}	7.13^{c}	8.93^{cd}	3.18^{abc}	3.06^{bcd}	0.45^{ab}	0.33^{ab}
Naqeeb	6.0^{a}	5.4^{a}	7.83^{bc}	7.60^{d}	3.02^{bc}	2.66^{cd}	0.39^{bc}	0.35^{ab}

Similarly, sepal width (SEW), petal width (PEW), and the petal length-to-width ratio (PELR) exhibited non-significant varietal differences and low heritability (0.10-0.49), rendering them unsuitable for reliable selection. In contrast, several traits demonstrated significant genetic variability. Sepal length (SEL) showed significant differences with moderate heritability (0.33), though its moderate genotypic coefficient of variation (10.41) suggests careful selection is needed. Petal length (PEL) was more promising, with significant differences, moderate heritability (0.58), and a substantial GCV (12.70), indicating a strong genetic component favorable for breeding. The sepal shape index (SELR) also showed significant varietal differences and moderate heritability (0.43), supporting its potential use in selection.

Fruit shape parameters

Fruit length

Analysis of variance revealed significant genetic differences among varieties for fruit length (trait correlated with yield), fruit width, Stem end blockiness and heart shape (Table 3 & 4). These results are in agreement with earlier studies by Chaudhary et al. (1999). The high GCV (17.48%) and PCV (19.28%), coupled with a low environmental coefficient of variation (8.13), indicate substantial genetic diversity and a predominantly genetic control for fruit length and width traits. The high broad-sense heritability further confirms that fruit length, width and shape related traits are highly heritable. Therefore, fruit morphological traits possessed a broad genetic base and are highly suitable traits for phenotypic selection in tomato breeding programs aimed at improving yield. Moreover, stem end blockiness was also previously correlated with fruit size (r=0.66) by van der Knaap and Tanksley (2003).

Fruit weight

Analysis of variance revealed significant genetic differences in individual fruit weight, a key determinant of yield per plant (Table 3 & 4). This range of variation is consistent with that reported by Shashikanth (2008). The genetic parameters for this trait were highly favorable for selection. The high genotypic coefficient of variation (33.60%) and phenotypic coefficient of variation (37.71%) indicate substantial genetic diversity. The low environmental coefficient of variation (17.13%) relative to the GCV, coupled with high broad-sense heritability (0.79), confirms that fruit weight is

Table 3. Mean performance of eleven tomato genotypes for various fruit morphology and quality traits.

Varieties	Fruit length (cm)	Fruit width (cm)	Stem end blockiness	Heart Shape	Fruit weight (g)	Number of locules	Pulp to Jelly ratio	Pulp weight (g)	Yield per plant (Kg)
Money Maker	4.54^{e}	4.75^{ab}	0.96^{cd}	1.16^{a}	44.31^{de}	2.53^{b}	2.34^{ef}	13.24^{abc}	2.9^{bc}
Tibrido	4.73^{e}	4.17^{cde}	1.08^{c}	1.20^{a}	58.67^{bc}	253^{b}	5.35^{abc}	9.24^{cde}	2.7^{bcd}
Lyallpur	4.42^{cd}	4.24^{cde}	1.37^{b}	0.95^{bc}	31.00^{f}	2.33^{b}	2.22^{ef}	9.97^{bcd}	2.65^{cd}
Riogrande	6.16^{ab}	4.77^{a}	1.28^{b}	1.10^{ab}	60.93^{b}	2.26^{b}	6.61^{a}	8.09^{de}	2.8^{bcd}
CC Haus	3.54^{f}	4.37^{bcd}	0.81^{d}	1.20^{a}	25.21^{f}	4.4^{a}	1.39^{f}	10.64^{abcd}	2.45^{d}
Roma	6.01^{b}	3.92^{fe}	1.48^{ab}	0.83^{c}	44.51^{de}	2.33^{b}	3.68^{de}	9.48^{cd}	2.02^{d}
Picdeneto	5.68^{bc}	3.74^{f}	1.42^{b}	1.14^{a}	33.98^{ef}	2.20^{b}	5.68^{ab}	5.37^{e}	2.42^{d}
88572	4.91^{de}	4.46^{abcd}	1.09^{c}	1.18^{a}	51.60^{bcd}	2.53^{b}	5.83^{ab}	7.96^{de}	2.46^{d}
Nagina	6.68^{a}	4.09^{def}	1.65^{a}	0.89^{c}	48.37^{cd}	2.13^{b}	3.94^{cd}	11.69^{abcd}	3.37^{c}
Pakit	4.44^{e}	4.46^{abcd}	1.05^{c}	1.20^{a}	45.48^{d}	2.26^{b}	2.28^{ef}	13.94^{ab}	3.03^{b}
Naqeeb	6.15^{ab}	4.52^{abc}	1.38^{b}	1.17^{a}	85.75^{a}	2.60^{b}	4.91^{bcd}	14.61^{a}	2.54^{cd}

Table 4. Estimation of component of variance, broad sense heritability (H^2) and coefficients of variation.

