https://doi.org/10.17221/54/2026-CJGPB

Evaluation of *Tomato yellow leaf curl virus* (TYLCV) resistance and yield performance of different genotypes of tomato

Mollah Naimuzzaman[1], *Faizur Rahman*[2], *Md. Fayez Al-Hakim Khan*[2], *Md Mahabub Hasan*[2], *Farhana Tasmim*[2], *Real Chandra Das*[2], *Md. Rishad Khan*[2], *Md. Mahdi Hasan Munna*[3], *Md Abdul Halim*[4,7], *Kun Cho*[5,6]*, *Md. Omar Sharif*[1], *Swapan Kumar Roy*[2], *Farjana Sultana*[2], *Fahim Ahmed*[2]*

[1]*Department of Agroforestry and Environmental Science, Faculty of Agriculture, Sylhet Agricultural University, Sylhet, Bangladesh*
[2]*College of Agricultural Sciences, IUBAT – International University of Business Agriculture and Technology, Dhaka, Bangladesh*
[3]*Department of Agronomy and Haor Agriculture, Faculty of Agriculture, Sylhet Agricultural University, Sylhet, Bangladesh*
[4]*Global Center for Environmental Remediation (GCER), College of Engineering Science and Environment, The University of Newcastle, Newcastle, Australia*
[5]*Biopharmaceutical Mass Spectrometry Research Unit, Korea Basic Science Institute (KBSI), Ochang Center, Cheongju-si, Chungcheongbuk-do, Republic of Korea*
[6]*Division of Bio-Analytical Science, University of Science and Technology (UST), Daejeon, Republic of Korea*
[7]*Department of Biotechnology, Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka, Bangladesh*

**Corresponding authors: fahim.ahmed@iubat.edu; chokun@kbsi.re.kr*

Citation: Naimuzzaman M., Rahman F., Khan M.F.A.-H., Hasan M.M., Tasmim F., Das R.C., Khan M.R., Munna M.M.H., Halim M.A., Cho K., Sharif M.O., Roy S.K., Sultana F., Ahmed F. (2026): Evaluation of *Tomato yellow leaf curl virus* (TYLCV) resistance and yield performance of different genotypes of tomato. Czech J. Genet. Plant Breed., 62: 201–212.

Abstract: Since *Tomato yellow leaf curl virus* (TYLCV) causes severe losses in tomato crops worldwide the search for genetic resources for breeding high-yielding, disease-resistant varieties remains challenging. We tested 25 tomato genotypes under field conditions to identify high-yielding disease-resistant genotypes. We identified several promising genotypes using advanced statistical methods, particularly genotype G13 which had a high yield of 8.8 kg per plant with 8.7 fruits per cluster and showed a low disease severity under high natural infection pressure. The genotypes G2, G3, G10, G11 showed moderate resistance, with disease severity ranging from 12.5% to 19.4%. The highest-yielding genotypes also had higher numbers of branches and fruit clusters. The high heritability of these traits indicates their potential usefulness as selection criteria in breeding programmes. The identified genotypes might provide useful genetic resources for developing high-yielding tomato varieties suitable for cultivation in TYLCV-prone areas. This work bridges the critical gap between disease resistance and yield potential, giving farmers actionable options to protect their harvests.

Keywords: disease severity; genetic variability; heritability; principal component analysis; whitefly (*Bemisia tabaci*)

Supported by the Ministry of Trade, Industry and Energy (MOTIE) and Korea Institute for Advancement of Technology (KIAT), Project No. 2410019416 "Development of an Innovative Drug R&D Acceleration Platform".

© The authors. This work is licensed under a Creative Commons Attribution 4.0 International (CC BY 4.0).

https://doi.org/10.17221/54/2026-CJGPB

Tomato (*Solanum lycopersicum* L.) is a vital global horticultural crop, prized for nutrition and economic value. In Bangladesh, it supports food security, nutrition, and the agricultural economy, cultivated year-round nationwide (Quamruzzaman et al. 2023). Tomatoes are rich in water, niacin, calcium, and essential vitamins (A, C, E) and minerals (K, Ca, P, Fe, Zn), supporting health and disease prevention (Wang et al. 2023). They also contain lycopene, carotenoids, and polyphenols, which act as antioxidants and help lower prostate cancer risk (Abu Haraira et al. 2022). These nutrients remain after cooking, and tomato pulp and juice are digestible and purify the blood. Tomato production is hindered by various biotic and abiotic stresses, with *Tomato yellow leaf curl virus* (TYLCV) being one of the most damaging, causing significant global economic losses (Avedi 2022; Naimuzzaman et al. 2025). TYLCV is a single-stranded DNA virus belonging to the Begomovirus genus, within the Geminiviridae family (Idrees et al. 2024). This virus is transmitted persistently and circulatively by the whitefly (*Bemisia tabaci*), one of the most notorious insect pests affecting Solanaceous crops (Shah et al. 2022). The transmission process is circulative and persistent, meaning the virus circulates within the whitefly's body and can be transmitted throughout the insect's lifespan. Once a whitefly feeds on an infected plant, it acquires the virus, which then replicates within the insect's midgut and salivary glands (Czosnek et al. 2017). The virus spreads to healthy plants via whitefly feeding, injecting it into phloem tissue. This efficient transmission enables rapid spread across fields and regions, particularly where whiteflies are abundant (Mandahar 2018). TYLCV infections cause a range of severe symptoms, including leaf curling, yellowing, vein clearing, and plant stunting, which ultimately lead to substantial reductions in yield and fruit quality (Hanssen et al. 2010; Ammara et al. 2017). The virus impacts nearly all growth stages, with early infections often causing total crop failure (Jones 2020). *Bemisia tabaci*'s adaptability and insecticide resistance complicate control. Chemical overuse causes environmental pollution and health risks, harming soil, water, air, and non-target organisms like beneficial insects and aquatic life (Punniyakotti et al. 2024). The decline in populations of natural predators, such as parasitoid wasps and ladybugs, has disrupted biological control mechanisms, leading to increased pest pressure and further reliance on chemical interventions (Naimuzzaman et al. 2024). Additionally, global climate change has intensified the spread and incidence of TYLCV, as rising temperatures and erratic weather patterns favour the proliferation of whiteflies (Yan et al. 2018; Lobin et al. 2022). In Bangladesh, TYLCV outbreaks in major tomato-growing areas cause 30–100% yield loss, depending on infection level and environment (Valverde et al. 2001). TYLCV's rapid spread threatens smallholder farmers due to limited pest control and awareness. Bangladesh's diverse agro-climatic zones produce commercial varieties with distinct growth, fruit, and stress traits. These varieties reduce virus impact, chemical use, and stabilise production. Assessing these identifies trait linkages, helping breeders improve TYLCV resistance (El Sappah et al. 2022; Tiwari et al. 2022; Shahriari et al. 2023). This study aims to evaluate TYLCV resistance and yield performance in commercially available tomato genotypes in Bangladesh by examining morphological, physiological, and yield traits under natural infection. It also seeks to identify key genetic factors through character association analyses to support the development of improved, locally adapted, TYLCV-resistant tomato varieties.

