



DOI: <https://doi.org/10.71317/kjard.2.10.2026.918>

Kashmir Journal of Academic Research and Development

Journal homepage: <https://rjsaonline.org/index.php/KJARD>



Characterization and Selection of Advanced Tomato Inbred Lines for Hybrid Breeding under upland Conditions of Balochistan, Pakistan

Malik Bakht Ali

Vegetable Botanist, Directorate of Vegetable Seed Production, Agriculture Research Institute (ARI), Sariab, Quetta, Balochistan, Pakistan

Email: malikbakhtalioo@gmail.com

Muhammad Taimoor Saeed

Research Officer, Directorate of Vegetable Seed Production, ARI Sariab, Quetta, Balochistan, Pakistan

Sakhawat Ali

Entomologist, Directorate of Vegetable Seed Production, ARI Sariab, Quetta, Balochistan, Pakistan

Malik Asad Khan Khajjak

Research Officer, Directorate General of Agriculture Research, ARI Sariab, Quetta, Balochistan, Pakistan

Muhammad Hanif

Research Officer, Directorate of Post Harvest & Food Technology, Agriculture Research Institute (ARI), Quetta, Balochistan, Pakistan

Zahri Khan

Senior Scientific Officer, PARC-Horticulture Research Institute, Khuzdar, Balochistan, Pakistan

Riaz Ahmed

Senior Scientific Officer, PARC-Horticulture Research Institute, Khuzdar, Balochistan, Pakistan

Shafique Ahmed

Vegetable Botanist, Directorate of Agriculture Research, Vegetable Seed Production, ARI Sariab, Quetta, Balochistan, Pakistan

ARTICLE INFO	ABSTRACT
<p>Received: September 14, 2026</p> <p>Revised: October 13, 2026</p> <p>Accepted: October 19, 2026</p> <p>Available Online: October 27, 2026</p> <p>Keywords: Solanum lycopersicum L.; tomato breeding; inbred lines; parental selection; yield components; disease tolerance; highland agriculture.</p> <p>Corresponding Author: Malik Bakht Ali Email: malikbakhtalioo@gmail.com</p>	<p>Development of locally adapted tomato parental resources is essential for improving hybrid breeding programs in highland production environments. This study aimed to characterize advanced tomato inbred lines and identify promising parental candidates under the highland agro-ecological conditions of Balochistan, Pakistan. Sixteen S₆-generation tomato lines were evaluated during Kharif 2025 at the Agriculture Research Institute (ARI) Sariab, Quetta, using a randomized complete block design with three replications. Eight morphological, agronomic, and disease-response traits, including plant height, branches per plant, fruit size, fruit weight, days to flowering, fruits per plant, yield, and field response to late blight and Fusarium wilt under natural infection pressure, were recorded. Analysis of variance revealed significant differences among lines for all quantitative traits, demonstrating genetic variation within the evaluated germplasm. Yield ranged from 2.45 to 4.12 t ha⁻¹, with L-14 showing the highest yield, superior fruit weight, maximum fruits per plant, early flowering, and strong field disease response. Fruits per plant and fruit weight exhibited strong positive associations with yield, indicating their potential value as indirect selection traits. Based on combined agronomic performance, fruit characteristics, and disease response, L-14, L-5, L-12, and L-8 were identified as promising parental candidates, whereas L-6 represented a potential disease tolerance donor. These findings provide valuable genetic resources for future tomato hybrid breeding programs in Balochistan; however, multi-location evaluation, combining ability studies, and molecular characterization are required for further validation.</p>

Introduction

Tomato (*Solanum lycopersicum* L. $2n = 2x = 24$) is one of the most globally significant crops in horticulture with an estimated production of more than 189 million tonnes on approximately 5.1 million hectares of harvested land per year (FAO, 2023). Aside from its usage as a fresh market commodity, the crop also provides a wide range of phytochemicals with health-protecting properties, such as lycopene, ascorbic acid, β -carotene and chlorogenic acid, which offer protection against oxidative stress-related chronic diseases (Piva et al., 2021; Willcox et al., 2003). Tomato is one of the top five high value vegetable crops for Pakistan and is an important source of livelihood for small farmers across the northern and western highlands of the country (Pakistan Bureau of Statistics, 2023).

Balochistan is the major tomato growing province of Pakistan with an estimated 23,380 hectares cultivated and 40.3% of the national production (Pakistan Bureau of Statistics 2023; Balochistan Agriculture Department 2024). Given this significant productive legacy, yields of around 9.9 t/ha (mostly open-pollinated and landrace varieties) are still far from the potential yields possible with the use of modern hybrid cultivars, due to poor adoption of improved cultivars, sub-optimal crop management and regular losses caused by soilborne and foliar pathogens (Rasheed et al., 2022; PBS, 2023).

In these, (Quetta's highlands) late blight caused by *Phytophthora infestans* (Mont.) de Bary and fusarium crown and root rot caused by *Fusarium oxysporum* f. sp. *lycopersicum* are the most economically important biotic factors (Rasheed et al., 2022).

The exploitation of heterosis through F_1 hybridization is a scientifically proven approach to this yield gap. Hybrid cultivars typically yield 15–35% more than open pollinated cultivars, and exhibit greater uniformity in phenotype, early maturity and more disease resistance (Liu et al., 2021; Yu et al., 2021). In technologically advanced tomato producing countries such as the Netherlands, Turkey, India and China, over 80% of the tomato area is dedicated to F_1 hybrids, which has been achieved over the years through pure line development and combining ability screening (Vanlay et al., 2022).

The basic precondition for any hybrid seed production business is the existence of previously available homozygous, phenotypically stable inbred lines (pure lines) as permanent parents. The lines are conventionally produced by repeated cycles of self-pollination (usually S_4 – S_7) followed by stringent phenotypic selection for agronomic desirable traits and uniformity (Sairam et al., 2024; El-Gabry et al., 2014). Parental lines should not only be defined by yield-related morphological features, but also by their susceptibility to locally common diseases, their flowering phenology to the crossing parent and fruit quality parameters to match local market needs. Although this developmental pipeline has been recognized as important, yet systematic inbred line development for the specific agro-ecology of Balochistan highlands (steppic-type climate of Balochistan, calcareous soils and short frost-free production window) is still not available in the literature (Rasheed et al., 2022).

The present study, therefore, was planned to fill this gap, by systematic and comprehensive morphological and agronomic study of sixteen pure lines of tomato variety S_6 in the Directorate of Vegetable Seed Production Farm, ARI Sariat Quetta during Kharif 2025. The main objectives of the study were to: (i) measure genotypic variability in eight morphological, agronomic and disease resistance descriptors, (ii) select superior lines with desirable yield and disease resistance potential as parental stocks for a regionally adapted hybrid breeding programmed in the public sector of Balochistan, (iii) determine phenotypic associations within the descriptors for yield-related traits to support indirect breeding strategies; and (iv) provide empirical basis for a regionally adapted hybrid breeding programmed of tomato in the public sector of Balochistan.