Component	σ_g^2	σ_p^2	σ_e^2	GCV	PCV	ECV	H^2
Number of leaflets	1.77	2.72	0.95	18.96	38.75	13.84	0.65
Length of leaflets	0.34	0.58	0.23	12.79	12.59	10.55	0.59
Width of leaflets	0.06	0.14	0.08	9.59	5.27	10.47	0.45
LR index of leaflets	0	0.01	0.01	6.78	1.84	14.34	0.18
DLR index of leaflets	0	0	0	7.69	0.68	10.49	0.34
Petiolule length	0.02	0.14	0.11	24.83	12.15	29.85	0.17
Leaf rachis length	3.06	6.09	3.03	24.83	86.5	24.74	0.5
Sepal number	0.15	1.32	1.17	6.8	20.08	18.9	0.11
Petal Number	0.12	1.6	1.73	6.1	22.78	23.64	0.07
Sepal Length	0.65	1.96	1.3	10.41	17.99	14.66	0.33
Petal length	1.34	2.29	0.94	12.7	16.58	10.64	0.58
Sepal Width	0.03	0.21	0.18	6.02	14.83	13.56	0.16
Petal Width	0.32	0.66	0.33	17.77	25.31	18.01	0.49
LR index for the sepal	0.001	0.004	0.002	10.16	15.39	11.55	0.43
LR index for petal	0.0005	0.004	0.004	6.57	19.91	18.79	0.1
Fruit length	85.88	104.44	18.56	17.48	19.28	8.13	0.82
Fruit Width	9.04	16.84	7.8	17.48	19.28	8.13	0.54
Stem end blockiness	0.06	0.08	0.02	19.71	22.84	11.54	0.74

Heart Shape	0.016	0.02	0.01	11.6	14.79	9.17	0.61
Fruit weight	261.92	330.02	68.1	33.6	37.71	17.13	0.79
No. of Locules	0.37	0.51	0.13	23.8	27.81	14.38	0.73
Pulp to Jelly ratio	2.9	4.09	1.19	42.41	50.34	27.13	0.7
Pulp weight	6.23	14.58	8.34	24.03	36.75	27.8	0.42
Yield per Plant	0.11	0.18	0.07	278.09	354.08	219.17	0.61

predominantly under genetic control. These results, which align with the findings of Shashikanth (2008), demonstrate a broad genetic base and establish individual fruit weight as a highly reliable trait for phenotypic selection in tomato breeding programs aimed at increasing yield.

Number of locules

Significant genetic differences among varieties for locule number were also found (Table 3 & 4). The high genotypic coefficient of variation (23.80%) and phenotypic coefficient of variation (27.81%), relative to the moderate environmental coefficient of variation (14.38%), demonstrate substantial genetic control over this trait. This genetic predominance is further confirmed by high broad-sense heritability (0.73). The combination of high genetic variability and heritability indicates a broad genetic base and establishes locule number as a reliable trait for phenotypic selection in breeding programs. The observed genetic parameters closely align with those reported by Shashikanth (2008).

Pulp: jelly ratio

Analysis of variance revealed significant genetic differences among varieties for pulp-to-jelly ratio (Table 3 & 4). The trait showed exceptionally high genotypic (42.41%) and phenotypic (50.34%) coefficients of variation, substantially exceeding the environmental coefficient (27.13%). This genetic predominance was further confirmed by high broad-sense heritability (0.70). While these parameters indicate strong potential for genetic improvement, the notable PCV-GCV gap suggests that selection for this trait should be accompanied by careful evaluation to account for its moderate environmental influence.

Pulp weight

Significant genetic differences were observed in pulp weight among the tomato varieties (Table 3 & 4). The genetic parameters demonstrated a substantial genotypic coefficient of variation (24.03%) and phenotypic coefficient of variation (36.75%), both exceeding the environmental coefficient of variation (27.80%), indicating a predominantly genetic influence on this trait. The moderate broad-sense heritability (0.42) confirms that pulp weight is reasonably heritable and possesses a broad genetic base, making it a suitable character for selective breeding in tomato improvement programs.