MATERIAL AND METHODS

Plant material and experimental design

The experiment was conducted at the IUBAT Agricultural Research Station, Gazipur, Bangladesh. The site lies in the subtropical zone with a mean annual temperature of 25.4 °C and average rainfall of 1 550 mm. The soil belongs to the agro-ecological zone "Madhupur Tract" (AEZ No. 28), characterised as silty clay loam with a pH of 6.8. AEZ refers to Agro-Ecological Zone, a land classification system used in Bangladesh. To conduct this experiment, a total of 25 genotypes (Table 1) were collected from the local sources. The experiment was laid out in a randomised complete block design (RCBD) with three replications. Each block measured 0.9144 by 0.6096 meters. There were 0.6096 meters between the blocks and 0.6096 meters between the plots. Each plot contained four tomato plants per genotype. All morphological and yield traits were recorded on a per plant basis and then averaged to obtain plot means for statistical analysis.

Whitefly-mediated natural inoculation

For the whitefly-mediated natural inoculation in the open field, the experimental plots were established in an area with a known presence of *Bemisia tabaci*.

https://doi.org/10.17221/54/2026-CJGPB

Table 1. List of plant materials

Sl	Codes	Genotypes	Sl	Codes	Genotypes
1	G1	Raja Babu	14	G14	Pathar kuchi
2	G2	BARI 18	15	G15	Kollani
3	G3	Big Boy	16	G16	BINA11
4	G4	SR Red	17	G17	BARI 14
5	G5	Gaint red	18	G18	Success
6	G6	Mongol Raja	19	G19	Laltu
7	G7	Bahuboli	20	G20	BARI 17
8	G8	Red ball	21	G21	Delta
9	G9	BINA 12	22	G22	BARI 19
10	G10	Roma VF	23	G23	Tomato RAJ
11	G11	Deepali	24	G24	BARI 15
12	G12	Gulfham	25	G25	BARI 20
13	G13	Sunshine			

Virus-infected plants exhibiting typical symptoms were used as sources of inoculum. Whitefly populations were monitored regularly using yellow sticky traps to assess density. Healthy tomato plants were placed in proximity to the infected plants to facilitate natural virus transmission through whitefly feeding.

Morphological traits measurement

Morphological traits of tomato genotypes were assessed for growth, yield, and *Tomato yellow leaf curl virus* (TYLCV) resistance in experimental plots, with each plot containing four plants per variety in every replicate. The same plants were evaluated for both virus tolerance and yield parameters. Traits measured included plant height (PH), leaf number (LN), leaf diameter (LD), branch number (BN), branch length (BL), number of clusters (NC), fruits per cluster (FPC), total yield (TY), and TYLCV severity. PH and LN were recorded at 20 days. LD was measured using a digital calliper to estimate leaf expansion. BN and BL were recorded to assess the canopy and fruit potential. NC and FPC served as key yield indicators, while TY was measured as the total fruit weight per plant. TYLCV severity was scored based on symptoms (leaf curl, yellowing, stunting), and the infection percentage was calculated.

Observations and measurements

Disease severity. Symptom development will be evaluated according to the symptom severity scale and using the Equation (1) (Lapidot & Friedmann 2002) and the pictorial scale (Figure 1).

Disease incidence. Disease incidence, which measures the proportion of a disease within a given field, will be estimated using the Equation (2) (Strange & Scott 2005).

TYLCV was identified visually by characteristic symptoms and was scored using a standard disease rating scale, following the disease rating scale given by Ali et al. (2005) (Table 2).

$$\%\ \text{Disease severity} = \frac{\text{Sum of total disease rating}}{\text{Total No. of observation} \times \text{Maximum grade in the scale}} \times 100 \quad (1)$$

$$\text{Disease incidence}(\%) = \frac{\text{Number of diseased plant}}{\text{Number of total plants observed}} \times 100 \quad (2)$$

Figure 1. *Tomato yellow leaf curl virus* (TYLCV) severity is scored 0–4 scale, as outlined by Muniyappa et al. (1991)
0 – symptomless; 1 – resistant; 2 – tolerant; 3 – susceptible; 4 – highly susceptible; images are not to scale and are presented for qualitative comparison of TYLCV symptoms

https://doi.org/10.17221/54/2026-CJGPB

Analysis of data

Statistical analysis was performed using R Studio (R Core Team 2021) and Statistix 10 (Analytical Software, Tallahassee, FL, USA).To avoid pseudo-replication, the data from individual plants were averaged to calculate plot means (n = 75). Analysis of variance (ANOVA) was employed using a linear model:

$$Yij = \mu + Gi + Bj + \varepsilon ij \quad (3)$$

where:
Yij – the plot mean;
M – the grand mean;
Gi – the fixed effect of genotype (i = 1…25);
Bj – the fixed effect of block/replication (j = 1,2,3);
Eij – the residual error.

Model assumptions (normality and homogeneity of variances) were assessed using Shapiro-Wilk and Levene's tests on the ANOVA residuals, supplemented by QQ plots. The corresponding assumption-test results are provided in Table S1 in ESM, and representative residual diagnostic plots for plant height (PH) are shown in Figure S1 in ESM. For TY, homogeneity of variances was violated (Levene's P = 0.03); therefore, a non-parametric Kruskal-Wallis test was applied for this specific trait, followed by Dunn's post-hoc test. Tukey's HSD was used for all other traits. Genetic parameters, including heritability (h^2), genetic variance (σ^2_G) was estimated as:

$$\frac{MSg - MSe}{r} \quad (4)$$

where:
MSg – the genotype mean square;
MSe – the error mean square;
r – the number of replications (Allard 1999), and phenotypic variance (σ^2_P), were estimated from plot means.

