

RESEARCH ARTICLE

Genetic, biochemical and molecular characterization of exotic tomato lines for key economic traits

Jagesh Kumar Tiwari*, Nagendra Rai, Manish Kumar Singh, Gaurav Mishra, Shreya Panwar, Priyanka Sharma, Rajat Singh, Tushar Kant, Yagyat Singh, Harish Kumar, Yerasu Suresh Reddy, Atma Nand Tripathi, Tusr Kanti Behera and Rajesh Kumar

Abstract

This study aimed to characterize 60 newly acquired exotic genotypes to identify superior lines for use as parental material in breeding programs. The genotypes were evaluated under field conditions during 2023-25 for yield components, processing traits, and resistance to tomato leaf curl disease (ToLCD). Gene-specific DNA markers were employed to detect ToLCD resistance genes Ty-2 and Ty-3. Substantial genetic variation was observed among the genotypes for the traits assessed. The genotypic coefficient of variation (GCV) ranged from 5.41 to 94.82%, which was lower than the phenotypic coefficient of variation (PCV), which ranged from 5.70 to 97.11%. High heritability values (> 60%) combined with high genetic advance as a percentage of the mean (> 20%) suggest that additive gene action is responsible, supporting the effectiveness of selection. Hierarchical clustering using the unweighted pair group method with arithmetic mean (UPGMA) classified the genotypes into four clusters (I-IV), revealing distinct variation among genotypes from the United States and Taiwan. Principal component analysis (PCA) explained a total of 76.56% of the variation, with the first and second principal components accounting for 49.16 and 27.40%, respectively. Field assays for ToLCD resistance identified 11 genotypes as highly resistant (HR), 4 as resistant (R), 5 as moderately resistant (MR), and the remaining 40 genotypes as moderately susceptible to highly susceptible. Genotypes AVTO1174, AVTO1219, AVTO1424, AVTO1707, and AVTO2151 possessed both Ty-2 and Ty-3 genes in homozygous form and exhibited field resistance to ToLCD. The following genotypes, AVTO1174, AVTO1219, AVTO1424, AVTO2101, AVTO1906, AVTO1907, AVTO2149, AVTO2151, AVTO1909, and AVTO1915, are recommended as parental lines for advanced breeding programs.

Keywords: Genetic parameters, Tomato, Yield components, ToLCD resistance, Processing, Markers, MGID

ICAR-Indian Institute of Vegetable Research, Varanasi- 221305, Uttar Pradesh, India

***Corresponding author;** Email: jageshtiwari@gmail.com

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Introduction

Tomato (*Solanum lycopersicum* L.) is a major vegetable crop cultivated for both fresh consumption and processing. It provides significant amounts of vitamins A and C, dietary fibre, carotenoids, potassium, phenolic compounds, and antioxidants such as lycopene, which exhibits anti-cancer properties (Nasir et al., 2015). In 2023, global tomato production reached 192.32 million tons from 5.41 million hectares, with an average productivity of 35.33 tons per hectare (FAOSTAT, 2024). In India, production was 21.54 million tons from 0.85 million hectares, with a productivity of 25.28 tons per hectare (MoAFW, Govt. of India, 1st Adv. Est. 2024-25). Despite its importance, tomato cultivation is challenged by biotic and abiotic stresses, climate change, the need to meet industrial fruit quality standards, and post-harvest losses (Causse et al., 2016). Over the past

century, thousands of tomato varieties have been developed worldwide for traits such as high yield, fruit size, shape, colour, resistance to biotic stresses including tomato leaf curl disease (ToLCD), tolerance to high temperatures, and suitability for processing. The development of cultivars that address these challenges is essential to sustain tomato production in India.

With the rapidly growing global population, limited cultivable land, and the impacts of climate change, boosting tomato production is essential to ensure food and nutritional security. Developing high-yielding varieties and hybrids remains one of the most effective and eco-friendly strategies. The success of breeding new varieties relies on a diverse genetic pool and the assessment of variability parameters to effectively utilize germplasm in breeding programs (Zhou et al., 2015). Tomatoes originated in South America, Mexico, and Central America. However, the narrow genetic base of cultivated tomatoes limits access to diverse germplasm for breeding, resulting in a shortage of high-yielding cultivars and, consequently, lower yield potential (Rasheed et al., 2023). Therefore, analyzing genetic variability is crucial for developing new cultivars with desired traits (Zannat et al., 2023). Acquiring diverse germplasm is the first step in breeding for genetic improvement. Recently, we have identified elite tomato lines using both conventional and molecular tools (Tiwari et al., 2024; 2025).

Tomato leaf curl disease (ToLCD) is recognized as the most severe disease affecting tomato crops globally. Severe infestations can result in total crop loss (Yerasu et al., 2025). ToLCD is caused by the begomovirus known as tomato leaf curl virus (ToLCV), which is transmitted by the whitefly *Bemisia tabaci*. The primary ToLCD resistance genes include *Ty-1* and *Ty-3*, located on chromosome 6, *Ty-4* on chromosome 3, and *Ty-6* on chromosome 10, all derived from *Solanum chilense*. *Ty-2*, located on chromosome 11, originates from *S. habrochaites*, while the recessive gene *ty-5* on chromosome 4 is found in the cultivar Tyking or *S. peruvianum* (Prasanna et al., 2015). Marker-assisted selection (MAS) has been employed for several decades in tomato breeding to accelerate early-stage selection and facilitate gene pyramiding (Tiwari et al., 2022). Gene pyramiding strategies have been used to introgress resistance to multiple diseases, including ToLCD, late blight, and root-knot nematode in tomato (Kumar et al., 2019). Therefore, identification of ToLCD resistance sources is essential for the development of high-yielding cultivars.

Materials and Methods

Plant materials and field experiments

Sixty exotic accessions were obtained earlier from the international gene banks, including 20 accessions from the World Vegetable Centre, Taiwan, and 40 accessions from the Tomato Genetic Resource Centre, UC Davis, California,

USA. Field experiments were executed in a randomized block design (RBD) for two years (2023-24 and 2024-25) in the rabi (winter) crop season at ICAR-Indian Institute of Vegetable Research, Varanasi (25.18° N Latitude and 82.83° E Longitude). Seeds were sown in mid-September and transplanting was done in the first week of October. Ten plants per accession were grown in two replications in the paired row on the raised bed at 60 cm × 45 cm spacing. The crops were grown following the recommended package of practices for tomato (Tiwari et al., 2024; 2025).

Evaluation for yield components and processing traits

Fourteen horticultural traits were recorded for two years (2023-25) in tomato genotypes such as *i*) days to first harvest, *ii*) days to last harvest, *iii*) average fruit weight (g), *iv*) fruit length (cm), *v*) fruit width (cm), *vi*) number of locules, *vii*) pericarp thickness (cm), *viii*) total soluble solids (TSS) (°Brix), *ix*) yield (kg/plant), *x*) plant height (cm), *xi*) lycopene (mg/100 g), *xii*) β-carotene (mg/100 g), *xiii*) titratable acidity (%), and *xiv*) pH. All traits were measured using previously established protocols (Tiwari et al., 2024). Data were collected from five randomly selected plants in each replication. Pericarp thickness was measured with a Vernier caliper. Average fruit weight was calculated from the mean weight of ten fruits. TSS was determined using a hand refractometer. Additionally, four qualitative traits—plant growth habit, fruit shape, fruit firmness, and fruit color—were also recorded (Tiwari et al., 2024).

Tomato leaf curl disease (ToLCD) resistance test under field conditions

Tomato genotypes were evaluated for ToLCD for two years (2023-2025) under natural field conditions. A total of 60 genotypes, including controls such as cv. Punjab Chhuhara (highly susceptible) and cv. Kashi Chayan (highly resistant), was utilized in the field trials. Disease symptoms were documented based on leaf infection (%) observed at 45 and 90 days after transplanting. Percent disease incidences were recorded according to the following scale: 0 (0-5%, HR = highly resistant), 1 (5.1-12.0%, R = resistant), 2 (12.1-25%, MR = moderately resistant), 3 (25.1-50.0%, MS = moderately susceptible), 4 (50.1-75%, S = susceptible), and 5 (75.1-100%, HS = highly susceptible) (Banerjee and Kalloo, 1987). The average data collected over the two years were compiled for the final scoring and categorization of genotypes into various classifications.