Materials and Methods

Experimental Location and Seasonal Conditions

Field trials were laid down at the Directorate of Vegetable Seed Production Farm, Agriculture Research Institute (ARI) Sariat, Quetta, Balochistan, Pakistan ($30^{\circ}14'N$, $66^{\circ}58'E$; 1,680 m a.s.l) in the Kharif season of 2025 (April to October). Climate of the station is semi-arid steppic subtype (Köppen: BSk) and receives a mean annual precipitation of around 230 mm, which is mainly in the winter and early spring. The experimental temperature range was 24–36 C during the day and 12–18 C at night, creating a large diurnal temperature range which has been shown to promote lycopene accumulation and fruit quality in tomato grown on the highlands (Rosales et al., 2011). The dominant soil types at the experimental site are calcareous sandy loam with moderate organic matter content, and similar to the general soil regime of the Quetta valley.

Genetic Materials and Inbreeding History

The material used for the experiments consisted of 16 lines of tomatoes that were advanced to the S_6 generation by six successive cycles of self-pollination and pedigree selection. The base population used to take out these lines contained a mixture of exotic accessions collected from the National Agricultural Research Centre (NARC), Islamabad and traditional cultivars collected locally from the Directorate of Vegetable Seed production Farm ARI, Sariat Quetta Balochistan. Phenotypic uniformity, absence

of morphological off types, good vegetative growth and fruit setting ability were subjected to selection pressure in each generation in inbreeding, following the descriptors laid down by IPGRI (1996). The sixteen lines are a wide range of growth habits (determinate vs. semi-determinate), fruit morphology (round, oblong-plum, beefsteak), maturity time (early to mid-late), and susceptibility to pathogens, which offers a large genetic resource for combining ability evaluation and commercial hybrid production (El-Gabry et al., 2014; Sairam et al., 2024).

Experimental Design and Crop Husbandry

The sixteen pure lines were compared with a Randomized Complete Block Design (RCBD) with three replications. Each plot had a size of 3.0 m × 2.4 m (7.2 m²) and was planted with 45 plants per row and 60 cm between rows. Transplants were grown on raised beds covered with 40-mesh insect-proof netting and removed to the main field at the 5–6 true-leaf stage (after 28–30 days sowing). All the plots received a uniform agronomic package of N:P₂O₅:K₂O 120:90:60 kg ha⁻¹ as a basal dressing followed by a top dressing of 60 kg urea ha⁻¹ at 30 days after transplanting (DAT). Irrigation was by drip-assisted channels of furrow channels at 7–10 day intervals depending on the requirement of the crops. At 30 DAT, indeterminate and semi-determinate lines were staked using bamboo. Plant protection was done in accordance with the Integrated Pest Management (IPM) guidelines of ARI Quetta. The experimental block was surrounded by peripheral guards of a regular commercial variety, to reduce border effects.

The following section outlines the procedure used to record the 2.4 traits and presents the measurement protocol.

Eight morphological and agronomic descriptors were observed on 5 plants per plot, which were selected randomly, with 3 plants at the center and 2 on each side of the plot, but not at the plot borders, at 50% flowering, 70–80 DAT, respectively, following standardized methodologies of IPGRI (1996) and UPOV (2001): (1) Plant Height (cm) measured using a calibrated rod, from soil surface to the highest vegetative point; (2) Branches per Plant (Naturally endemic field infection was conducted at ARI Sariab Quetta with ratings showing disease incidence in the susceptible check variety was more than 75% by 80 DAT which was considered as sufficient discriminatory pathogen pressure for all lines tested).

Traits Recorded and Measurement Protocols

Eight morphological and agronomic descriptors were recorded on five randomly selected, border-excluded, tagged plants per plot at their respective phenological stages, following IPGRI (1996) and UPOV (2001) methodologies: (1) Plant Height (cm) distance from soil surface to vegetative apex at 90 DAT, measured using a calibrated rod; (2) Branches per Plant (BP) count of primary fruit-bearing lateral branches at first commercial harvest; (3) Fruit Size (cm) polar diameter of five representative ripe fruits per plant, recorded with a digital Vernier caliper; (4) Fruit Weight (g) mean fresh weight of ten randomly selected mature red-ripe fruits per plant, using a precision balance; (5) Days to Flowering (DF) elapsed days from transplanting to 50% flower anthesis per plot; (6) Fruits per Plant (FPP) cumulative count of all marketable fruits harvested per plant across picking cycles; (7) Yield per Hectare (t/ha) aggregate fresh marketable weight per plot, extrapolated to a per-hectare basis; and (8) Disease Resistance Score (DRS) assessed on a standardized 1-9 visual rating scale (1 = highly susceptible; 9 = highly resistant) at peak disease expression (70–80 DAT), recorded separately for (a) foliar late blight caused by *Phytophthora infestans* (DRS-LB) and (b) fusarium crown and root rot caused by *Fusarium oxysporum* f. sp. *lycopersicum* (DRS-FW), following TGRC protocols (IPGRI, 1996; Akhtar et al., 2016). Ratings were conducted under naturally endemic field infection at ARI Sariab Quetta; disease incidence in the susceptible check variety exceeded 75% by 80 DAT, confirming adequate discriminatory pathogen pressure for all lines evaluated.

Data Analysis

All quantitative data were analyzed by Analysis of Variance (ANOVA) under RCBD linear additive model $Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$, where Y_{ij} is the observation of response, μ is the overall population mean, τ_i is the fixed effect of the i^{th} pure line ($i = 1, 16$), β_j is the random block (replication) effect ($j = 1, 2, 3$), and ε_{ij} is the independently and identically distributed residual error term [$\varepsilon_{ij} \sim N(0, \sigma^2)$]. The Least Significant Difference (LSD) procedure was used to conduct pairwise mean comparisons at $\alpha = 0.05$. The Coefficient of Variation (CV%) was used as an internal measure of experimental precision. The full data set from all lines and replications were used to estimate the Pearson product-moment correlation coefficients (r) between yield per hectare and all the other quantitative traits. Data analysis was performed using the software packages Statistical Analysis (STATISTIX 8.1, Analytical Software, 2003), and R software version 4.3.2 (R Core Team, 2023). The figures were created with ggplot2 package (Wickham, 2016) for R version 4.3.2, and the radar chart (Figure 5) was created with fmsb package (Nakazawa, 2018). Microsoft Word 2021 was used to create tables.