Table 2. Disease incidence rating scale of *Tomato yellow leaf curl virus* (TYLCV)

Scale	Rating	Incidence range (%)
0	immune	0
1	highly resistant	1–10
2	moderately resistant	11–25
3	tolerant	26–50
4	moderately susceptible	51–60
5	susceptible	61–70
6	highly susceptible	71–100

Genetic advance (GA) and genetic advance as a percentage of mean (GAM) were estimated using standard formulas (Johnson et al. 1955). Phenotypic correlation coefficients were calculated using genotype means. Principal component analysis (PCA) and K-means clustering were used to identify patterns of trait variation. Path analysis was conducted to partition the phenotypic correlations into direct and indirect effects on yield.

RESULTS

Disease severity. Disease severity was assessed to classify resistance levels of tomato genotypes to TYLCV (Figures 2, 3). Severity was rated on a 0–6 scale, where 0 indicates no symptoms and 6 indicates severe symptoms. Genotype G9 exhibited the highest severity (rating 6, highly susceptible), followed by G22 (rating 6), G15 (rating 5), and G14 (rating 5). Genotypes G7 (rating 4) and G23 (rating 3) were highly and moderately susceptible, respectively. Genotypes G1 (rating 2), G8 (rating 2), G16 (rating 2), and G19 (rating 2) showed moderate susceptibility (tolerant to moderately susceptible). In contrast, genotypes G2 (rating 1), G3 (rating 1), G10 (rating 1), and G11 (rating 1) were moderately resistant. Genotypes G6 (rating 1), G12 (rating 1), G13 (rating 1), and G17 (rating 1) also exhibited moderate resistance, highlighting significant variability in TYLCV resistance.

Genotypic variation. Genetic parameters for 25 tomato genotypes and 12 number of plants per genotypes used to calculate for each genotype are shown in Table 3. PH ranged 40–120 cm (mean 68.98), with σ^2_G = 163.85, σ^2_E = 126.29, h^2= 0.56, GA = 19.81 cm (GAM 28.72%). LN ranged 5–57 (mean 19.44), with σ^2G = 68.48, h^2 = 0.66, GA = 13.85 (GAM 71.29%). LD ranged 87.12–868 cm^2 (mean 272.91), with σ^2_G = 10 136.85, h^2 = 0.42. BN ranged 1–6 (mean 2.29), BL ranged 10–42.8 cm (mean 26.21). NC ranged 1–16 (mean 6, h^2 = 0.78). FPC ranged 1–12 (mean 4.33, h^2 = 0.70). TY ranged 30–9779.8 g (mean 1 224.49), with h^2 = 0.88 and GA = 3 661.23 g (GAM 299%), suggesting high genetic improvement potential, especially for TY, NC, and FPC.

Mean performance for the measured traits. The 25 tomato genotypes showed significant trait variation (Table 4, Figure 4). PH ranged from 49.87 cm (G9) to 115 cm (G19). LN varied from 8.67 (G3) to 51.33 (G19). LD was highest in G7 (572.82 cm^2) and lowest in G8 (123.37 cm^2). BN ranged from 1 (G2, G3, G5)

https://doi.org/10.17221/54/2026-CJGPB

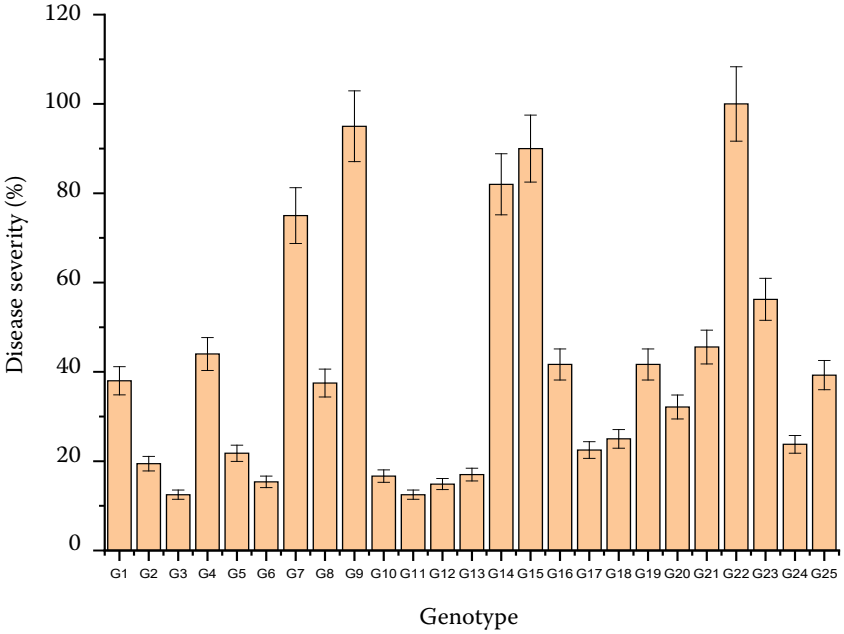

Figure 2. Disease severity distribution across genotypes
Bars represent mean disease severity (%) ± SE

to 5.67 (G13). BL was longest in G6 (37.6 cm) and shortest in G22 (12.1 cm). NC ranged from 1.66 (G8) to 15.33 (G21). FPC were highest in G1 (10) and G13 (8.67), and lowest in G14 (1.67). TY ranged from 53.3 g (G5) to 8839.1 g (G13). G13 excelled in TY, BN, and FPC, while G5, G3, and G14 showed poor yield, indicating genetic variability for breeding. The ANOVA analysis included degrees of freedom (*df*) with df for genotypes at 24 and df for error at 74. Homogeneity of variances was met for all traits except TY (Levene's $P = 0.03$); however, with equal group sizes ($n = 3$ per genotype), the F-test remains reliable.

Figure 3. Highly susceptible tomato genotypes to *Tomato yellow leaf curl virus* (TYLCV); images show genotypes G22 (A), G15 (B), G14 (C), and G9 (D) at 45 days after whiteflymediated inoculation
Images are not to scale and are presented for qualitative comparison of TYLCV symptoms

https://doi.org/10.17221/54/2026-CJGPB

Table 3. Genetic parameters for traits evaluated across 25 tomato genotypes.