Molecular marker assays for ToLCD

Genotypes were examined for resistance genes associated with ToLCD (*Ty-2* and *Ty-3*) through the use of molecular markers (Prasanna et al., 2015). Leaf samples were taken from plants grown in the field and utilized for DNA extraction via the CTAB method. The quality of the DNA was assessed

on a 1% agarose gel, while the quantity was measured with a NanoDrop 2000 Spectrophotometer (Thermo Fisher Scientific, Wilmington, USA). For the *Ty-2* gene, SCAR marker AW910upF2R3 (F: AGAAGGTTAACGCGCTAAATT; and R: AAGCCAAGAAGTTGAAAACAC) was used, which shows 523 (resistant) and 821 (susceptible) bands (Garcia et al., 2007). Likewise, for *Ty-3* gene, *Ty3*-SCAR1 marker (F: GCTCAGCATCACCTGAGACA; R: TGCAGGAACAGAAATGATAGAAAA) were deployed that amplified 519 bp (resistant) and 269 bp (susceptible) bands (Dong et al., 2016). The PCR (polymerase chain reaction) mixture was prepared in a total volume of 15 μ L, consisting of 7.5 μ L of 2X PCR buffer, 1- μ L of forward and 1- μ L of reverse primers, 3 μ L of each sample's DNA, and 2.5 μ L of PCR-grade water (Genei Laboratories Pvt Ltd, Bangalore, India). The PCR cycle was programmed at 94°C for 4 minutes, followed by 36 cycles at 94°C for 1 minute, 55°C for 1-minute, and 72°C for 1 minute, concluding with 72°C for 7 minutes in a thermal cycler (BIO-RAD, CA, USA). The PCR products were separated on 1.5% agarose gels and observed using the Alpha Innotech Gel-Doc system (Alpha Innotech, CA, USA) (Tiwari et al., 2024).

Statistical analysis

A total of 15 horticultural traits were evaluated across 60 tomato genotypes. These findings were utilized in analyses for genetic variability, diversity, principal component analysis (PCA), correlations, multi-trait genotype-ideotype distance index (MGIDI), and resistance to TolCD. Data from two years were analyzed through a one-factor pooled ANOVA (RBD) using the OPSTAT tool (<https://opstat.somee.com/>). Data from multiple years were combined to pinpoint genotypes that exhibit stable and favorable average effects throughout the years. The Bartlett's Chi-square test ($p < 0.05$) was applied to assess the homogeneity of error variances. Each trait with homogeneous variance was then subjected to a combined analysis of variance for the pooled data. The analysis of genetic variability utilized the library (variability) and the correlation coefficient was computed using the library (readxl) from the R package. Genetic diversity was assessed through the Neighbor-Joining method with 100 bootstraps, employing DARwin 6.0.11 software. PCA was also conducted to investigate the genetic relationships among the accessions using the same DARwin software. The analysis of MGIDI was performed to identify promising genotypes using the default settings of the «metan» package within R software (Olivoto and Nardino, 2021).

Results and Discussion

Evaluation for yield components and processing traits:

A total of 60 genotypes were assessed for a variety of yield parameters and processing characteristics (Table 1).

The genotype that produced the earliest first picking was AVTO2036 (57.5 days), whereas the latest genotype was LA3120 (130 days). The duration from planting to the final harvest ranged from 105 days (AVTO1909) to 157.5 days (LA4345). This indicated that the genotype with the longest collection period was AVTO2037 (79.5 days), followed by AVTO1349 and AVTO1174 (76 days), whereas the shortest harvest period was recorded in LA4347 (16 days). The highest average fruit weight was found in LA2086 (176.5 g) and was followed by AVTO2101 (121.5 g), while the lowest was recorded for LA1310 (8.1 g). The maximum fruit length was noted in LA4347 (6.75 cm), while the shortest length was measured for LA1579 (1.06 cm). The greatest fruit width was observed in LA2086 (6.24 cm), while the smallest was noted in LA1579 (1.13 cm). In terms of fruit shape, 28 genotypes were classified as round-fruited, 27 as oblong, 4 as flat-round, and 1 as pear-shaped. The genotype LA1502 exhibited the highest number of locules (6.07), while AVTO1349 and AVTO2037 had the fewest locules (2). The maximum thickness of the pericarp was seen in LA4104 (0.95 cm), followed by AVTO2149 (0.93 cm) and AVTO1219 (0.66 cm), with the minimum thickness recorded in LA2093/LA1579 (0.11 cm). Firmness of the fruit was classified as tough in 11 genotypes, medium in 26, and loose in 23.

In terms of processing parameters, the highest total soluble solids (TSS) were noted in LA2093 (7.69 °Brix), followed by AVTO2037 (7.48 °Brix) and AVTO2036 (6.48 °Brix), while the lowest was recorded in AVTO1914 (3.28 °Brix). The genotypes that produced the most fruit yield per plant included AVTO0102 (1.88 kg), AVTO2101 (1.59 kg), and AVTO1707 (1.48 kg), while the least productive genotypes were LA3120 (0.08 kg) and LA2093 (0.09 kg). The tallest plants were measured in AVTO2037 (217.1 cm) and AVTO1174 (217.0 cm), while the shortest were found in LA3911 (15.34 cm) and LA3006 (46.67 cm). In total, 23 genotypes exhibited determinate growth, 11 were indeterminate, and 26 had semi-determinate growth habits. Regarding processing characteristics, the highest lycopene content was found in AVTO2149 (4.9 mg/100 g), while the lowest was noted in LA3898 (0.4 mg/100 g). Genotype LA2093 had the greatest β -carotene content (4.6 mg/100 g), followed by AVTO1707 (4.26 mg/100g), with the minimum being in LA2086 (0.33 mg/100 g). The highest titrable acidity was recorded in LA3320 (0.45%), whereas the lowest was in LA2086 (0.17%). The maximum pH was observed in AVTO2017 (4.75), while the minimum was found in LA3120 (3.81). Overall, there were 50 red genotypes, 7 orange, 2 dark red, and 1 pink color (Table 1). Similar to this, genotypic parameters have been extensively investigated earlier for yield-related traits in tomato (Singh et al., 2015). Hence, the information generated in our study would be informative for increasing fruit yield-related traits in tomato.

Table 1: Mean performance of exotic tomato genotypes under field conditions for two years (2023-24 and 2024-25).