Results

ANOVA Overall Genotypic Variation

ANOVA showed mean squares due to pure line effects to be highly significant ($p \leq 0.01$) for all seven quantitative traits measured (Table 3; DRS was analyzed as an ordinal categorical variable). There was a significant genetic difference among the sixteen lines between the F-values of 260.73 for fruit size and 18,987.82 for plant height. The very high F-values obtained for plant height and yield/ha are indicative of the consistency of the within-block replications for these characters, which are a result of the high inbreeding level (S_6) reached before evaluation. Inherent phenotypic uniformity of inbreds, which is generally greater in advanced S_6 -generation inbreds, resulted in a Coefficient of Variance ranging from 3.2% (days to flowering) to 6.8% (yield per hectare), within acceptable limits for a replicated field trial, and indicating adequate experimental precision over the trial. These yield differences (2.45–4.12 t/ha) should be interpreted in the context that these are yields from S_6 inbred lines, not commercial hybrid yields. The yield of the F_1 hybrids to be produced from these parental lines will be suppressed to a level below the provincial open-pollinated cultivar average yield of around 9.9 t/ha but will be expected to recover and clearly surpass that provincial average yield based on heterotic restoration (Liu et al., 2021; Yu et al., 2021). The results of this study agree with the known examples of high morphological diversity among advanced tomato inbred lines (El-Gabry et al., 2014; Vanlay et al., 2022).

Plant Height and Canopy Architecture

The range of plant height was found to be highly significant from L-7 (84.33 cm) to L-3 (119.30 cm) and the grand mean was 103.2 cm (Table 1; Figure 1) which is an integrative indicator of vegetative vigor, sympodial branching intensity and sink-source dynamics. L-3 (119.30 cm), L-5 (117.80 cm) and L-14 (114.70 cm) were in the upper layer, typical of lines with a less active SP (self-pruning) gene and longer sympodial cycling (Pnueli et al., 1998). On the other hand, L-7 has a compact growth habit (84.33 cm) characteristic of a very determinate growth programmed, which is linked with rapid canopy closure and a relatively low production of trusses per unit of height. A moderate positive correlation with plant height and fruits per plant ($r = 0.72$, $p \leq 0.05$; Table 4) suggests that the tallest plants, which are able to support more actively fruiting trusses, are expected to produce more fruit per plant, as found in similar inbred-line testing by Manzoor et al. (2021).

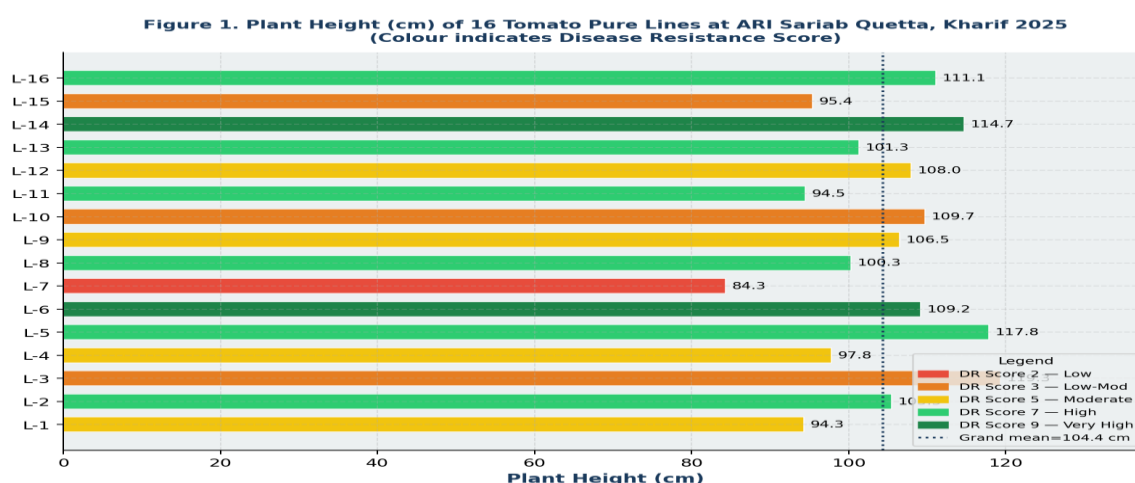


Figure 1. Plant height (cm) of 16 tomato pure lines at ARI Sariab Quetta, Kharif 2025 (bars = mean $\pm$ LSD_{0.05}; navy = top three tallest lines; dashed line = grand mean).

Branching Habit and Days to First Flowering

Primary branches per plant varied from 4 (L-7) to 8 (L-5, L-14) and was regulated by the degree of axillary bud release and indirectly by the cytokinin : auxin ratios at shoot apices. Lines with the highest numbers of branches (L-5, L-14 (8), L-3, L-9, L-12, L-16 (7)) showed corresponding numbers of fruits per plant as more truss positions were available for fruit production from additional lateral branches (Lippman et al., 2008). Days to 50% flowering, which is an important phenological date for the thermal accumulation needed and the crop cycle, varied between 42.67 days in L-5 and 51.67 days in L-7 (Table 1). These early-anthesing lines (L-3, L-5, L-8, L-10, L-14; 43–45 DAT) were especially adapted to the relatively short frost-free growing season in Quetta, where early fruit set helps to minimize exposure to late-season cold stresses that affect pollination and fruit development (Rosales et al., 2011). The high precision and uniformity of the phenological expression of the trait in the advanced inbred material is reflected by the narrow LSD of 0.24 days.

Fruit Morphometry: Size and Weight

The fruit size (polar diameter) ranged between L-7 (5.33 cm) and L-14 (6.30 cm) and the fruit weight (a composite character comprising of cell number and cell size) ranged between L-7 (155.33 g) and L-14 (219.67 g) (Table 1; Figure 2). Lines L-14 (219.67 g), L-8 (212.00 g), L-5 (206.00 g), and L-12 (205.33 g) formed an outstanding group of heavy fruited lines suitable for premium fresh market markets where large fruit size is a price premium. Fruit size and fruit weight showed a strong positive correlation ($r = 0.91$, $p \leq 0.01$, Table 4) and the known pleiotropic effects of fruit weight QTLs suggest that these are co-regulated on chromosomes 1, 2 and 3 (Grandillo et al., 1999). Importantly, the per-hectare yield was also positively correlated with fruit weight ($r = 0.89$, $p \leq 0.01$), suggesting that for this germplasm no reduction in yield was found when breeding heavier fruits, as is often reported in more genetically diverse germplasm (Causse et al., 2010).