Traits	N	Max	Min	GM	SEM	CD_5%	CD_1%	σ^2_E	σ^2_G	σ^2_P	ECV	GCV	PCV	h^2	GA	GAM
PH (cm)	75	120	40	68.98	6.48	18.44	24.61	126.29	163.85	290.14	16.29	18.55	24.69	0.56	19.81	28.72
LN (No.)	75	57	5	19.44	3.42	9.73	12.98	35.14	68.48	103.62	30.49	42.57	52.36	0.66	13.85	71.29
LD (cm^2)	75	868	87.12	272.91	66.98	190.47	254.09	13 461.38	10 136.85	13 598.23	42.51	36.89	56.28	0.42	135.93	49.8
BN (No.)	75	6	1	2.29	0.5	1.42	1.89	0.75	0.91	1.67	37.77	41.81	56.34	0.55	1.46	63.9
BL (cm)	75	42.8	10	26.21	3.45	9.82	13.1	35.81	38.47	74.29	22.82	23.66	32.87	0.51	9.19	35.07
NC (No.)	75	16	1	6	0.91	2.59	3.46	2.5	9.39	11.9	25.86	50.36	56.36	0.78	5.61	91.66
FPC (No.)	75	12	1	4.33	0.67	1.93	2.57	1.38	3.25	4.63	27.13	41.61	49.67	0.7	3.11	71.81
TY (g)	75	9 779.8	30	1 224.49	388.02	1 103.33	1 471.86	451 691.25	3 559 612.38	4 011 303.64	54.88	154.07	163.56	0.88	3 661.23	299

N = 75 plot means; GM – grand mean; SEM – standard error; CD – critical difference; σ^2_E – environmental variance; σ^2_G – genotypic variance; σ^2_P = phenotypic variance; ECV – environmental coefficient of variance; GCV – genotypic coefficient of variance; PCV – phenotypic coefficient of variance; h^2= heritability (broad sense); GA – genetic advance; GAM – genetic advance (% of mean); PH – plant height; LN – leaf number; LD – leaf diameter; BN – branch number; BL – branch length; NC – number of clusters; FPC – fruit per cluster; TY – total yield

Phenotypic correlation analysis among different yield-associated characters. Correlation analysis of 25 tomato genotypes showed key traityield relationships (Table 5). PH strongly correlated with LN (r = 0.86, P < 0.01), BN (r = 0.54, P < 0.01), BL (r = 0.64, P < 0.01), and clusters (NC) (r = 0.53, P < 0.01), but weakly with TY (r = –0.07, P > 0.05). LN correlated with BN (r = 0.45,

Figure 4. *Tomato yellow leaf curl virus* (TYLCV) resistance of resistant genotypes G13 (A) and G12 (B), and highly susceptible genotypes G9 (C) and G22 (D)
Images are not to scale and are presented for qualitative comparison of TYLCV symptoms

https://doi.org/10.17221/54/2026-CJGPB

$P < 0.05$) and BL ($r = 0.41$, $P < 0.05$), but not with TY ($r = -0.17$, $P > 0.05$). BN was strongly correlated with TY ($r = 0.67$, $P < 0.01$), NC ($r = 0.52$, $P < 0.01$), and FPC ($r = 0.53$, $P < 0.01$). NC was linked with FPC ($r = 0.64$, $P < 0.01$) and TY ($r = 0.34$). FPC correlated with TY ($r = 0.48$, $P < 0.05$). LD and BL were weakly correlated with TY ($r = 0.36$ and -0.21, respectively, $P > 0.05$).

Phenotypic path analysis of yield-associated traits in tomato. Path analysis of 25 tomato genotypes revealed trait effects on TY (Figure 5). BN had the strongest positive direct effect (1.24) and indirect effects via PH, LN, NC, and FPC. NC showed a moderate direct effect (0.39) and indirect effects through BN (0.66) and FPC (0.25). BL had a weak direct effect (0.45). FPC had a negative direct effect (–0.35) but positive indirect effects via BN (0.67) and NC (0.25). PH (–0.98) and LN (–0.20) had strong negative direct effects but indirect contributions via BN, NC, and FPC. LD had minimal impact (0.04). BN, NC, and FPC are key yield drivers, while high PH and LN may lower yield.

Characterisation of individual clusters. *K*-means clustering grouped 25 tomato genotypes into three clusters based on yield traits (Figure 6). Cluster 1 (G11, G14, G15) showed low values for plant height (PH: 64.3 cm), clusters (NC: 4.67), and total yield (TY: 674 g), indicating limited yield potential. Cluster 2 (G10, G19, G6, G21) had taller plants

Table 4. Post-hoc test (Tukey's HSD) results for pairwise comparisons of 25 tomato genotypes

Genotypes	PH (cm)	LN (No.)	LD (cm^2)	BN (No.)	BL (cm)	NC (No.)	FPC (No.)	TY (g)
G1	67.83^{c-i}	16.33^{d-h}	261.13^{c-f}	2.33^{c-f}	27.20^{b-i}	13.67^{a}	10^{a}	1 978.7^{a-d}
G2	77.50^{b-e}	19.00^{d-g}	483.96^{ab}	1.00^{f}	35.97^{abc}	5.00^{cde}	3.33^{e-i}	340.7^{f-k}
G3	51.00^{hi}	8.67^{h}	144.73^{ef}	1.00^{f}	26.60^{c-i}	3.33^{def}	3.33^{e-i}	80.0^{jk}
G4	86.13^{bc}	19.67^{d-g}	185.31^{def}	1.67^{def}	33.83^{a-e}	4.33^{de}	5.00^{b-e}	144.6^{ijk}
G5	74.67^{c-f}	16.33^{d-h}	131.14^{f}	1.00^{f}	30.30^{a-g}	4.66^{cde}	4.33^{b-f}	53.3^{k}
G6	79.57^{bcd}	20.67^{d-g}	255.95^{c-f}	3.33^{bc}	37.60^{a}	9.33^{b}	5.00^{b-e}	2 733.9^{abc}
G7	62.00^{d-i}	17.33^{d-h}	572.82^{a}	2.00^{c-f}	16.03^{jkl}	5.00^{cde}	3.33^{e-i}	406.6^{c-j}
G8	65.77^{d-i}	14.67^{d-h}	123.37^{f}	2.00^{c-f}	31.80^{a-f}	1.66^{f}	5.33^{bcd}	140.5^{ijk}
G9	49.87^{i}	9.00^{h}	232.91^{def}	1.67^{def}	18.00^{i-l}	3.66^{def}	2.00^{hi}	217.4^{hijk}
G10	68.47^{c-h}	34.00^{b}	224.93^{def}	3.33^{bc}	36.70^{ab}	4.00^{def}	5.00^{b-e}	144.3^{ijk}
G11	59.33^{e-i}	18.00^{d-h}	482.80^{ab}	1.67^{def}	26.43^{c-i}	5.00^{cde}	5.00^{b-e}	1 700.0^{a-f}
G12	71.63^{c-g}	23.33^{cde}	313.11^{b-f}	3.33^{bc}	25.57^{d-j}	8.33^{b}	5.00^{b-e}	4 259.7^{ab}
G13	69.10^{c-h}	11.67^{gh}	375.77^{bcd}	5.67^{a}	21.00^{g-l}	9.33^{b}	8.67^{a}	8 839.1^{a}
G14	68.00^{c-i}	23.67^{cd}	307.78^{b-f}	1.66^{def}	22.63^{f-k}	5.66^{cd}	1.67^{i}	2 286.0^{a-f}
G15	60.17^{e-i}	13.67^{e-h}	151.07^{ef}	2.00^{c-f}	22.20^{f-k}	2.66^{ef}	3.33^{e-i}	237.4^{f-k}
G16	73.73^{c-g}	19.00^{d-g}	304.53^{b-f}	2.66^{cde}	34.47^{a-d}	5.66^{cd}	3.67^{d-h}	113.7^{ijk}
G17	55.63^{ghi}	14.33^{d-h}	326.08^{b-e}	2.33^{c-f}	26.00^{d-i}	7.00^{bc}	4.33^{b-f}	972.0^{a-h}
G18	74.40^{c-f}	22.33^{c-f}	217.17^{def}	2.33^{c-f}	19.13^{h-l}	5.66^{cd}	5.67^{bc}	268.5^{d-k}
G19	115.00^{a}	51.33^{a}	226.49^{def}	4.33^{ab}	28.57^{a-h}	9.00^{b}	4.00^{c-g}	399.4^{b-i}
G20	65.90^{d-i}	16.33^{d-h}	154.63^{ef}	2.00^{c-f}	25.80^{d-j}	5.66^{cd}	2.00^{hi}	182.7^{g-k}
G21	95.33^{b}	32.00^{bc}	151.39^{ef}	3.00^{bcd}	35.33^{a-d}	15.33^{a}	6.00^{b}	133.6^{ijk}
G22	57.83^{f-i}	13.00^{fgh}	195.04^{def}	2.33^{c-f}	12.10^{l}	3.66^{def}	2.67^{f-i}	499.8^{e-k}
G23	57.67^{f-i}	16.67^{d-h}	443.17^{abc}	1.67^{def}	22.17^{f-k}	5.00^{cde}	2.33^{ghi}	394.9^{b-i}
G24	59.37^{e-i}	21.67^{def}	291.41^{c-f}	1.67^{def}	24.43^{e-k}	5.33^{cd}	4.00^{c-g}	2 431.0^{a-e}
G25	58.63^{f-i}	13.33^{fgh}	266.26^{c-f}	1.33^{ef}	15.53^{kl}	5.00^{cde}	3.33^{e-i}	1 654.5^{a-g}
Tukey HSD ($P \leq 0.05$)	35.20	19.03	368.18	2.87	18.61	5.16	3.67	2 144.03