Sample code	Genotype	Solanum species	Days to first harvest	Days to last harvest	Average fruit weight (g)	Fruit length (cm)	Fruit width (cm)	Number of locules	Pericarp thickness (cm)
G1	AVTO0102	<i>Solanum lycopersicum</i>	81.50	121.00	58.40	4.45	4.61	2.30	0.38
G2	AVTO1174	<i>S. lycopersicum</i>	63.50	139.50	26.50	3.92	3.09	2.47	0.38
G3	AVTO1219	<i>S. lycopersicum</i>	77.50	133.00	101.80	5.34	5.44	3.17	0.66
G4	AVTO1349	<i>S. lycopersicum</i> var. <i>cerasiforme</i>	62.50	138.50	25.30	3.99	3.07	2.00	0.38
G5	AVTO1424	<i>S. lycopersicum</i>	86.00	127.00	72.80	5.90	5.12	4.13	0.42
G6	AVTO1706	<i>S. lycopersicum</i>	67.50	126.50	69.50	5.27	4.71	2.48	0.43
G7	AVTO1707	<i>S. lycopersicum</i>	78.00	127.50	68.40	5.29	4.65	3.10	0.44
G8	AVTO1906	<i>S. lycopersicum</i>	81.00	128.00	86.80	5.44	4.71	3.10	0.49
G9	AVTO1907	<i>S. lycopersicum</i>	77.50	126.00	86.40	5.92	4.89	3.43	0.53
G10	AVTO1909	<i>S. lycopersicum</i>	73.50	105.00	48.75	5.10	4.37	3.48	0.25
G11	AVTO1914	<i>S. lycopersicum</i>	75.00	118.50	98.90	6.67	5.35	2.48	0.38
G12	AVTO1915	<i>S. lycopersicum</i>	77.50	117.50	58.90	5.52	4.42	2.48	0.35
G13	AVTO2017	<i>S. lycopersicum</i>	81.50	146.00	101.50	4.96	5.67	3.27	0.52
G14	AVTO2036	<i>S. lycopersicum</i> var. <i>cerasiforme</i>	57.50	127.50	20.10	3.36	2.62	2.17	0.31
G15	AVTO2037	<i>S. lycopersicum</i> var. <i>cerasiforme</i>	66.00	145.50	17.70	3.25	2.39	2.00	0.29
G16	AVTO2101	<i>S. lycopersicum</i>	74.50	118.50	121.50	5.08	5.60	5.20	0.48
G17	AVTO2149	<i>S. lycopersicum</i>	77.50	137.50	96.20	5.61	5.23	3.00	0.93
G18	AVTO2151	<i>S. lycopersicum</i>	98.00	140.50	90.70	6.00	4.96	3.00	0.56
G19	AVTO9706	<i>S. lycopersicum</i>	79.00	153.50	28.40	3.59	3.54	2.53	0.44
G20	AVTO9801	<i>S. lycopersicum</i>	69.00	127.50	36.30	3.84	3.82	2.27	0.45
G21	AVTO9802	<i>S. lycopersicum</i>	76.50	126.00	69.40	5.85	4.84	2.73	0.62
G22	AVTO9805	<i>S. lycopersicum</i>	92.00	139.00	25.40	4.09	3.00	2.37	0.36
G23	LA0089	<i>S. lycopersicum</i> cv. <i>Principe Borghese</i>	120.00	155.00	37.70	4.58	3.16	2.40	0.36
G24	LA0315	<i>S. lycopersicum</i>	96.00	150.00	39.50	3.76	3.94	2.37	0.46
G25	LA1017	<i>S. lycopersicum</i>	80.00	145.50	22.50	3.68	3.59	3.10	0.42
G26	LA1019	<i>S. lycopersicum</i>	107.00	146.00	45.90	4.10	4.24	3.43	0.50
G27	LA1028	<i>S. chmielewskii</i>	84.50	144.50	27.50	4.96	3.11	2.57	0.42
G28	LA1162	<i>S. lycopersicum</i> cv. <i>Cuba Plum</i>	75.50	135.00	21.60	3.40	2.24	2.47	0.29
G29	LA1222	<i>S. lycopersicum</i> cv. <i>VF-1457 8-79</i>	90.00	141.50	69.20	4.99	4.61	3.17	0.47
G30	LA1310	<i>S. lycopersicum</i> var. <i>cerasiforme</i>	95.00	141.00	8.10	1.72	1.67	2.10	0.16
G31	LA1421	<i>S. lycopersicum</i> var. <i>cerasiforme</i>	74.00	144.00	9.40	2.30	2.57	2.60	0.18
G32	LA1500	<i>S. lycopersicum</i>	97.50	145.50	71.40	4.51	5.19	4.33	0.40

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TSS (Brix)	Yield (kg/plant)	Plant height (cm)	Lycopene (mg/100g)	β-Carotene (mg/100g)	Titrable acidity (%)	pH	Plant growth habit	Fruit shape	Fruit firmness	Fruit colour
4.91	1.88	93.17	2.35	3.66	0.31	4.23	SD	Round	Loose	Orange
5.61	1.01	217.00	1.82	3.10	0.37	4.49	I	Oblong	Tough	Orange
3.77	1.31	121.67	2.83	2.18	0.24	4.62	SD	Round	Tough	Red
5.31	0.93	165.50	1.79	2.61	0.28	4.39	I	Oblong	Medium	Red
3.57	1.22	102.67	2.80	1.31	0.24	4.59	SD	Oblong	Tough	Red
4.36	0.96	58.00	1.41	1.49	0.19	4.75	D	Oblong	Medium	Red
3.86	1.48	55.67	4.56	4.26	0.25	4.22	D	Round	Tough	Red
4.05	1.02	88.33	3.16	2.99	0.23	4.56	SD	Oblong	Medium	Red
4.20	1.19	78.17	4.14	3.45	0.28	4.56	SD	Oblong	Tough	Red
3.32	0.80	59.17	1.43	1.05	0.27	4.61	D	Oblong	Medium	Red
3.28	0.86	85.67	1.94	1.30	0.25	4.45	SD	Oblong	Medium	Red
3.56	0.86	74.75	1.79	2.15	0.22	4.52	SD	Oblong	Medium	Red
4.49	1.08	128.67	1.89	1.99	0.28	4.75	SD	Round	Medium	Red
6.48	0.87	128.17	2.01	2.13	0.30	4.46	I	Oblong	Medium	Red
7.48	1.19	217.17	2.56	2.19	0.27	4.32	I	Oblong	Loose	Pink
3.71	1.59	57.83	1.56	1.06	0.27	4.33	D	Round	Medium	Red
4.80	1.33	87.83	4.90	2.39	0.26	4.69	SD	Round	Medium	Red
4.83	1.20	105.00	4.29	3.77	0.28	4.49	SD	Oblong	Medium	Red
5.74	0.99	169.67	2.46	3.25	0.28	4.14	I	Round	Medium	Orange
4.85	0.66	48.67	3.61	3.66	0.31	4.24	D	Round	Medium	Red
4.45	0.97	74.67	4.06	4.17	0.21	4.44	SD	Oblong	Medium	Red
6.04	0.86	147.17	1.31	2.91	0.26	4.64	SD	Oblong	Medium	Orange
4.83	0.57	90.00	2.03	2.83	0.38	3.96	SD	Oblong	Loose	Red
4.83	0.99	102.50	0.86	1.02	0.36	3.89	SD	Round	Loose	Red
4.97	0.11	190.00	1.80	1.30	0.29	4.69	I	Round	Medium	Red
5.20	0.11	92.17	0.73	0.64	0.26	3.83	SD	Round	Loose	Red
4.47	0.12	70.00	3.34	3.16	0.25	4.57	D	Oblong	Medium	Red
4.97	0.90	154.83	2.75	1.89	0.42	4.45	I	Oblong	Loose	Red
5.05	0.83	66.67	1.53	1.83	0.30	4.30	D	Round	Medium	Red
5.70	0.13	154.67	0.80	0.96	0.41	4.25	I	Round	Loose	Red
5.47	0.30	167.67	2.73	3.05	0.44	3.86	I	Round	Loose	Red
5.91	0.23	71.67	0.77	1.15	0.36	4.05	D	Round	Loose	Red