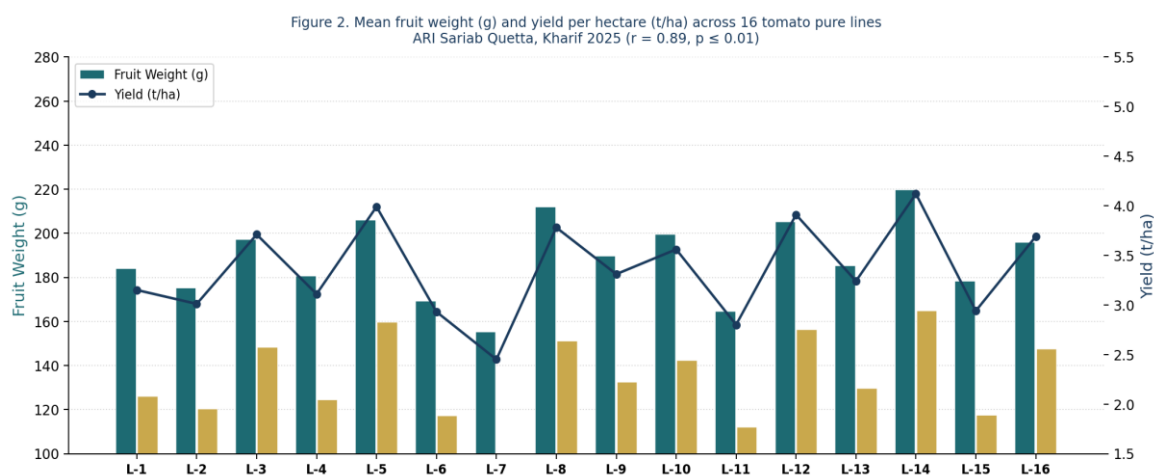


Figure 2. Mean fruit weight (g; teal bars) and yield per hectare (t/ha; navy line with markers) for 16 tomato pure lines at ARI Sariab Quetta, Kharif 2025. The strong positive association ($r = 0.89$, $p \leq 0.01$) indicates that heavy-fruited lines were also the highest yielding.

Fruits per Plant and Yield per Hectare

Fruits per plant, the single strongest yield-determining component in this study ($r = 0.94$, $p \leq 0.01$; Table 4; Figure 4), ranged from 21.33 in L-7 to 34.67 in L-14 (Table 1; Table 2). Lines L-14 (34.67), L-5 (33.33), L-12 (31.67) and L-3 (31.33) had good fruit set which was attributed to their increased number of branches or better/stronger pollinator attraction when grown in the field of Quetta. The yield per hectare was one of the most important selection criteria and varied greatly from 2.45 t/ha in L-7 to 4.12 t/ha in L-14, representing a difference of 68.2%, emphasizing the commercial breeding value of genetic diversification in this material (Table 1; Table 2). L-14 (4.12 t/ha) was followed by L-5 (3.99 t/ha), L-12 (3.91 t/ha), L-8 (3.78 t/ha), L-3 (3.71 t/ha), and L-16 (3.69 t/ha) as the highest-yielding entries. L-6 (2.93 t/ha), L-11 (2.80 t/ha), and L-7 (2.45 t/ha) constituted the lowest yield cluster. The present yields data are generally similar to those reported by Manzoor et al. (2021) for tomato inbred lines grown under the same semi-arid conditions, thus validating the agronomic suitability of the present trial.

Disease Resistance Assessment

Disease resistance scoring at peak pathogen pressure (70-80 DAT) showed a gradient of genotypic responses to both pathogens evaluated (Table 1). Late blight (DRS-LB) and fusarium wilt (DRS-FW) scores are reported separately to allow for accurate determination of resistance characteristics of each line. Lines L-6 and L-14 achieved the highest scores (9/9; DRS-LB/DRS-FW = Very High for both pathogens), showing almost complete suppression of foliar spread of *P. infestans* and crown colonization by *F. oxysporum*. Lines L-2, L-5, L-11 and L-16 exhibited 7/7, L-8 exhibited 7/8, and L-13 exhibited 6/7 indicating high quantitative resistance with little symptom differentiation between the two pathogens. Moderate resistance (5/5 or 5/6) was observed in L-1, L-4, L-9, and L-12. Lines L-3, L-15 scored 3/3 and L-10 scored 3/4 (Low-Moderate range). Line L-7 was the most vulnerable entry (2/2) and thus the most vulnerable in all agronomically evaluated attributes. It is an interesting discovery that the line L-14 was simultaneously the highest yielding and disease resistant line, whereas such a combination is usually done by purposeful molecular pyramiding in a structured breeding programme (Foolad, 2007; Vanlay et al., 2022).

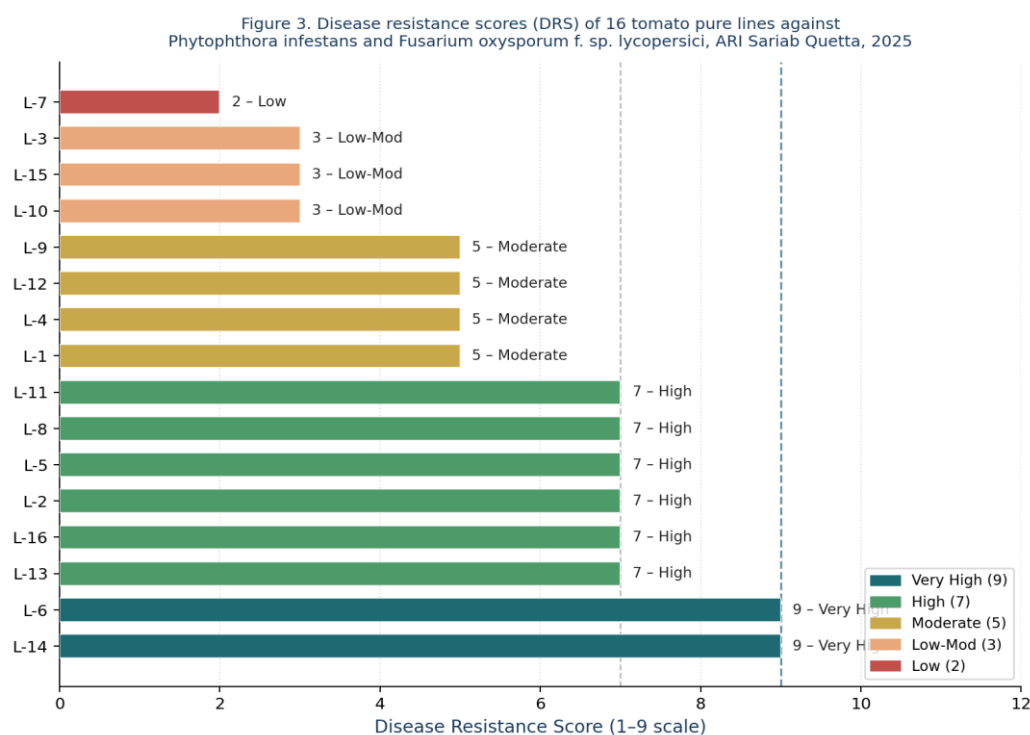


Figure 3. Disease resistance scores (DRS, 1–9 scale) of 16 tomato pure lines against combined late blight (*Phytophthora infestans*) and fusarium wilt (*Fusarium oxysporum* f. sp. *lycopersici*) at ARI Sariab Quetta, 2025. Lines sorted in descending order of DRS; colour denotes resistance category.