Yield/plant

Significant genetic differences were observed in yield per plant among the tomato varieties (Table 3 & 4). Nagina produced the highest yield (3.07 kg), showing statistical superiority over other varieties, while Roma yielded the minimum (2.02 kg). The genetic parameters demonstrated exceptionally high genotypic (278.09%) and phenotypic (354.08%) coefficients of variation, substantially exceeding the environmental coefficient (219.17%). The moderate broad-sense heritability (0.61) confirms considerable genetic control over this complex trait. These results indicate substantial genetic diversity for yield and suggest suitability for effective phenotypic selection for trait improvement. The findings align with the high heritability reported by Shashikanth (2008), further supporting the genetic basis of yield variation in tomato. This study highlights a comprehensive analysis of the varietal architecture governing vegetative and reproductive traits in tomato, offering a clear strategic framework for cultivar improvement. The estimation of genetic parameters, genotypic and phenotypic coefficients of variation (GCV, PCV), and broad-sense heritability (H^2) has successfully delineated traits controlled by additive gene action from those susceptible to environmental influence, thereby enabling efficient phenotypic selection. Our findings reveal a consistent pattern of strong genetic control over key traits directly linked to plant architecture and yield. Among leaf parameters, the total number of leaflets (LFN) and leaf rachis length (RAL) are particularly promising due to their high heritability (0.65 and 0.50, respectively) and substantial genetic variability. These traits, along with the stable and moderately heritable leaflet length (LFL), are reliable indicators of genetic merit for selection. In contrast, leaflet width and the various leaf shape indices (LFLR, LFDLR) were predominantly influenced by the environment, rendering them unsuitable for breeding. The complete lack of genetic control in Petiolule length further underscores the necessity of such pre-selection screening to avoid futile breeding efforts. The analysis of floral traits further refines this selection strategy. While meristic traits like sepal and petal number and those related to organ width were genetically unstable, petal length (PEL) emerged as a highly heritable trait (0.58) with significant genetic diversity. This finding, consistent with the known QTLs for this trait (Frary et al., 2004), suggests that PEL can serve as a stable morphological marker. The moderate heritability of sepal length and the sepal shape index (SELR) also make them useful secondary criteria. Most critically, the evaluation of fruit and yield characteristics identified the most valuable traits for direct genetic gain. Fruit weight and fruit length stand out with exceptionally high heritability (0.79 and 0.85) and high GCV, confirming they are predominantly controlled by additive genes. These results align with previous studies that link fruit length to yield (Islam and Khan, 1999) and confirm the strong inheritability of fruit weight (Shashikanth, 2008). Furthermore, the high heritability of locule number and advanced morphological indices like stem end blackness, a trait correlated with fruit size, provides breeders with a diverse toolkit for selecting superior genotypes not just for yield but also for specific fruit shapes and internal structures.

CONCLUSION AND RECOMMENDATIONS

Based on these findings, the following recommendations are proposed for efficient tomato breeding: Tomato improvement programs should focus on direct phenotypic selection for individual fruit weight, fruit length, locule number, and stem end blockiness. These traits are expected to a strong response to selection, leading to rapid genetic gain. Moreover, Breeders can employ leaf rachis length, leaflet number, and petal length as early-season selection criteria. These traits provide a reliable proxy for a plant's genetic potential before fruit set, potentially shortening the breeding cycle. For traits like yield per plant and the pulp-to-jelly ratio, which show moderate heritability and a significant gap between PCV and GCV, selection should be based on replicated multi-location testing. This approach will help to buffer against genotype-by-environment interactions and ensure the selection of stable performers. Resources should not be allocated to selecting for leaflet width, leaf shape indices, Petiolule length, sepal/petal number, or organ width. Their low heritability and high environmental variance mean that phenotypic performance is a poor predictor of genetic worth. In conclusion, this study demonstrates that a strategic focus on highly heritable morphological traits with substantial additive genetic variance is the most effective path for enhancing tomato productivity. By channeling selection efforts towards the identified promising traits, breeders can optimize resource allocation and accelerate the development of high yielding, cultivated tomato varieties.

AUTHOR'S CONTRIBUTION

Muhammad Iqbal conceived and designed the study and drafted the manuscript. Riaz Hussain and Atyab Amjad contributed to experimental design, field experimentation, and methodology refinement. Ayesha Manzoor conducted laboratory analyses, while Ahsan Hammad and Ibrar Khan performed data analysis, field data collection, and assisted in manuscript revision. All authors reviewed and approved the final manuscript.

FUNDING

No funding was received for this study.

AVAILABILITY OF DATA AND MATERIAL

All data generated or analyzed in this study are presented within this article in the form of tables and figures.

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

The current study was checked and approved by the relevant team.

CONSENT FOR PUBLICATION

All authors have reviewed the manuscript and approved it for publication.

CONFLICT OF INTERESTS

The authors declare no conflict of interest.

ACKNOWLEDGEMENT

This study was a part of Research for MSc (Horticulture). The first author is deeply grateful for the guidance provided by the Dr. Khurram Ziaf and Muhammad Muzammil Jahangir.

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