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G33	LA1501	<i>S. lycopersicum</i>	114.50	148.50	84.30	4.63	5.00	4.60	0.50
G34	LA1502	<i>S. lycopersicum</i>	88.00	143.50	69.90	3.73	4.45	6.07	0.36
G35	LA1503	<i>S. lycopersicum</i>	106.00	155.50	77.80	4.36	4.99	4.77	0.44
G36	LA1563	<i>S. lycopersicum</i>	107.00	146.00	77.70	4.25	5.47	5.43	0.51
G37	LA1579	<i>S. pimpinellifolium</i>	95.00	144.00	10.90	1.06	1.13	2.10	0.11
G38	LA1996	<i>S. lycopersicum</i>	85.00	135.00	91.50	4.59	5.59	4.43	0.52
G39	LA2019	<i>S. lycopersicum</i>	91.50	147.00	53.00	5.22	3.51	2.30	0.48
G40	LA2086	<i>S. lycopersicum</i>	125.00	150.00	176.60	5.63	6.24	4.83	0.52
G41	LA2093	<i>S. pimpinellifolium</i>	70.50	138.00	9.60	1.41	1.48	2.10	0.11
G42	LA2375	<i>S. lycopersicum</i> cv. San Marzano	87.50	144.00	47.50	5.38	3.86	2.53	0.48
G43	LA2661	<i>S. lycopersicum</i> cv. Nagcarlang	70.50	134.00	28.60	3.32	3.43	2.43	0.45
G44	LA2662	<i>S. lycopersicum</i> cv. Saladette	87.00	153.50	50.70	4.71	4.27	2.27	0.52
G45	LA2711	<i>S. lycopersicum</i> cv. Edkawi	87.50	140.50	117.50	5.03	5.69	5.50	0.54
G46	LA3006	<i>S. lycopersicum</i>	81.50	141.50	34.00	5.69	1.82	2.25	0.44
G47	LA3120	<i>S. lycopersicum</i> cv. Malintka 101	85.00	130.00	27.50	4.02	3.49	2.20	0.41
G48	LA3320	<i>S. lycopersicum</i> cv. Hotset	81.50	137.00	100.20	4.71	5.94	4.07	0.58
G49	LA3847	<i>S. lycopersicum</i> cv. NC HS-1	92.50	147.00	88.20	4.61	4.95	4.00	0.40
G50	LA3897	<i>S. lycopersicum</i>	87.50	140.50	61.00	4.15	4.16	2.27	0.46
G51	LA3898	<i>S. lycopersicum</i>	88.00	141.00	57.70	4.22	4.67	2.47	0.56
G52	LA3899	<i>S. lycopersicum</i>	90.50	143.00	46.00	4.93	4.12	2.37	0.49
G53	LA3911	<i>S. lycopersicum</i> cv. Micro-Tom	70.00	117.50	11.30	1.94	2.08	2.67	0.23
G54	LA4082	<i>S. lycopersicum</i>	81.00	137.50	69.70	5.13	4.43	2.43	0.65
G55	LA4104	<i>S. lycopersicum</i>	97.50	138.00	29.50	4.79	4.22	3.30	0.95
G56	LA4345	<i>S. lycopersicum</i> cv. Heinz 1706-BG	82.50	157.50	31.90	4.95	3.07	2.53	0.40
G57	LA4347	<i>S. lycopersicum</i> cv. B-L-35	130.00	146.00	52.30	6.75	4.04	2.10	0.57
G58	LA4410	<i>S. lycopersicum</i> cv. Meek	72.50	148.00	63.80	5.11	4.33	2.60	0.57
G59	LA4453	<i>S. lycopersicum</i>	92.50	144.00	66.40	4.48	3.74	2.80	0.48
G60	LA4454	<i>S. lycopersicum</i>	93.00	150.50	44.40	5.09	3.73	3.27	0.49
Mean			85.54	138.6	57.37	4.50	4.07	3.04	0.44
CD (p < 0.05)		Years	2.29	2.81	5.54	0.21	0.30	0.31	0.07
		Varieties	18.69	21.44	25.32	1.3	1.48	1.09	0.31
		Years × Varieties	4.16	4.51	2.57	0.23	0.21	0.19	0.05

CD: Critical Difference; D: Determinate; I: Indeterminate; SD: Semi-determinate; Percent disease incidence were recorded based on the scale: 0 (0-5%, HR = highly resistant), 1 (5.1-12.0%, R = resistant), 2 (12.1-25%, MR = moderately resistant), 3 (25.1-50.0%, MS = moderately susceptible), 4 (50.1-75%, S = susceptible), and 5 (75.1-100%, HS = highly susceptible) Source: Banerjee MK, Kalloo G (1987) Sources and inheritance of resistance to leaf curl virus in *Lycopersicon*. Theor Appl Genet 73:707-710. Note: Show selected genotypes based on the MGIDI analysis: AVTO2149 (G17), AVTO2151 (G18), LA2711 (G45), AVTO2017 (G13), LA2375 (G42), LA2086 (G40), LA4345 (G56), AVTO9706 (G19), and LA1501 (G33).

Cont...

6.12	0.50	76.50	0.61	0.96	0.30	4.40	SD	Round	Loose	Red
6.17	0.45	78.00	0.74	1.21	0.38	4.06	SD	Round	Loose	Red
5.49	0.69	59.50	0.48	0.70	0.36	4.26	D	Round	Medium	Red
5.54	0.49	76.50	1.23	1.06	0.21	4.47	D	Flat-round	Loose	Red
5.94	0.10	162.17	1.05	1.14	0.37	4.06	I	Round	Loose	Red
5.03	1.25	70.17	2.76	1.52	0.25	4.53	D	Flat-round	Loose	Dark red
4.75	0.32	83.00	2.90	1.74	0.25	4.19	SD	Pear Shape	Loose	Red
6.14	1.08	87.83	0.44	0.33	0.17	4.33	SD	Round	Loose	Red
7.69	0.09	146.33	4.02	4.60	0.28	4.22	I	Round	Loose	Red
5.08	0.98	89.00	3.59	3.91	0.24	4.47	SD	Oblong	Medium	Red
5.80	1.33	83.33	3.20	0.91	0.37	4.33	SD	Round	Loose	Red
4.45	0.98	52.50	2.41	1.36	0.29	4.58	D	Round	Loose	Dark red
5.81	0.68	137.67	1.66	1.82	0.28	4.44	SD	Flat-round	Loose	Red
5.21	0.10	46.67	1.68	0.70	0.22	4.03	D	Oblong	Medium	Red
4.20	0.08	52.33	2.04	1.51	0.32	3.81	D	Oblong	Loose	Red
5.54	0.89	116.17	1.86	1.60	0.45	4.07	SD	Flat-round	Loose	Red
4.68	1.43	74.17	1.31	0.89	0.36	4.05	SD	Round	Medium	Red
4.66	0.42	52.00	1.24	1.89	0.35	4.47	D	Round	Medium	Orange
4.53	0.53	57.83	0.40	0.81	0.30	4.04	D	Round	Tough	Orange
3.93	0.66	51.17	1.48	2.46	0.34	4.13	D	Oblong	Tough	Orange
4.27	0.21	15.34	3.08	2.42	0.43	4.08	D	Round	Medium	Red
4.69	0.42	50.83	2.55	3.32	0.40	4.71	D	Round	Tough	Red
5.79	0.37	61.00	0.56	0.82	0.39	4.21	D	Oblong	Tough	Red
5.63	0.18	74.67	3.03	2.69	0.30	4.48	SD	Oblong	Medium	Red
5.71	0.25	69.83	0.73	0.70	0.38	4.34	SD	Oblong	Loose	Red
4.35	0.96	56.17	0.94	1.24	0.28	4.03	D	Oblong	Medium	Red
5.95	0.35	61.83	1.81	1.78	0.34	4.49	D	Oblong	Tough	Red
5.27	0.50	52.50	0.86	1.47	0.30	4.46	D	Oblong	Tough	Red
5.04	0.74	93.66	2.07	2.00	0.30	4.31				
0.23	0.24	3.44	0.25	0.24	0.02	0.24				
1.65	0.50	48.70	1.88	1.85	0.22	0.27				
0.13	0.14	3.91	0.18	0.12	0.08	0.22				

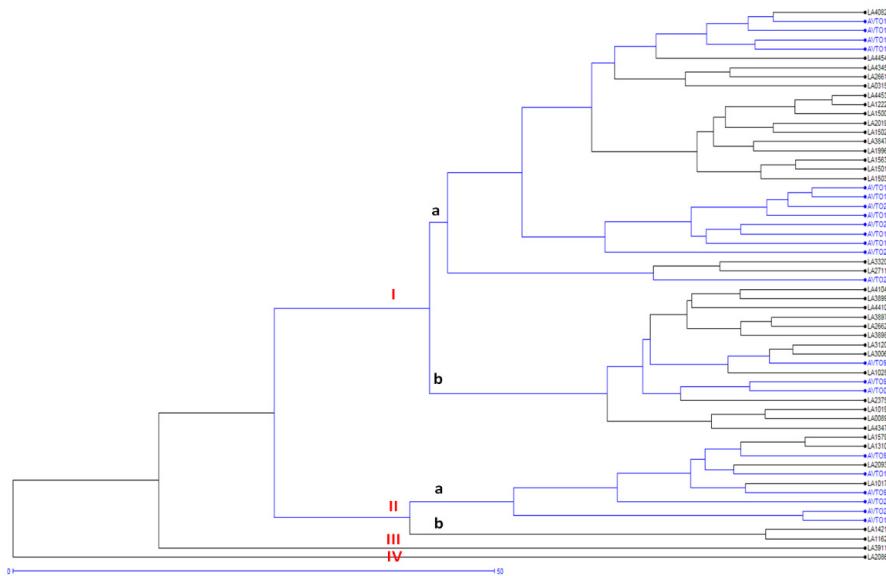


Fig. 1: Genetic diversity analysis in 60 tomato genotypes by the Hierarchical clustering based on the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) method using the DARwin 6.0.11 software.