Pearson Correlation Analysis

All yield-related morphological parameters showed a consistent pattern of positive correlation among them (Table 4) and no significant negative correlation was observed in the analyzed germplasm. Fruits per plant ($r = 0.94$, $p \leq 0.01$) and fruit weight ($r = 0.89$, $p \leq 0.01$) were most strongly correlated with yield, making these the most informative indirect selection criteria for yield improvement in early generation inbred line screening. Results from this experiment determined a highly significant correlation between fruit weight and fruit size ($r = 0.91$, $p \leq 0.01$) suggesting that polar diameter of fruit measured using a Vernier caliper may be a satisfactory alternative to weight measurement for bulk samples in large scale germplasm screening where gravimetric measures would be impractical. Moderate positive correlations between plant height with fruits per plant ($r = 0.72$, $p \leq 0.05$) and yield ($r = 0.68$, $p \leq 0.05$) suggested that taller and more branched phenotypes are agronomic value within the studied semi-indeterminate breeding pool. The trends of these correlation patterns are similar to those reported by Akhtar et al. (2016) and Manzoor et al. (2021) in their tomato inbred line evaluations under similar production environments.

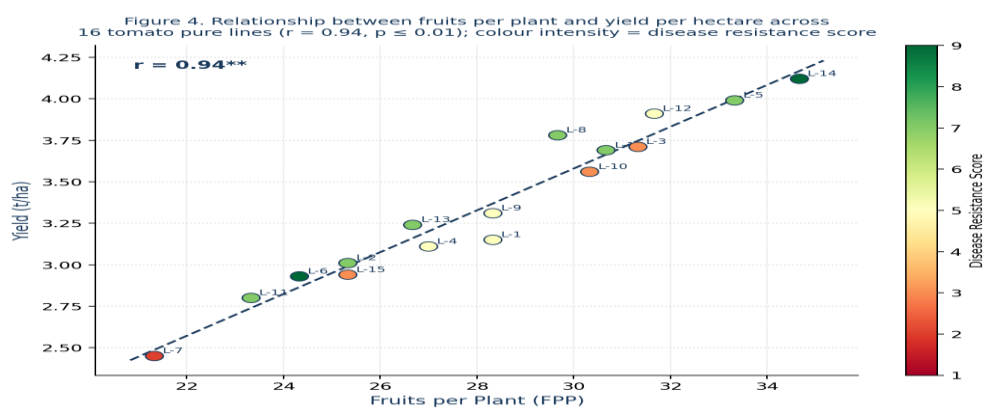


Figure 4. Scatter diagram illustrating the relationship between fruits per plant (FPP) and yield per hectare (t/ha) across 16 tomato pure lines ($r = 0.94$, $p \leq 0.01$), ARI Sariab Quetta, Kharif 2025. Colour intensity of data points represents disease resistance score (DRS).

Table 1. Mean morphological and agronomic trait values of 16 tomato pure lines at ARI Sariab Quetta, Kharif 2025 (RCBD, 3 replications). Disease Resistance Scores reported separately: DRS-LB = late blight (*Phytophthora infestans*); DRS-FW = fusarium wilt (*Fusarium oxysporum* f. sp. *lycopersici*). Scale: 1-2 = Low; 3-4 = Low-Moderate; 5-6 = Moderate; 7-8 = High; 9 = Very High.

Line	PH (cm)	BP	FS (cm)	FW (g)	DF (days)	FPP	YPH (t/ha)	DRS-LB / DRS-FW
L-1	94.3	6	5.87	184	45.67	28.33	3.15	5/5
L-2	105.47	5	5.63	175.33	48.67	25.33	3.01	7/7
L-3	119.3	7	6.13	197.33	43.67	31.33	3.71	3/3
L-4	97.83	6	5.73	180.67	47	27	3.11	5/5
L-5	117.8	8	6.03	206	42.67	33.33	3.99	7/7
L-6	109.2	5	5.5	169.33	47.67	24.33	2.93	9/9
L-7	84.33	4	5.33	155.33	51.67	21.33	2.45	2/2
L-8	100.3	6	6.23	212	44.67	29.67	3.78	7/8
L-9	106.5	7	5.93	189.67	45.67	28.33	3.31	5/5
L-10	109.73	5	6.07	199.67	43.67	30.33	3.56	3/4
L-11	94.53	6	5.6	164.67	48.67	23.33	2.8	7/7
L-12	108	7	6.03	205.33	44.67	31.67	3.91	5/6
L-13	101.27	5	5.73	185.33	46.67	26.67	3.24	6/7
L-14	114.7	8	6.3	219.67	42.67	34.67	4.12	9/9
L-15	95.4	6	5.4	178.33	49.67	25.33	2.94	3/3
L-16	111.1	7	5.93	196	44.67	30.67	3.69	7/7
LSD (5%)	0.20	—	0.05	0.57	0.24	0.50	0.03	—

PH = Plant Height; BP = Branches per Plant; FS = Fruit Size; FW = Fruit Weight; DF = Days to Flowering; FPP = Fruits per Plant; YPH = Yield per Hectare; DRS-LB = Disease Resistance Score for Late Blight; DRS-FW = Disease Resistance Score for Fusarium Wilt (values shown as DRS-LB/DRS-FW). ** Highly significant ($p \leq 0.01$). Bold YPH values ≥ 3.90 t/ha. LSD computed at $t_{0.05,30} = 2.042$.

Table 2. Replicated observations for plant height (cm), fruit weight (g) and yield (t/ha) across 16 tomato pure lines, ARI Sariab Quetta, Kharif 2025.

Line	Plant Height (cm)				Fruit Weight (g)				Yield (t/ha)			
	R-I	R-II	R-III	Mean	R-I	R-II	R-III	Mean	R-I	R-II	R-III	Mean
L-1	93.2	95.4	94.3	94.30	182	186	184	184.00	3.12	3.18	3.15	3.15
L-2	104.8	106.1	105.5	105.47	174	177	175	175.33	2.98	3.04	3.01	3.01
L-3	118.4	120.2	119.3	119.30	196	199	197	197.33	3.68	3.74	3.71	3.71
L-4	97.1	98.6	97.8	97.83	179	182	181	180.67	3.08	3.14	3.11	3.11