PH – plant height; LN – leaf number; LD – leaf diameter; BN – branch number; BL – branch length; NC – number of clusters; FPC – fruit per cluster; TY – total yield; different letters indicate statistically significant differences ($P \leq 0.05$) according to Tukey's HSD test; genotypes sharing the same letter are not significantly different

https://doi.org/10.17221/54/2026-CJGPB

Table 5. Phenotypic correlation analysis among different yield-associated characters

Traits	PH (cm)	LN (No.)	LD (cm^2)	BN (No.)	BL (cm)	NC (No.)	FPC (No.)	TY (g)
PH (cm)	1**							
LN (No.)	0.86**	1**						
LD (cm^2)	–0.31 NS	–0.11 NS	1**					
BN (No.)	0.54**	0.45*	0.07 NS	1**				
BL (cm)	0.64**	0.41*	–0.32 NS	0.06 NS	1**			
NC (No.)	0.53**	0.35 NS	0.03 NS	0.52**	0.24 NS	1**		
FPC (No.)	0.21 NS	0.04 NS	–0.08 NS	0.53**	0.31 NS	0.64**	1**	
TY (g)	–0.07 NS	–0.17 NS	0.38 NS	0.67**	–0.21 NS	0.34 NS	0.48**	1**

PH – plant height; LN – leaf number; LD – leaf diameter; BN – branch number; BL – branch length; NC – number of clusters; FPC – fruit per cluster; TY – total yield; correlations are phenotypic correlations based on genotype means (n = 25); NS – not significant; *,**P < 0.05, 0.01

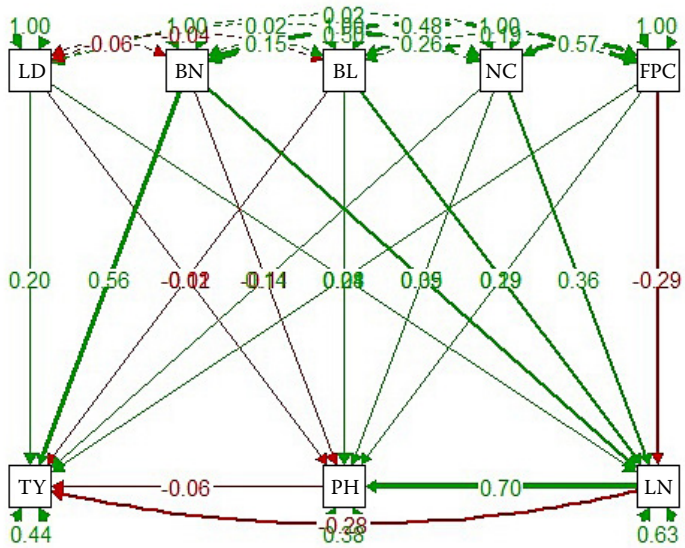

Figure 5. Phenotypic path analysis of yield-associated traits in tomato

PH – plant height; LN – leaf number; LD – leaf diameter; BN – branch number; BL – branch length; NC – number of clusters; FPC – fruit per cluster; TY – total yield

(PH: 89.6 cm), more branches (BN: 3.5), and moderate yield (TY: 853 g). Cluster 3 (G1, G12, G13) exhibited high yield (TY: 5026 g), clusters (NC: 10.4), and fruits per cluster (FPC: 7.89), marking it as the top-performing group for breeding.