Table 2: Genetic variability parameters for different traits in exotic tomato genotypes

Sr. No.	Traits	SS	SSE	σ^2g	σ^2p	σ^2e	h^2b (%)	GCV	PCV	ECV	GA	GA as % of mean
1.	Days to first harvest	37541**	3193	203.07	230.13	27.06	88	16.63	17.70	6.07	27.57	32.18
2.	Days to last harvest	20415.4**	4280.8	103.24	139.52	36.27	74	7.33	8.52	4.34	18.00	12.99
3.	Average fruit weight (g)	197764**	5644	1101.36	1149.19	47.83	95	57.84	59.08	12.05	66.92	116.65
4.	Fruit length (cm)	239.52**	14.81	1.31	1.43	0.12	91	25.45	26.64	7.87	2.25	50.08
5.	Fruit width (cm)	246.33**	18.88	1.33	1.49	0.16	89	28.43	30.08	9.83	2.25	55.35
6.	Number of locules	175.28**	10.50	0.96	1.04	0.08	91	32.20	33.66	9.80	1.93	63.46
7.	Pericarp thickness (cm)	3.93**	0.88	0.01	0.02	0.007	72	31.39	36.88	19.41	0.24	55.04
8.	TSS (Brix)	148.09**	23.82	0.76	0.97	0.20	79	17.44	19.60	8.93	1.60	31.98
9.	Yield (kg/ plant)	34.87**	2.12	0.19	0.20	0.01	91	58.71	61.41	18.01	0.86	115.63
10.	Plant height (cm)	351500**	20713	1927.36	2102.90	175.53	91	46.90	48.98	14.15	86.58	92.49
11.	ToLCD (%)	199838**	6407	1110.93	1165.22	54.29	95	94.82	97.11	20.96	67.04	190.73
12.	Lycopene (mg/100 g FW)	229.45**	30.92	1.20	1.47	0.26	82	53.25	58.73	24.79	2.05	99.45
13.	β -Carotene (mg/100 g FW)	202.403**	30.03	1.05	1.31	0.25	80	51.63	57.50	25.31	1.90	95.51
14.	Titrable acidity (%)	0.76**	0.42	0.003	0.006	0.003	46	18.52	27.23	19.86	0.07	25.95
15.	pH	10.04**	0.71	0.05	0.06	0.006	90	5.41	5.70	1.79	0.45	10.59

SS: sum of the square of genotype, SSE: sum of the square of error, σ^2g : genotypic variance, σ^2p : phenotypic variance, σ^2e : environmental variance, h^2b : heritability, GCV: genotypic coefficient of variation, PCV: phenotypic coefficient of variation, ECV: environmental coefficient of variation, GA: genetic advance; ** highly significant ($p < 0.01$).

Genetic variability parameters

The findings indicated significant genetic diversity among the tomato genotypes for the majority of traits examined (Table 2). The genotypic and phenotypic variances were found to be substantial for traits such as days to first harvest, days to last harvest, average fruit weight, plant height, and

ToLCD, while the remaining traits exhibited low variances. In general, the genotypic variance was smaller than the phenotypic variance for most characteristics. Likewise, the GCV and PCV were high for most traits including days to first harvest, average fruit weight, fruit length, fruit width, number of locules, pericarp thickness, TSS, yield, plant

height, ToLCD, lycopene, β -carotene, and titrable acidity, with the exception of two traits (days to last harvest and pH) that received low values. Overall, GCV was found to be less than PCV for all traits assessed. The broad-sense heritability varied from 46% (titrable acidity) to 95% (either average fruit weight or ToLCD), with most traits exhibiting high heritability (> 60%), apart from titrable acidity, which showed medium heritability. The genetic advance expressed as a percentage of the mean ranged from 10.59 (pH) to 190.93 (ToLCD). These were categorized as low (< 10%), moderate (10-20%), and high (> 20%) (Table 2). Most traits displayed both high heritability and high genetic advance as a percent of the mean, suggesting the presence of additive gene action, which is crucial for effective breeding selection methods.

The majority of traits demonstrated very high GCV, PCV, broad-sense heritability (h^2_b), and genetic advance, which are essential for successful breeding. In line with our results, previous research has reported high GCV, PCV, heritability, and genetic advance for traits such as the number of fruits per plant, height of the plant, and weight of the fruit (Kumar et al., 2013). It is indeed true that both parents and hybrids are chosen based on these genetic variability parameters (GCV, PCV, h^2 , and genetic advance) (Rasheed et al., 2023; Hussain et al., 2024). High heritability and substantial genetic advance are crucial elements for enhancing traits via hybridization and efficient selection techniques in tomato breeding (Ene et al., 2022). Therefore, our research suggests that genetic variability parameters are fundamental in selecting parents and prioritizing traits in tomato breeding programs.

Genetic diversity

The analysis of genetic diversity classified 60 genotypes into four primary clusters (I-IV) through Hierarchical clustering analysis utilizing the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) method (Fig. 1). Cluster I (46) and Cluster II (12) were subsequently separated into two sub-clusters each (Ia/Ila and Ib/Ilb), respectively. Cluster Ia comprised 30 genotypes (WVC: 13 + USA: 17), whereas cluster Ib contained 16 genotypes (WVC: 3 + USA: 13). Cluster Ila included 10 (WVC: 6 + USA: 4) genotypes, while Ilb had only 2 genotypes (LA1421 and LA1162) from the USA. Similarly, clusters III (LA3911) and IV (LA2086) each had a single genotype. Therefore, a considerable diversity was noted among the exotic collections for the selection of varied parental lines, which may be utilized in breeding to produce new crosses with significant heterosis.

Genetic diversity is one of the most essential elements in a breeding program for selecting varied parents for crossing to produce significant heterosis. The mixing of diverse genotypes facilitates advantageous allelic combinations due to extensive genetic variation (Javed et al., 2022). In our research, we noted a considerable amount of genetic diversity among the genotypes. Zannat et al. (2023) indicated a strong genetic divergence and elevated heterosis in tomatoes. Therefore, our research indicates that utilizing genetic diversity is crucial for creating variability aimed at attaining high yield.

PCA and correlation analysis

Genotypes were additionally represented in PCA plots. A total of 76.56% of variability was captured in the first