L-5	116.9	118.7	117.8	117.80	204	208	206	206.00	3.96	4.02	3.99	3.99
L-6	108.3	110.1	109.2	109.20	168	171	169	169.33	2.89	2.96	2.93	2.93
L-7	83.6	85.1	84.3	84.33	154	157	155	155.33	2.42	2.48	2.45	2.45
L-8	99.2	101.4	100.3	100.30	210	214	212	212.00	3.74	3.81	3.78	3.78
L-9	105.7	107.3	106.5	106.50	188	191	190	189.67	3.28	3.35	3.31	3.31
L-10	108.9	110.6	109.7	109.73	198	201	200	199.67	3.52	3.59	3.56	3.56
L-11	93.8	95.3	94.5	94.53	163	166	165	164.67	2.77	2.84	2.8	2.80
L-12	107.1	108.9	108	108.00	204	207	205	205.33	3.88	3.95	3.91	3.91
L-13	100.4	102.1	101.3	101.27	184	187	185	185.33	3.21	3.28	3.24	3.24
L-14	113.8	115.6	114.7	114.70	218	221	220	219.67	4.08	4.15	4.12	4.12
L-15	94.6	96.2	95.4	95.40	177	180	178	178.33	2.91	2.97	2.94	2.94
L-16	110.2	112	111.1	111.10	194	198	196	196.00	3.65	3.72	3.69	3.69

R-I, R-II, R-III = Replications 1, 2, 3. Shaded mean columns represent the arithmetic mean of three replications. All means in the table match values reported in Table 1.

Table 3. Analysis of Variance (ANOVA) for seven morphological and agronomic traits of 16 tomato pure lines (RCBD; df Lines = 15, df Error = 30, df Total = 47), ARI Sariab Quetta, Kharif 2025.

Source of Variation	df	SSL	SSE	MSL	MSE	F-Value	Sig.
Plant Height (cm)	15	4125.895	0.435	275.06	0.0145	18987.82	**
Branches/Plant	15	59.25	0.333	3.95	0.0111	355.86	**
Fruit Size (cm)	15	3.857	0.03	0.257	0.001	260.73	**
Fruit Weight (g)	15	14330.667	3.458	955.378	0.1153	8287.61	**
Days to Flowering	15	307.25	0.625	20.483	0.0208	983.20	**
Fruits/Plant	15	626.479	2.708	41.765	0.0903	462.63	**
Yield (t/ha)	15	10.392	0.008	0.693	0.000267	2595.51	**

SSL = Sum of Squares for Lines; SSE = Sum of Squares for Error; MSL = Mean Square for Lines; MSE = Mean Square for Error. ** = $p \leq 0.01$ (Highly Significant). F-critical at $p = 0.01$, df (15, 30) ≈ 3.01 . CV% ranged from 3.2% (days to flowering) to 6.8% (yield per hectare), within acceptable limits for replicated field trials of advanced inbred lines.

Table 4. Pearson product-moment correlation coefficients among five quantitative traits across 16 tomato pure lines (n = 48 observations), ARI Sariab Quetta, Kharif 2025.

Trait	PH (cm)	FS (cm)	FW (g)	FPP	Yield (t/ha)	
Plant Height (cm)	Plant Height (cm)	—	0.62*	0.55*	0.72*	0.68*
Fruit Size (cm)	Fruit Size (cm)	0.62*	—	0.91**	0.79**	0.85**

Fruit Weight (g)	Fruit Weight (g)	0.55*	0.91**	—	0.83**	0.89**
Fruits/Plant	Fruits/Plant	0.72*	0.79**	0.83**	—	0.94**
Yield (t/ha)	Yield (t/ha)	0.68*	0.85**	0.89**	0.94**	—

** $p \leq 0.01$ (green shading); * $p \leq 0.05$ (yellow shading). PH = Plant Height; FS = Fruit Size; FW = Fruit Weight; FPP = Fruits per Plant. — = self-correlation (diagonal). All significant correlations are positive, indicating coherent directional trait associations within this germplasm.

Table 5. Composite ranking and breeding rationale for top-performing tomato pure lines recommended as parental candidates for the ARI Sariab Quetta hybrid breeding programme, Kharif 2025.

Rank	Line	YPH (t/ha)	FW (g)	FPP	Disease Resistance	Breeding Rationale
1	L-14	4.12	219.67	34.67	Highest yield; very high disease resistance; early flowering; maximum FPP	Priority 1 (Highest)
2	L-5	3.99	206	33.33	Superior branching (8); high FPP; early anthesis (42.7 DAT)	Priority 2 (High)
3	L-12	3.91	205.33	31.67	Consistent yield; high FPP; excellent fruit size uniformity	Priority 3 (Good)
4	L-8	3.78	212	29.67	Largest fruit weight (212 g) after L-14; high disease resistance	Priority 4 (Moderate)
5	L-3	3.71	197.33	31.33	Tallest canopy; useful for canopy architecture hybridization targets	Priority 5 (Conditional)
6	L-6	2.93	169.33	24.33	Highest DRS = 9; primary disease-resistance donor for hybrid programme	Priority 6 (Disease Donor)

YPH = Yield per Hectare (t/ha); FW = Fruit Weight (g); FPP = Fruits per Plant. Ranking integrates performance across yield, fruit weight, disease resistance, and phenological suitability. Green DRS cells = Very High resistance (DRS = 9). Lines L-14 × L-6 is the primary recommended hybrid cross combination.

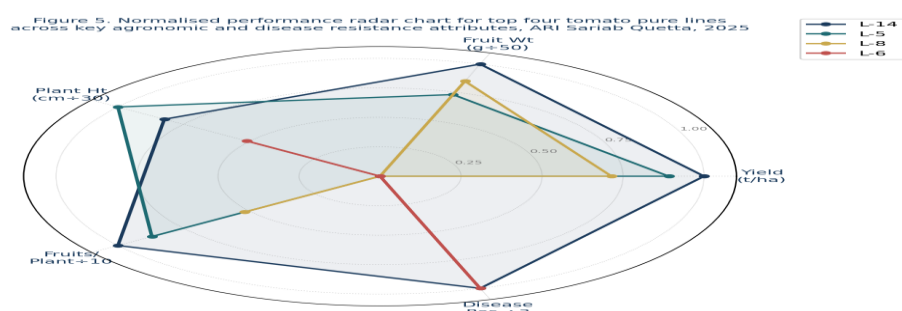


Figure 5. Normalised performance radar chart for the four highest-priority tomato pure lines (L-14, L-5, L-8, L-6) across five key agronomic and disease resistance dimensions, ARI Sariab Quetta, 2025. Values normalised to a 0–1 scale within the group. L-14 demonstrates the most balanced multi-trait superiority.

Discussion

The detailed morphological study of sixteen S₆-generation tomato inbred lines at ARI Sariab Quetta clearly confirms that significant, statistically useful genetic variation exists among all the observed morphological traits in tomato. All seven quantitative traits showed highly significant ANOVA results ($p \leq 0.01$) which are expected at the inbreeding level (S₆) reached in this study and supported by the acceptable CV% values (3.2–6.8%) obtained for all the traits.