Principal component analysis (PCA) for morphological traits of tomato genotypes under field conditions. PCA was conducted to evaluate relationships among eight morphological traits (PH, LN, LD, BN, BL, NC, FPC, TY) across 25 tomato genotypes under field conditions (Table 6). The first three principal components (PCs) explained 72.63% of the total variance. PC1 (39.11%) was primarily driven by the number of clusters (NC, 20.83%), branch number (BN, 18.43%), plant height (PH, 16.76%), and fruits per cluster (FPC, 15.12%), reflecting traits associated with plant architecture and fruiting potential. PC2 (20.99%) was dominated by total yield (TY, 34.34%), leaf number (LN, 17.75%), and branch length (BL, 14.67%), indicating variation in yield and vegetative growth. PC3 (12.53%) was almost entirely explained by leaf diameter (LD, 91.48%), highlighting leaf size as a distinct source of variation. The PCA biplot (Figure 7) illustrates these relationships, with NC, BN, PH, and FPC clustering along PC1, and TY, LN, and BL along PC2. Genotypes with high PC1 scores (e.g., G6, G13, G19) exhibited superior plant architecture and fruiting traits, while those with high PC2 scores (e.g., G12, G13) showed elevated yield and vegetative growth, suggesting their potential for breeding programs targeting high-yield, robust genotypes. This genetic variation, visualised in the biplot, aids

https://doi.org/10.17221/54/2026-CJGPB

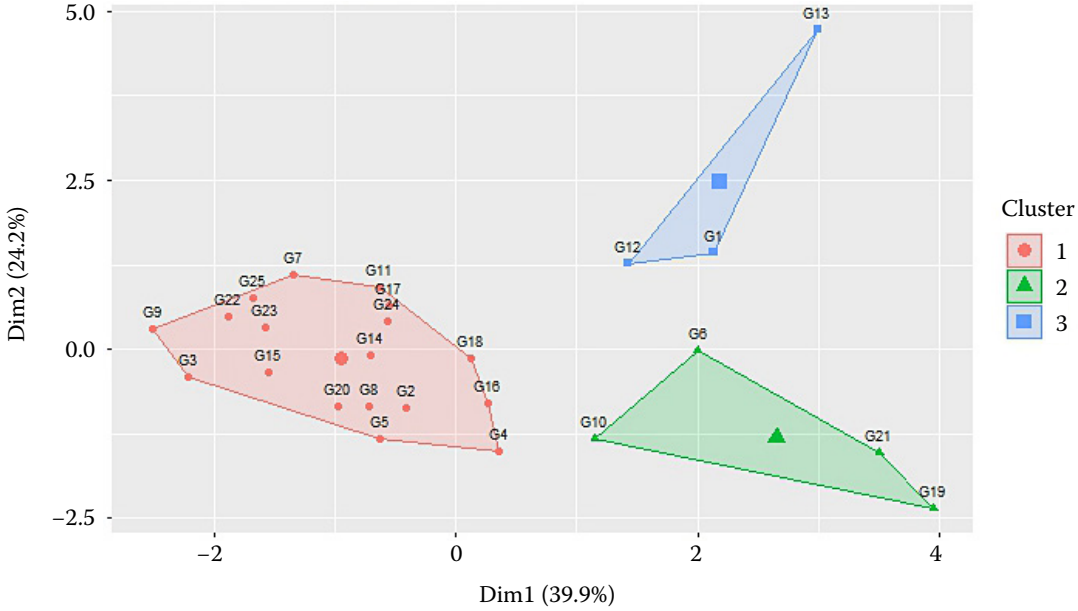

Figure 6. *K*-means clustering of 25 tomato genotypes based on phenotypic traits
Genotypes are grouped into three clusters (1, 2, 3) according to yieldrelated characteristics

in selecting genotypes for breeding to improve yield and architectural traits under field conditions.

DISCUSSION

The evaluation of 25 tomato genotypes for resistance to TYLCV and yield performance demonstrated significant genetic variability, offering valuable insights for breeding high-yielding, TYLCV-resistant cultivars. The study employed a RCBD with three replicates, assessing 300 plants (12 per genotype) under uniform field conditions with standard agronomic practices to reduce environmental influence. TYLCV severity, evaluated on a 0–4 scale, and incidence (percentage of symptomatic plants). This robust design ensured reliable estimation of genetic parameters and trait relationships, addressing the need for reproducible results in plant breeding studies. Significant variability in TYLCV resistance was observed; four genotypes (G2, G3, G10, and G11) exhibited moderate resistance (with a rating of 1), consistent with Lapidot and Friedmann (2002), who emphasised genetic resistance as a key strategy for TYLCV management. On the other hand, some tomato plants like G9, G15, and G22 were highly susceptible to TYLCV (scoring 5–6 on the severity scale). The high susceptibility of these genotypes aligns with (Pico et al. 1999), who associated TYLCV

Table 6. Principal component analysis (PCA) for morphological traits of tomato genotypes under field conditions

Characters	Eigenvalue	%Variance	PC.1	PC.2	PC.3	PC.4
PH (cm)	3.12	39.10	16.76	14.16	1.59	4.10
LN (No.)	1.60	20.99	14.95	17.75	1.61	15.98
LD (cm^2)	1.00	12.53	0.01	4.21	91.48	0.05
BN (No.)	0.76	9.59	18.43	4.68	3.34	8.40
BL (cm)	0.57	7.17	6.22	14.68	0.48	55.05
NC (No.)	0.38	4.80	20.83	0.58	0.01	0.69
FPC (No.)	0.28	3.52	15.12	9.60	1.46	15.46
TY (g)	0.18	2.27	7.68	34.34	0.03	0.27

PH – plant height; LN – leaf number; LD – leaf diameter; BN – branch number; BL – branch length; NC – number of clusters; FPC – fruit per cluster; TY – total yield

https://doi.org/10.17221/54/2026-CJGPB

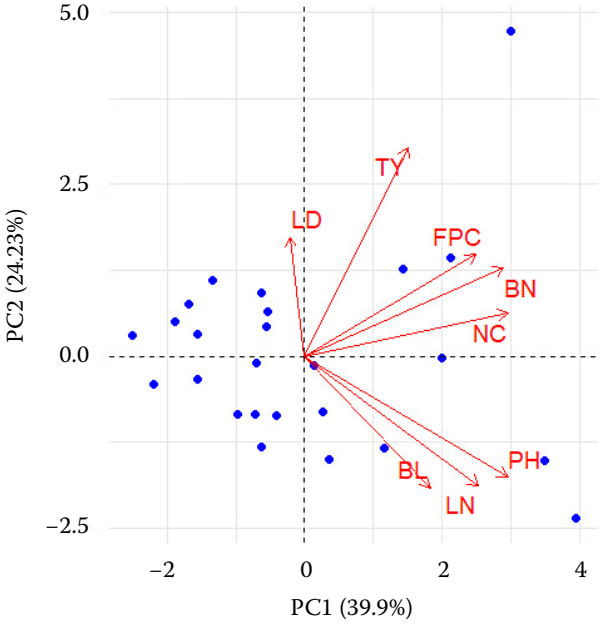

Figure 7. Biplot among the first two principal components (PC1 and PC2)