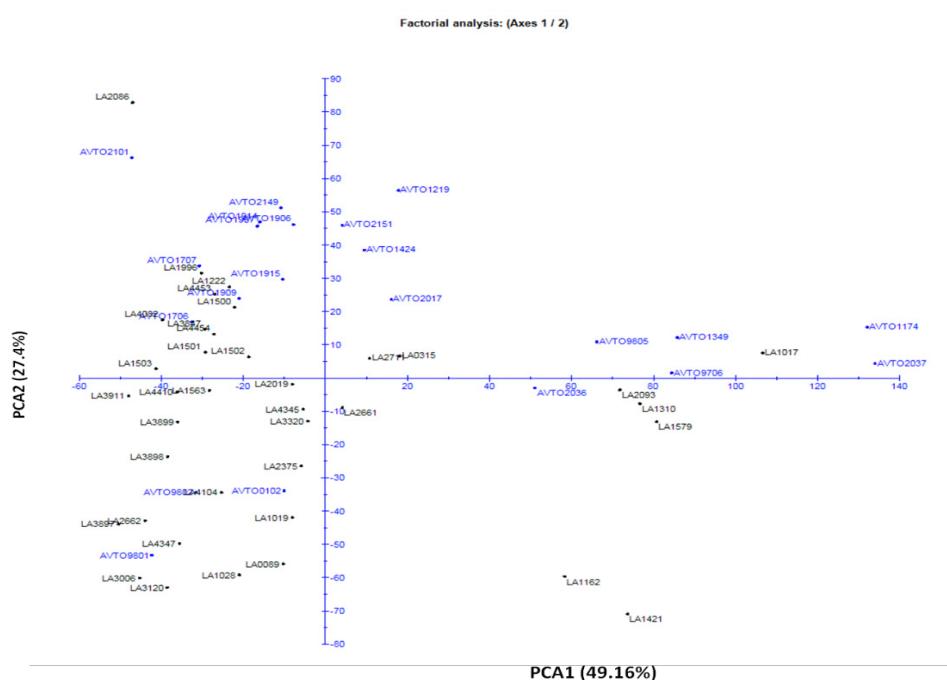


Fig. 2: The Principal Component Analysis (PCA) explaining the first component PCA1 (49.16%) explaining higher variability than the second component PCA2 (27.4%) and distribution of all 60 tomato genotypes into PCA components using the DARwin 6.0.11

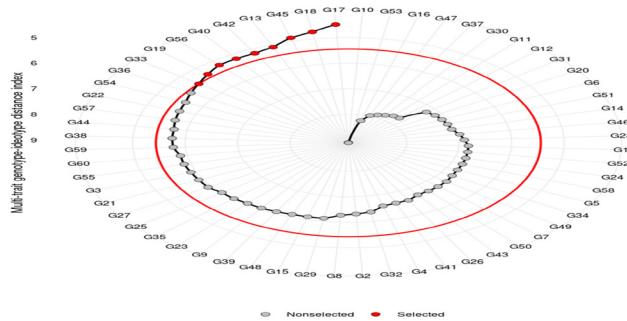


Fig. 3: The multi-trait genotype-ideotype distance index (MGIDI) views of the 60 tomato genotypes (G1-G60) using the default parameters of “metan” package of the R software (Scaling = 1, Centering = 2, SVP = 2). Red colour circles indicate selected genotypes, whereas grey colour for non-selected one.



Fig. 4: Tomato fruits of some selected genotypes identified in this study.

Table 3: Correlation studies in traits studied in tomato genotypes

Trait	DFH	DLH	FWt	FL	FWd	Loc	PT	TSS	YL	PHt	ToLCD	Lyco	Caro	TA	pH
DFH	1 **	0.59**	0.22**	0.12**	0.21**	0.26**	0.27*	0.26*	-0.27**	-0.10**	0.26**	-0.53**	-0.44**	0.15	-0.22*
DLH	0.59**	1 **	-0.08	-0.15	-0.12	0.03	0.11	0.44**	-0.26**	0.09*	0.32 **	-0.39**	-0.29*	0.16*	-0.25*
FWt	0.22**	-0.08	1 **	0.66**	0.95**	0.67**	0.62**	-0.31**	0.48**	-0.21**	-0.13	-0.05	-0.15*	-0.35**	0.27**
FL	0.12**	-0.15	0.66**	1 **	0.57**	0.31**	0.56**	-0.50**	0.31**	-0.32 **	0.15	0.15	0.03	-0.54**	0.37**
FWd	0.21**	-0.12	0.95**	0.57**	1 **	0.73 **	0.61**	-0.30**	0.49**	-0.16**	-0.11	-0.11	-0.19*	-0.33**	0.25**
Loc	0.26 **	0.03	0.67**	0.31**	0.73**	1 **	0.37**	-0.07	0.22	-0.09*	-0.17	-0.17**	-0.25**	-0.17	0.14
PT	0.27*	0.11	0.62**	0.56**	0.61**	0.37**	1 **	-0.17**	0.25 **	-0.29**	0.13	-0.02	-0.11	-0.18	0.19**
TSS	0.26 *	0.44**	-0.31**	-0.50**	-0.30**	-0.07	-0.17**	1 **	-0.28**	0.40**	0.17	-0.29*	-0.15	0.31**	-0.21*
YL	-0.27**	-0.26**	0.48**	0.31**	0.49**	0.22	0.25**	-0.28**	1 **	0.17	-0.37 **	0.30**	0.19*	-0.31**	0.30**
PHt	-0.10**	0.09*	-0.21**	-0.32**	-0.16**	-0.09*	-0.29**	0.40**	0.17	1 **	-0.20**	0.12	0.18*	-0.0	0.08
ToLCD	0.26**	0.32**	-0.13	-0.15	-0.11	-0.17	0.13	0.17	-0.37 **	-0.20**	1 **	-0.18	-0.16	0.30**	-0.42**
Lyco	-0.53**	-0.39**	-0.05	0.15	-0.11	-0.17**	-0.02	-0.29*	0.30 **	0.12	-0.18	1 **	0.76**	-0.23*	0.30**
Caro	-0.44**	-0.29*	-0.15*	0.03	-0.19*	-0.25**	-0.11	-0.15	0.19 *	0.18*	-0.16	0.76**	1 **	-0.11	0.26*
TA	0.15NS	0.16*	-0.35**	-0.54**	-0.33**	-0.17	-0.18	0.31**	-0.31**	-0.0	0.30**	-0.23*	-0.11	1 **	-0.40**
pH	-0.22*	-0.25*	0.27**	0.37**	0.25**	0.14	0.19**	-0.21*	0.30**	0.08	-0.42**	0.30**	0.26*	-0.40**	1 **

Abbreviations: DFH (days to 1st harvest), DLH (days to last harvest), FWt (average per fruit weight (g)), FL (fruit length (cm)), FWd (fruit width (cm)), Loc (number of locules), PT (pericarp thickness (cm)), TSS (total soluble solids (°Brix)), YL (yield (kg/plant)), PHt (plant height (cm)), ToLCD (tomato (yellow) leaf curl viral disease (%)), Lyco (lycopene (mg/100 g)), Caro (β-carotene (mg/100 g)), TA (titrable acidity (%)), and pH. Correlation co-efficient ranges between -1 (negative) to 1 (positive). Statistical significance indicates: * ($p < 0.05$) and ** ($p < 0.01$). Dark grey colour shows Correlation co-efficient: 1.

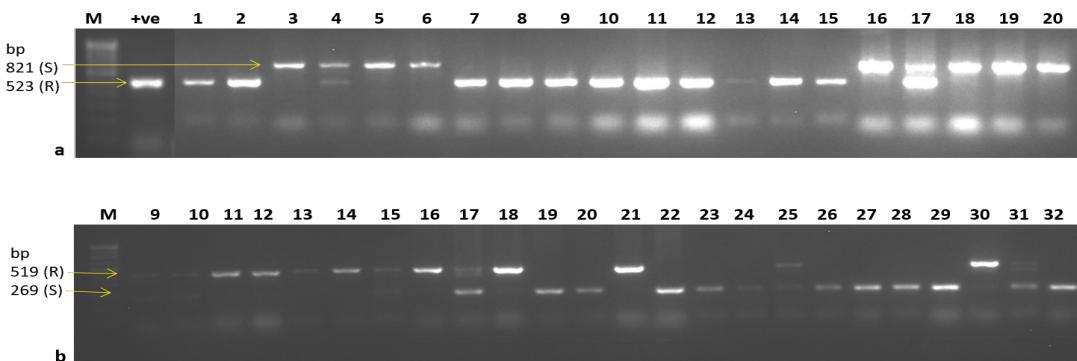


Fig. 5: Identification of host resistance genes in selected samples using gene-specific molecular markers for tomato leaf curl disease (ToLCD) resistance genes a) Ty-2 (resistant: 523 bp, susceptible: 821 bp), and b) Ty-3 (resistant: 519 bp, susceptible: 269 bp). M = StepUp 100 bp DNA ladder (GeNeiTm). Samples #1. AVTO1219, 2. AVTO1424, 3. AVTO2017, 4. AVTO2101, 5. AVTO9801, 6. AVTO9802, 7. AVTO1707, 8. AVTO1906, 9. AVTO1907, 10. AVTO2149, 11. AVTO2151, 12. AVTO1706, 13. AVTO1909, 14. AVTO1914, 15. AVTO1915, 16. AVTO1349, 17. AVTO2036, 18. AVTO2037, 19. AVTO9805, 20. AVTO0102, 21. AVTO1174, 22. AVTO9706, 23. LA0089, 24. LA0315, 25. LA1017, 26. LA1019, 27. LA1028, 28. LA1162, 29. LA1222, 30. LA1310, 31. LA1421, and 32. LA1500.