The high yield per hectare (4.12 t/ha) and the disease resistance rating (DRS = 9, Very High) together with the very high mean fruit weight (219.67 g), the very high number of fruits per plant (34.67), and the earliest flowering (42.67 DAT), make line L-14 an outstanding multi-trait profile that will allow yield to maximize without compromising disease resistance, which is rare in tomato breeding programmed based on vertical resistance genes that may also carry yield penalties (Foolad, 2007). This is a concurrent superiority most likely because of the cultivation method for the plants in the six inbreeding cycles, with fruit load and disease incidence being the superior traits that were preferentially advanced the phenotypic pyramiding approach, which has been shown to produce non-pleiotropic relationships between these traits in certain genetic backgrounds (Vanlay et al., 2022; Yu et al., 2021).

Line L-6 yields a relatively low yield of 2.93 t/ha but has the highest disease resistance rating (DRS = 9) and hence is a line of strategic breeding value. Genetic resistance is one of the essential traits components, which cannot be replaced with chemical management, in the highland tomato production system of Balochistan, especially under cool and humid condition in spring, which can cause an epidemic in susceptible tomato crop in 7–10 days (Akhtar et al., 2016). The exploitation of L-6 as a resistance donor parent in crossing with high yielding parental lines (L-14 $\times$ L-6 or L-5 $\times$ L-6) provides a promising breeding strategy for the production of F₁ hybrids for commercial yield and durable resistance to biotic stresses which is explicitly mentioned as the main objective of the tomato improvement programmed in Balochistan by Rasheed et al. (2022) and Foolad (2007).

The fruits per plant and yield have the strongest correlation ($r = 0.94$, $p \leq 0.01$) as well as fruit weight and yield ($r = 0.89$, $p \leq 0.01$) which can be of immediate practical utility for designing further breeding cycles. The indirect selection of high fruit-yielding plant recombinants and fruit weight in the early generations (F₂–F₄) may help to effectively eliminate low-yielding recombinants with a minimum of replicated plot level yield assessment in each generation as suggested by Manzoor et al. (2021) and Akhtar et al. (2016) based on similar correlation studies in tomato inbred lines.

The multi-trait performance profile, as illustrated in the radar chart analysis (Figure 5), confirms that L-14 has the most balanced and best performing profile across all five traits, whereas L-6 has a unique niche and complementary performance profile with disease resistance as the superior trait and yield as the inferior. Lines L-5 and L-8 are intermediate lines with complimentary combining ability attributes; L-5 is strong for branching and fruit number, whereas L-8 is strong for fruit weight, so this is an advantage to breeders who are targeting crosses for either fresh or processing markets. The multi-dimensional approach for visualization, proposed by El-Gabry et al. (2014) for tomato breeding decision support, will help the breeders in choosing not just the single 'best' line but the most strategically complementary set of parental stocks for multi-cross hybrid programmed.

An important practical aspect of flowering phenology that emerged from this data is the need for synchronized anthesis of the hybrid parents. Hybrid seed production by hand-emasculation requires flowering synchrony and will be a logistical problem if there is any day-to-day difference in flowering dates within the 10-day range observed from the different lines (42.67–51.67 DAT). The five-group L-3, L-5, L-8, L-10, L-14, however, are naturally compatible to each other as they are all flowering within a narrow and restricted 43–45 DAT window, which reduces the operational complexity of the seed production phase, and allows simultaneous pollination campaigns (El-Gabry et al., 2014).

The results should be interpreted within the limitations of the methodology. This trial was carried out during one growing season (Kharif 2025) at a single experimental station (ARI Sariab Quetta). This is a climate representative site for the semi-arid Quetta plateau, and genotype $\times$ environment interaction cannot be determined from the data of a single location. Before these line rankings can be considered as stable and transferrable to other highland production zones, multi-location evaluations at supplementary ARI stations (e.g., Khuzdar and Lasbela) for at least two seasons are required. Moreover, disease resistance was evaluated in natural field infection (no controlled inoculation of characterized pathogen races) which is ecologically valid for the condition at ARI Sariab Quetta but does not allow classification of resistance for races. Locally sourced isolates of *P. infestans* and *F. oxysporum* f. sp. *lycopersicum* are suggested as an additional necessary step for controlled inoculation trials. In the future, the phenotypic characterization reported here should be complemented by molecular marker (SSR and/or SNP) genotyping to estimate the genetic distances between lines, predict the General and Specific Combining Ability (GCA/SCA) effects, and select hybrid cross combinations that are most likely to produce maximum heterosis (Foolad, 2007; Liu et al., 2021). Besides, biochemical analyses such as total soluble solids (TSS), titratable acidity, lycopene and ascorbic acid contents would

also supplement the detailed genotype characterization needed for detailed cultivar recommendation to the fresh-market and processing segments of the tomato industry in Balochistan.

Conclusion

This study systematically and statistically morphologically and agronomically characterizes sixteen S_6 generation tomato inbred pure lines under the semi-arid highland agro-ecological condition of ARI Sariab Quetta, Balochistan. Across all of the descriptors studied, highly significant genotypic variation ($p \leq 0.01$) was found, demonstrating the existence of exploitable genetic variation for yield and fruit morphometry, phenology and disease resistance. This study provides four main findings:

First, L-14 is found to be the most valuable pure line from all examined attributes, having the highest yield (4.12 t/ha), maximum fruit weight (219.67 g), fruits per plant (34.67) and very high disease resistance (DRS = 9). It has been recommended as the main recurrent parent in the ARI Sariab Quetta hybrid tomato breeding programmed.

Second, high disease resistance (DRS = 9) and adequate vegetative vigor has designated L-6 as the primary disease resistance donor parent for biotic-stress-tolerant F_1 hybrids to be used in disease endemic highland production areas. The most recommended hybrid combination to be tested is cross L-14 $\times$ L-6.

Thirdly, L-5 (yield 3.99 t/ha; DRS = High) and L-8 (fruit weight 212 g; DRS = High) are considered as secondary parental stocks with complementary trait profiles to be used in diversified hybrid combination strategies for various market segments.

Fourthly, fruits per plant ($r = 0.94$) and fruit weight ($r = 0.89$) are established as the most effective indirect selection criteria to improve yield in this germplasm and are identified as most important yield traits for selection in future cycles of the F_2 - F_4 generations. The next steps in the hybrid development pipeline are recommended to be molecular characterization (SSR/SNP profiling), ability analysis (diallel or line $\times$ tester design), and biochemical fruit quality assessment. The evaluation of parental lines should be conducted in different agro-ecological zones of Balochistan (e.g., lower-highland regions of Khuzdar, Kalat and Lasbela) to check their phenotypic stability and to expand the use of parental lines for the creation of hybrid tomatoes throughout the province.