Phenotypic traits were: PH – plant height; LN – leaf number; LD – leaf diameter; BN – branch number; BL – branch length; NC – number of clusters; FPC – fruit per cluster; TY – total yield

susceptibility with specific genetic markers such as Ty-1 and Ty-3. However, it remains uncertain whether the observed tolerance in resistant genotypes (G2, G3, G10, and G11) stems from these same genes or involves novel loci. Marker-assisted selection (MAS) offers a promising approach to expedite the identification and pyramiding of resistance alleles such as those potentially present in G2 or G3 into high-yielding cultivars, enhancing overall resilience. For instance, integrating resistance genes from G2 or G3 into high-yielding backgrounds could enhance cultivar resilience. Yield performance varied widely (53.3–8 839.1 g), with genotype G13 standing out for its exceptional yield (8 839.1 g), high fruits per cluster (FPC, 8.67), and robust vegetative growth (e.g., BN = 5.67). The high heritability of yield (h^2 = 0.88) and substantial genetic advance (GA = 3 661.23 g) indicate strong potential for genetic improvement, corroborating Ramos et al. (2019), who, who reported similar heritability for yield-related traits in tomato. High heritability for BN (h^2 = 0.78) and FPC (h^2 = 0.70) further suggests that these traits are under strong genetic control, making them reliable targets for selection. Correlation analysis revealed strong positive associations between yield and BN (r = 0.67, P < 0.01) and NC (r = 0.64, P < 0.01), consistent with Singh et al. (2015) and Nagar et al. (2018), who identified BN and NC as key yield determinants. Conversely, negative correlations with plant height (PH, r = –0.98) and leaf number (LN, r = –0.20) suggest that excessive vegetative growth may divert resources from fruit production, as noted by (Monamodi et al. 2013). Path analysis further clarified these relationships, with BN showing a strong direct effect on yield (1.24) and NC a moderate effect (0.39), aligning with (Hossain et al. 2011). These findings suggest that selecting for high BN and NC, while moderating PH and LN, could optimise yield in breeding programs. Path analysis provided additional insight beyond simple correlations: although PH showed a weak negative correlation with yield, its strong negative direct effect (–0.98) was masked by positive indirect effects via BN and NC. This highlights the importance of selecting for moderate plant height to optimise yield. PCA elucidated trait relationships, with the first three PCs explaining 72.63% of the total variance (Table 6). PC1 (39.11%) was driven by NC (20.83%), BN (18.43%), PH (16.76%), and FPC (15.12%), reflecting plant architecture and fruiting potential. PC2 (20.99%) was dominated by total yield (TY, 34.34%), LN (17.75%), and branch length (BL, 14.67%), highlighting yield and vegetative growth variation. PC3 (12.53%) was primarily explained by leaf diameter (LD, 91.48%), indicating leaf size as a distinct trait. The PCA biplot (Figure 7) visualised these relationships, with genotypes like G13 and G12 positioned far from the origin along PC1 and PC2, indicating superior performance in TY and architectural traits (BN, NC). This genetic variation is critical for breeding, as genotypes with high PC1 scores (e.g., G6, G13, G19) offer robust plant architecture, while those with high PC2 scores (e.g., G12, G13) are ideal for yield improvement (Sarkar et al. 2024). For example, crossing G13 (high yield, moderate TYLCV susceptibility) with G2 or G3 (TYLCV-resistant) could combine resistance and yield traits, enhancing cultivar performance in TYLCV-endemic regions. The results underscore the potential for breeding TYLCV-resistant, high-yielding tomato cultivars by leveraging genetic variability in BN, NC, FPC, and TY. Marker-assisted selection targeting resistance genes (Pico et al. 1999) and quantitative trait loci (QTL) for yield components (Ramos et al. 2019) could accelerate progress. Additionally, the negative effects of excessive PH and LN suggest that breeding programs should balance vegetative

https://doi.org/10.17221/54/2026-CJGPB

and reproductive growth to maximise yield. Future studies should validate these findings across diverse environments and incorporate molecular markers to enhance selection efficiency. This integrated approach, combining phenotypic selection, PCA, and genetic markers, offers a robust strategy for developing superior tomato cultivars tailored to TYLCV-affected regions.

CONCLUSION

In conclusion, this study highlights significant genetic diversity among tomato genotypes in terms of TYLCV resistance and yield potential, providing valuable insights for breeding programs. Genotypes G2, G3, G10, and G11 showed moderate resistance (12.5–19.44%) and are promising candidates for developing TYLCV-resistant varieties, while G9, G15, and G22 were highly susceptible, emphasising the urgent need for resistant cultivars. G13 emerged as the top performer, combining high yield (8 839.1 g), more fruits per cluster (8.67), and strong vegetative growth. Traits like BN and NC showed strong positive effects on yield. High heritability and genetic advance in yield-related traits suggest strong potential for genetic improvement. Overall, genotypes like G13, G2, G3, G10, and G11 are valuable for breeding TYLCV-resistant, high-yielding tomatoes.

Acknowledgements. The authors gratefully acknowledge the support of this collaborative research provided by the research project for conducting the research from the National Research Foundation of Korea (NRF), Ministry of Science and ICT (MSIT), Republic of Korea.

REFERENCES

Abu Haraira A., Ahmad A., Khalid M.N., Tariq M., Nazir S., Habib I. (2022): Enhancing health benefits of tomato by increasing its antioxidant contents through different techniques: A review. Advancements in Life Sciences, 9: 131–142.

Ali S., Khan M., Habib A., Rasheed S., Iftikhar Y. (2005): Correlation of environmental conditions with okra yellow vein mosaic virus and *Bemisia tabaci* population density. International Journal of Agriculture and Biology, 7: 142–144.

Allard R.W. (1999): Principles of Plant Breeding. John Wiley & Sons.

Ammara U., Al-Sadi A.M., Al-Shihi A., Amin I. (2017): Real-time qPCR assay for the TYLCV titer in relation to symptoms-based disease severity scales. International Journal of Agriculture & Biology, 19: 145–151.

Avedi E.K. (2022): Distribution and Genetic Diversity of Tomato Yellow Leaf Curl Virus, Associated Whitefly Vectors and the Response of Selected Tomato Varieties to the Virus. Nairobi University of Nairobi.

Czosnek H., Hariton-Shalev A., Sobol I., Gorovits R., Ghanim M. (2017): The incredible journey of *begomo* viruses in their whitefly vector. Viruses, 9: 273.