Table 4: Screening of tomato genotypes for ToLCD under field conditions and identification of host resistance genes using molecular markers

Sample Code	Genotypes	Tomato leaf curl disease infection (%)			DNA marker assay		
		2023-24	2024-25	Mean	Class	Ty-2 gene	Ty-3 gene
G1	AVTO0102	90.50	95.00	92.75	HS	-	-
G2	AVTO1174	0.00	0.00	0.00	HR	+	+
G3	AVTO1219	0.00	0.00	0.00	HR	+	+
G4	AVTO1349	0.00	20.00	10.00	R	-	+
G5	AVTO1424	0.00	0.00	0.00	HR	+	+
G6	AVTO1706	25.35	5.50	15.43	MR	+	+
G7	AVTO1707	0.00	40.00	20.00	MR	+	+
G8	AVTO1906	0.00	0.00	0.00	HR	+	NA
G9	AVTO1907	0.00	0.00	0.00	HR	+	Hetero
G10	AVTO1909	0.00	0.00	0.00	HR	+	Hetero
G11	AVTO1914	10.54	15.55	13.05	R	+	Hetero
G12	AVTO1915	0.00	0.00	0.00	HR	+	Hetero
G13	AVTO2017	50.55	5.50	28.03	MS	-	-
G14	AVTO2036	20.85	90.59	55.72	MS	Hetero	Hetero
G15	AVTO2037	10.25	20.50	15.38	MR	-	+
G16	AVTO2101	0.00	9.50	4.75	HR	Hetero	-
G17	AVTO2149	0.00	2.50	1.25	HR	+	Hetero
G18	AVTO2151	5.50	50.50	28.00	MR	+	+
G19	AVTO9706	20.50	90.50	55.50	MS	-	-
G20	AVTO9801	90.50	80.50	85.50	HS	-	+
G21	AVTO9802	90.50	100.00	95.25	HS	-	-
G22	AVTO9805	0.00	100.00	50.00	MS	-	-
G23	LA0089	90.32	50.45	70.39	HS	-	-
G24	LA0315	20.42	98.50	59.46	MS	NA	-
G25	LA1017	0.00	0.00	0.00	HR	+	Hetero
G26	LA1019	80.67	75.52	78.10	HS	-	-
G27	LA1028	90.54	95.35	92.95	HS	-	-
G28	LA1162	90.52	75.25	82.89	HS	-	-
G29	LA1222	10.50	95.25	52.88	MS	-	-
G30	LA1310	20.50	35.50	28.00	MS	-	+
G31	LA1421	95.50	100.00	97.75	HS	-	Hetero
G32	LA1500	30.50	100.00	65.25	S	-	-
G33	LA1501	50.50	100.00	75.25	S	-	-
G34	LA1502	40.50	100.00	70.25	S	-	-
G35	LA1503	50.50	100.00	75.25	S	-	-
G36	LA1563	90.50	100.00	95.25	S	-	-
G37	LA1579	25.50	50.00	37.75	MS	NA	-
G38	LA1996	35.50	100.00	67.75	S	-	-

G39	LA2019	50.50	80.43	65.47	MS	-	-
G40	LA2086	20.60	95.37	57.99	MS	-	-
G41	LA2093	10.25	20.45	15.35	R	-	-
G42	LA2375	70.57	100.00	85.29	S	-	-
G43	LA2661	30.48	100.00	65.24	S	-	-
G44	LA2662	95.67	93.69	94.68	HS	-	Hetero
G45	LA2711	82.31	100.00	91.16	HS	NA	-
G46	LA3006	90.50	100.00	95.25	HS	NA	-
G47	LA3120	95.50	100.00	97.75	HS	-	-
G48	LA3320	95.70	90.50	93.10	HS	-	-
G49	LA3847	40.50	95.50	68.00	S	-	-
G50	LA3897	90.50	100.00	95.25	HS	NA	-
G51	LA3898	60.50	100.00	80.25	HS	Hetero	-
G52	LA3899	60.50	60.50	60.50	MS	NA	-
G53	LA3911	5.50	0.00	2.75	HR	Hetero	-
G54	LA4082	20.50	80.50	50.50	MS	Hetero	-
G55	LA4104	85.50	100.00	92.75	HS	Hetero	Hetero
G56	LA4345	30.50	90.50	60.50	S	NA	-
G57	LA4347	100.00	75.50	87.75	HS	Hetero	NA
G58	LA4410	50.50	100.00	75.25	HS	Hetero	-
G59	LA4453	10.50	10.80	10.65	R	Hetero	-
G60	LA4454	5.50	21.50	13.50	MR	NA	-
Punjab Chhuhara (Suscept. control)		98	98.00	100.00	99.00	HS	
Kashi Chayan (Resistant control)		0	0.00	0.00	0.00	HR	
Mean		40.69	61.49	51.25			
CD (p < 0.05)		4.87	4.99	4.72			
CV (%)		6.78	9.69	8.24			

Symbols indicate: Resistant (+), Susceptible (-), Hetero = both (+/-) bands, N/A: No amplification. Resistant (+) reflects homozygous condition of both dominant alleles (AA) of the gene showing single band amplification. Whereas, 'Hetero' term indicates heterozygous (Aa) condition of the alleles showing two bands (one each for resistant and susceptible). Resistance gene for ToLCD: Ty-2 (R: 523 bp, S: 821 bp); Ty-3 (R: 519 bp, S: 269 bp). ToLCD scale is mentioned above.

two PCA components, namely PCA1 (49.16%; Eigenvalue: 2215.20) and PCA2 (27.4%; Eigenvalue: 1234.36) (Fig. 2). PCA1 revealed greater variability compared to PCA2. PCA1 contained 12 high-performing genotypes (such as AVTO1174, AVTO1219, AVTO1349, AVTO1424, AVTO2017, AVTO2037, AVTO2151, AVTO9706, AVTO9805, LA1017, LA2711, and LA3015), whereas PCA2 included 20 genotypes. In general, high-performing genotypes sourced from the WVC, Taiwan, were located on the positive side of the PCA1/PCA2 axes. PCA reflects the relevant variables and suitable traits into various components (Akinyode, 2023), which are useful in breeding programs. The correlation analysis identified relationships among the various traits examined in the study. Traits including average fruit weight, fruit length,

fruit width, pericarp thickness, lycopene, and pH showed highly significant positive correlations with yield (Table 3). Average fruit weight exhibited a strong link with fruit length, fruit width, number of locules, pericarp thickness, and yield. Moreover, TSS content exhibited a positive correlation with plant height and titratable acidity, while lycopene content was positively associated with β -carotene content. In line with our observations, Zannat et al. (2023) mentioned that traits such as the number of fruits per plant, fruit diameter, and fruit weight demonstrated strong positive relationships with fruit yield. Thus, notable and positive correlations were found among various traits that contribute to yield in tomatoes, which will aid in choosing breeding parents and prioritizing traits in tomato breeding.

Selection of tomato genotypes through MGIDI analysis

The MGIDI analysis revealed nine potential genotypes: AVTO2149 (G17), AVTO2151 (G18), LA2711 (G45), AVTO2017 (G13), LA2375 (G42), LA2086 (G40), LA4345 (G56), AVTO9706 (G19), and LA1501 (G33) utilizing the standard parameters of the «metan» package in R software, based on 15 traits (Fig. 3) for future application in breeding (Olivoto and Nardino, 2021). A total of four factors were identified in the MGIDI analysis, with the 15 traits contributing to various factors: FA1 included average fruit weight, fruit length, fruit width, and pericarp thickness; FA2 involved days to first harvest, number of locules, lycopene, and β -carotene; FA3 encompassed yield, ToLCD, titrable acidity, and pH; and FA4 consisted of days to last harvest, TSS, and plant height. Selected genotypes are displayed in Fig. 4.