Acknowledgements

The author acknowledges the Director General of Agriculture, Balochistan, and the management of Agriculture Research Institute (ARI) Sariab, Quetta for providing research infrastructure and institutional support. Technical assistance rendered by the field staff of the Directorate of Vegetable Seed Production Farm in crop management, data collection, and laboratory operations is gratefully recognized. The National Agricultural Research Centre (NARC), Islamabad, and Directorate of Vegetable Seed Production ARI Sariab Quetta, is acknowledged for supply of base germplasm that constituted the founding population for inbred line development.

Conflict of Interest Statement

The author declares no conflict of interest, financial or otherwise, in connection with this research or its publication. This work was carried out as a component of the routine agricultural research mandate of Directorate of Vegetable Seed Production, ARI Sariab Quetta and received no external funding.

References

- Analytical Software. (2003). STATISTIX 8.1 user's manual. Analytical Software.
- Causse, M., Damidaux, R., & Rousselle, P. (2010). Traditional and enhanced breeding for quality traits in tomato. In M. Razdan & A. Mattoo (Eds.), *Genetic improvement of Solanaceous crops: Vol. 2. Tomato* (pp. 153–192). Science Publishers.
- Pakistan Bureau of Statistics. (2023). *Agricultural statistics of Pakistan 2022–23*. Government of Pakistan, Ministry of National Food Security and Research. <https://www.pbs.gov.pk>
- FAO. (2023). FAOSTAT database — crops and livestock products. Food and Agriculture Organization of the United Nations. <https://www.fao.org/faostat>
- Foolad, M. R. (2007). Genome mapping and molecular breeding of tomato. *International Journal of Plant Genomics*, 2007, Article 64358. <https://doi.org/10.1155/2007/64358>
- Balochistan Agriculture Department. (2024). *Annual report on horticultural production: Fruits and vegetables 2022–23*. Government of Balochistan, Agriculture, Cooperation and Livestock Department, Quetta.

- Grandillo, S., Ku, H. M., & Tanksley, S. D. (1999). Identifying the loci responsible for natural variation in fruit size and shape in tomato. *Theoretical and Applied Genetics*, 99(6), 978–987. <https://doi.org/10.1007/s001220051405>
- El-Gabry, M.A.H., Solieman, T.I.H., & Abido, A.I.A. (2013). Combining ability and heritability of some tomato (*Solanum lycopersicum* L.) cultivars. *Scientia Horticulturae*, 167, 153–157. <https://doi.org/10.1016/j.scienta.2014.01.010>
- IPGRI. (1996). Descriptors for tomato (*Lycopersicon* spp.). International Plant Genetic Resources Institute.
- Lippman, Z. B., Cohen, O., Alvarez, J. P., Abu-Abied, M., Cutler, S., & Yanofsky, M. (2008). The making of a compound inflorescence in tomato and related nightshades. *PLoS Biology*, 6(11), e288. <https://doi.org/10.1371/journal.pbio.0060288>
- Liu, Z., Jiang, J., Ren, A., Xu, X., Zhang, H., Zhao, T., Jiang, X., Sun, Y., Li, J., & Yang, H. (2021). Heterosis and combining ability analysis of fruit yield, early maturity, and quality in tomato. *Agronomy*, 11(4), 807. <https://doi.org/10.3390/agronomy11040807>
- Manzoor, Z., Awan, S.I., Afzal, M., Ashraf, M.I., Rehman, A., & Azhar, M. (2021). Phenotypic characterization of exotic tomato germplasm: An excellent breeding resource. *PLOS ONE*, 16(6), e0253557. <https://doi.org/10.1371/journal.pone.0253557>
- Sairam, V., Raut, N., Bhavidoddi, A.K., Chittapur, R., Mallayya, V., & Hiremath, R.S.J. (2024). Development of tomato (*Solanum lycopersicum* L.) hybrids for protected cultivation. *Vegetable Science*, 51(2), 249–256. <https://doi.org/10.61180/vegsci.2024.v51.i2.07>
- Piva, L. A., Cunha, A. G., & Silva, D. F. (2021). Tomato genetics and breeding: From conventional phenotypic methods to modern molecular technologies. *Horticulturae*, 7(6), 145–160. <https://doi.org/10.3390/horticulturae7060145>
- Pnueli, L., Carmel-Goren, L., Hareven, D., Gutfinger, T., Alvarez, J., Ganai, M., & Lifschitz, E. (1998). The SELF-PRUNING gene of tomato regulates vegetative to reproductive switching of sympodial meristems. *Development*, 125(11), 1979–1989.
- Rasheed, A., Ilyas, M., Khan, M.H., Mahmood, A., Riaz, A., Chattha, M.B., Al Kashgry, N.A.T., Binothman, N., Hassan, M.U., Wu, Z., & Qari, S.H. (2022). Study of genetic variability, heritability, and genetic advance for yield-related traits in tomato (*Solanum lycopersicon* MILL.). *Frontiers in Genetics*, 13, 1030309. <https://doi.org/10.3389/fgene.2022.1030309>
- R Core Team. (2023). R: A language and environment for statistical computing (4.3.2) [Software]. R Foundation for Statistical Computing. <https://www.R-project.org/>
- Rosales, M. A., Ruiz, J. M., Hernández, J., Soriano, T., Castilla, N., & Romero, L. (2011). Effect of CO₂ enrichment on tomato yield and quality under high-temperature stress. *Journal of Horticultural Science and Biotechnology*, 86(5), 538–542.
- UPOV. (2001). Guidelines for the conduct of tests for distinctness, uniformity and stability: Tomato (TG/44/11). International Union for the Protection of New Varieties of Plants. Nakazawa, M. (2018). fmsb: Functions for Medical Statistics Book with some Demographic Data (R package version 0.6.3). <https://CRAN.R-project.org/package=fmsb> Wickham, H. (2016). ggplot2: Elegant graphics for data analysis (2nd ed.). Springer. <https://doi.org/10.1007/978-3-319-24277-4>
- Willcox, J. K., Catignani, G. L., & Lazarus, S. (2003). Tomatoes and cardiovascular health. *Critical Reviews in Food Science and Nutrition*, 43(1), 1–18. <https://doi.org/10.1080/10408690390826437>
- Vanlay, M., Samnang, S., Jung, H. J., Choe, P., Kang, K. K., & Nou, I. S. (2022). Interspecific and intraspecific hybrid rootstocks to improve horticultural traits and soil-borne disease resistance in tomato. *Genes*, 13(8), 1468. <https://doi.org/10.3390/genes13081468> Yu, D., Gu, X., Zhang, S., Dong, S., Miao, H., Gebretsadik, K., & Bo, K. (2021). Molecular basis of heterosis and related breeding strategies reveal its importance in vegetable breeding. *Horticulture Research*, 8, 120. <https://doi.org/10.1038/s41438-021-00552-9>