El-Sappah H.A., Qi S., Soaud S.A., Huang Q., Saleh A.M., Abourehab M.A.S., Wan L., Cheng G.-T., Liu J., Ihtisham M., Noor Z., Mir R.R., Zhao X., Yan K., Abbas M., Li J. (2022): Natural resistance of tomato plants to Tomato yellow leaf curl virus. Frontiers in Plant Science, 13: 1081549.

Hanssen I.M., Lapidot M., Thomma B.P. (2010): Emerging viral diseases of tomato crops. Molecular Plant-Microbe Interactions, 23: 539–548.

Hossain M., Akanda A., Rahman A. (2011): Character association and path coefficient analysis for yield components in TYLCV infected tomato (*Solanum lycopersicum* L.). Journal of the Bangladesh Agricultural University, 9: 203–208.

Idrees M.A., Abbas A., Saddam B., Bashir M.H., Naveed H., Khan A.K., Dara M.Z.N. (2024): A comprehensive review: Persistence, circulative transmission of *begomovirus* by whitefly vectors. International Journal of Tropical Insect Science, 44: 405–417.

Johnson H.W., Robinson H.F., Comstock R.E. (1955): Estimates of genetic and environmental variability in soybeans. Agronomy Journal, 47: 314–318.

Jones R.A. (2020): Disease pandemics and major epidemics arising from new encounters between indigenous viruses and introduced crops. Viruses, 12: 1388.

Lapidot M., Friedmann M. (2002): Breeding for resistance to whitefly-transmitted geminiviruses. Annals of Applied Biology, 140: 109–127.

Lobin K.K., Jaunky V.C., Taleb-Hossenkhan N. (2022): A meta-analysis of climatic conditions and whitefly *Bemisia tabaci* population: Implications for tomato yellow leaf curl disease. The Journal of Basic and Applied Zoology, 83: 57.

Mandahar C.L. (2018): Plant Viruses: Volume II: Pathology. CRC Press.

Monamodi E., Lungu D., Fite G. (2013): Analysis of fruit yield and its components in determinate tomato (*Lycopersicon lycopersicum*) using correlation and path coefficient. Journal of Agricultural Science, 5: 45–52.

Muniyappa V., Jalikop S., Saikia A., Chennarayappa, Shivashankar G., Bhat A.I., Ramappa H. (1991): Reaction of *Lycopersicon* cultivars and wild accessions to tomato leaf curl virus. Euphytica, 56: 37–41.

Nagar S.S., Kumar P., Vishwakarma S., Singh G., Tyagi B. (2018): Assessment of genetic variability and character as-

https://doi.org/10.17221/54/2026-CJGPB

sociation for grain yield and its component traits in bread wheat (*Triticum aestivum* L.). Journal of Applied and Natural Science, 10: 797.

Naimuzzaman M., Rahman F., Alvi A.T., Yeasmin L., Mittra P.K., Roy S.K. (2024): Plant growth–promoting fungi in plants: Insights from stress tolerance mechanism. In: Sa T.M. (ed.): Beneficial Microbes for Sustainable Agriculture Under Stress Conditions. Academic Press: 469–511.

Naimuzzaman M., Hasan M.M., Kumer A., Hossin A.Y., Harun-Ur-Rashid M., Roy S.K., Ahmmed A.N.F., Uddin J. (2025): Computational and *in silico* study of novel fungicides against combating root rot, gray mold, fusarium wilt, and cereal rust. PLoS ONE, 20: e0316606.

Pico B., Ferriol M., Diez M., Nuez F. (1999): Developing tomato breeding lines resistant to tomato yellow leaf curl virus. Plant Breeding, 118: 537–542.

Punniyakotti P., Vinayagam S., Rajamohan R., Priya S., Moovendhan M., Sundaram T. (2024): Environmental fate and ecotoxicological behaviour of pesticides and insecticides in non-target environments: Nanotechnology-based mitigation strategies. Journal of Environmental Chemical Engineering, 12: 113349.

Quamruzzaman A., Akter L., Islam F. (2023): Yield and pest performance of high-temperature tolerant tomato (*Lycopersicon esculentum*) lines for year-round tomato production in Bangladesh. Agricultural Sciences, 14: 855–863.

R Core Team (2021): R: A Language and Environment for Statistical Computing. Vienna, R Foundation for Statistical Computing.

Ramos R.S., Kumar L., Shabani F., Picanço M.C. (2019): Risk of spread of Tomato yellow leaf curl virus (TYLCV) in tomato crops under various climate change scenarios. Agricultural Systems, 173: 524–535.

Sarkar N.S., Kalaimagal T., Kavithamani D., Chandirakala R., Manonmani S., Raveendran M., Senthil A. (2024): Assessing genetic relationships, trait associations and diversity patterns in sorghum germplasm through correlation, cluster and principal component analysis. Agricultural Science Digest, 44: 445–452.

Shah M.A., Subhash S., Ellango R., Asokan R., Sharma S., Chakrabarti S. (2022): Biology and Management of Whiteflies in Potato Crops. Sustainable Management of Potato Pests and Diseases. Singapore, Springer.

Shahriari Z., Su X., Zheng K., Zhang Z. (2023): Advances and prospects of virus-resistant breeding in tomatoes. International Journal of Molecular Sciences, 24: 15448.

Singh N., Ram C., Deo C., Yadav G., Singh D.P. (2015): Genetic variability, heritability and genetic advance in tomato (*Solanum lycopersicum* L.). Plant Archives, 15: 705–709.

Strange R.N., Scott P.R. (2005): Plant disease: A threat to global food security. Annual Review of Phytopathology, 43: 83–116.

Tiwari A., Tikoo S.K., Angadi S.P., Kadaru S.B., Ajanahalli S.R., Rao M.V. (2022): Market-Driven Plant Breeding for Practicing Breeders. Vol. 411, Singapore, Springer Nature.

Valverde R., Lotrakul P., Landry A., Boudreaux J. (2001): First report of Tomato yellow leaf curl virus in Louisiana. Plant Disease, 85: 230–230.

Wang C., Li M., Duan X., Abu-Izneid T., Rauf A., Khan Z., Mitra S., Emran T.B., Aljohani A. S, Alhumaydhi F.A. (2023): Phytochemical and nutritional profiling of tomatoes; impact of processing on bioavailability-a comprehensive review. Food Reviews International, 39: 5986–6010.

Yan Z., Pérez-De-Castro A., Díez M.J., Hutton S.F., Visser R.G., Wolters A.-M.A., Bai Y., Li J. (2018): Resistance to tomato yellow leaf curl virus in tomato germplasm. Frontiers in Plant Science, 9: 1198.

Received: April 28, 2026
Accepted: July 29, 2026
Published online: August 20, 2026