ToLCD resistance under field conditions

Over two years of field evaluation, 11 genotypes demonstrated high resistance to ToLCD, showing either no or minimal infestation (HR: 0–5%) in contrast to control varieties like Punjab Chhuhara (HS: 99.33%) and Kashi Chayan (HR: 0%) (Table 4). Eleven highly resistant accessions included AVTO1174, AVTO1219, AVTO1424, AVTO1906, AVTO1907, AVTO1909, AVTO1915, AVTO2101, AVTO2149, LA1017, and LA3911. Additionally, four genotypes (AVTO1349, AVTO1914, LA2093, and LA4453) were classified as resistant (R: 5.1–12%), while five genotypes (AVTO1706, AVTO1707, AVTO2037, AVTO2151, and LA4454) were categorized as moderately resistant (MR: 12.1–25%). Besides, 12 were moderately susceptible (MS: 25.1–50%), 10 were susceptible (S: 50.1–75%), and 18 were highly susceptible (HS: 75.1–100%) category (Table 4).

Molecular markers analysis for ToLCD resistance genes

A total of 60 tomato genotypes were examined for the presence of ToLCD host resistance genes (*Ty-2* and *Ty-3*) using gene-specific molecular markers. The investigation into ToLCD resistance revealed that 13 accessions had a specific band for the *Ty-2* resistance gene (523 bp) (resistant: 523 bp, susceptible: 821 bp), while 10 accessions displayed the *Ty-3* resistance gene-specific band (519 bp) (resistant: 519 bp, susceptible: 269 bp) (Table 4). Selected samples that amplified the *Ty-2* and *Ty-3* genes are illustrated in Fig. 5. Additionally, heterozygous forms, showing both resistant and susceptible bands for *Ty-2* and *Ty-3* genes, were identified in 8 and 10 accessions, respectively (Table 3). Genotypes AVTO1174 (HR), AVTO1219 (HR), AVTO1424 (HR), AVTO1707 (MR), and AVTO2151 (MR) exhibited homozygous conditions (*TyTy*) with a single band amplification and were classified as HR or MR to ToLCD. However, some genotypes presented a heterozygous condition (*Ttyt*) with both resistant (*Ty*) and susceptible (*ty*) bands. It will be important

to further improve these heterozygous genotypes through single plant selection. Notably, certain genotypes like AVTO2101 and AVTO9805 displayed HR but did not show any amplification for the *Ty-2/Ty-3* genes. Genotypes AVTO1349, AVTO1909, AVTO1914, AVTO1915, AVTO2037, AVTO2149, AVTO2151, AVTO9805, and LA2093 amplified gene-specific markers for *Ty-2* or *Ty-3* while also showing field resistance (HR/R) to ToLCD. In summary, ToLCD-resistant genotypes (HR: 16, R: 6, MR: 11) were selected based on field trials, and a few showed correlations with marker-assisted selection as well. Consequently, this study has identified a significant number of genotypes, AVTO1174, AVTO1219, AVTO1424, AVTO1707, and AVTO2151, which showed both *Ty-2* and *Ty-3* gene-specific bands and ToLCD resistance under natural field conditions for future breeding programs.

Numerous studies demonstrate that ToLCD significantly harms the yield and quality of tomato fruits (Yan et al., 2021). Comparable research has been conducted on tomato resistance to ToLCD through both traditional and molecular breeding methods (Pozharskiy et al., 2022; Yerasu et al., 2025). The strategy of gene pyramiding in tomatoes has been employed to enhance resistance against ToLCV, along with other challenges such as late blight and root knot nematodes, resulting in lines that possess multiple resistances to diseases and pests (Kumar et al., 2019). In summary, our research highlights genetic resources suitable for breeding ToLCV resistance using marker-assisted selection (MAS).

Conclusion

To conclude, various exotic tomato lines were assessed for horticultural traits such as yield components, processing quality, and resistance to ToLCD. Significant genetic variation was observed in the studied genotypes. The MGIDI analysis revealed nine promising genotypes AVTO2149, AVTO2151, LA2711, AVTO2017, LA2375, LA2086, LA4345, AVTO9706, and LA1501 based on all above traits. Additionally, the genotypes with resistance to ToLCD, namely AVTO1174, AVTO1219, AVTO1424, AVTO1707, and AVTO2151 having both *Ty-2* and *Ty-3* genes, making them suitable candidates for parent lines in a resistance breeding program. Further, it will be essential to characterize these genotypes against additional biotic and abiotic stresses to determine stable genotypes across various environments in the future.

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सारांश

इस अध्ययन का उद्देश्य प्रजनन कार्यक्रमों में पैतृक सामग्री के रूप में उपयोग हेतु श्रेष्ठ वंशक्रमों की पहचान हेतु 60 नव-अधिग्रहित विदेशी जीनोटाइपों का अभिलक्षण करना था। उपज घटकों, प्रसंस्करण लक्षणों और टमाटर पत्ती मरोड़ रोग (ToLCD) के प्रति प्रतिरोध के लिए 2023-25 के दौरान क्षेत्रीय परिस्थितियों में जीनोटाइपों का मूल्यांकन किया गया। ToLCD प्रतिरोधी जीन Ty-2 और Ty-3 का पता लगाने के लिए जीन-विशिष्ट डोएनए मार्करों का उपयोग किया गया। मूल्यांकित लक्षणों के लिए जीनोटाइपों में पर्याप्त आनुवंशिक भिन्नता देखी गई। जीनोटाइपिक भिन्नता गुणांक (GCV) 5.41 से 94.82% तक था, जो कि फेनोटाइपिक भिन्नता गुणांक (PCV) से कम था, जो 5.70 से 97.11% तक था। उच्च आनुवंशिकता मान (> 60%) और माध्य के प्रतिशत के रूप में उच्च आनुवंशिक प्रगति (> 20%) यह दर्शाते हैं कि योगात्मक जीन क्रिया इसके लिए उत्तरदायी है, जो चयन की प्रभावशीलता का समर्थन करती है। अंकगणितीय माध्य (UPGMA) के साथ भारतीन युग्म समूह विभि का उपयोग करते हुए पदानुक्रमित क्लस्टरिंग ने जीनोटाइप को चार समूहों (I-IV) में वर्गीकृत किया, जिससे संयुक्त राज्य अमेरिका और ताइवान के जीनोटाइप के बीच स्पष्ट भिन्नता का पता चला। प्रमुख घटक विश्लेषण (PCA) ने कुल 76.56% भिन्नता की व्याख्या की, जिसमें पहले और दूसरे प्रमुख घटक क्रमशः 49.16% और 27.40% के लिए जिम्मेदार थे। ToLCD प्रतिरोध के लिए क्षेत्र परख ने 11 जीनोटाइप को अत्यधिक प्रतिरोधी (HR), 4 को प्रतिरोधी (R), 5 को मध्यम प्रतिरोधी (MR), और शेष 40 जीनोटाइप को मध्यम रूप से अतिसंवेदनशील से लेकर अत्यधिक अतिसंवेदनशील के रूप में पहचाना। जीनोटाइप AVTO1174, AVTO1219, AVTO1424, AVTO1707, और AVTO2151 में समयुग्मजी रूप में Ty-2 और Ty-3 दोनों जीन मौजूद थे और ToLCD के लिए क्षेत्र प्रतिरोध प्रदर्शित किया। निम्नलिखित जीनोटाइप AVTO1174, AVTO1219, AVTO1424, AVTO2101, AVTO1906, AVTO1907, AVTO2149, AVTO2151, AVTO1909, और AVTO1915 को उन्नत प्रजनन कार्यक्रमों के लिए पैतृक वंश के रूप में अनुशंसित किया जाता है।