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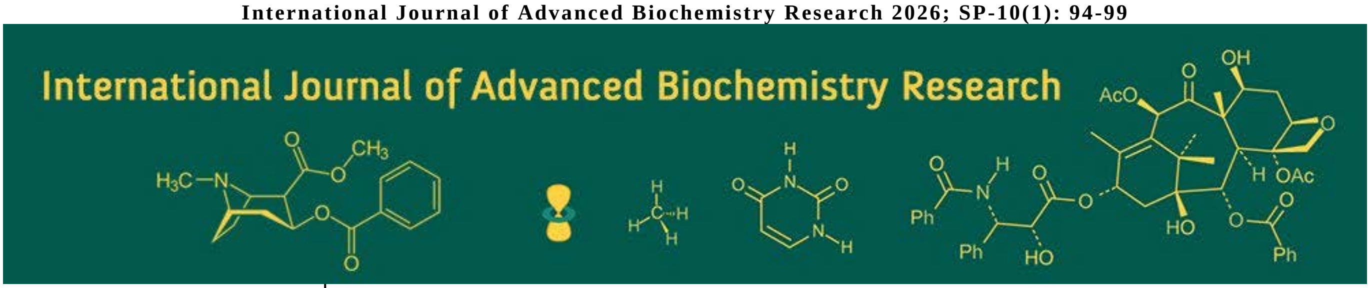

# Genetic variability for Tomato Leaf Curl Virus resistance and yield response in tomato (*Solanum lycopersicum* L.) under natural epiphytotic conditions

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## Abstract

Tomato Leaf Curl Virus (TLCV) is one of the most destructive viral diseases of tomato, causing severe yield losses in tropical and subtropical regions. The present study was undertaken to screen tomato genotypes for resistance to TLCV and to assess the impact of disease severity on yield under natural field conditions. A total of 74 tomato genotypes, comprising advanced breeding lines and hybrids, were evaluated during Kharif 2023 at ICAR-Indian Agricultural Research Institute, New Delhi, following a randomized block design with three replications. Disease reaction was assessed under natural epiphytotic conditions based on disease incidence (%) and percent disease index (PDI), while yield-related traits such as number of fruits per plant, yield per plant, and average fruit weight were recorded at maturity. Considerable variability was observed among genotypes for both TLCV incidence and disease severity. Disease incidence ranged from 0 to 74%, while PDI varied from 0.00 to 50.00, indicating substantial genetic diversity for resistance. A majority of genotypes exhibited zero or negligible disease incidence and low PDI, confirming predominance of resistant genotypes. Frequency distribution analysis revealed a highly skewed distribution towards resistant classes, whereas scatter plot analysis indicated a positive association between disease incidence and severity. Several genotypes exhibited complete resistance along with stable yield performance. The identified resistant genotypes represent valuable genetic resources for direct cultivation in TLCV-prone areas and for use as donor parents in tomato resistance breeding programmes.

**Keywords:** Tomato; Tomato Leaf Curl Virus; disease resistance; percent disease index; yield performance

## Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most economically important vegetable crops worldwide due to its high nutritional value and extensive use in fresh consumption and processing industries. In India, tomato productivity is significantly constrained by several biotic stresses, among which Tomato Leaf Curl Virus (TLCV) is considered one of the most destructive, causing substantial yield losses (Saikia and Muniyappa, 1989; Moriones and Navas-Castillo, 2000; Hanssen *et al.*, 2010) [1, 2, 3]. TLCV, a member of the genus *Begomovirus* (family *Geminiviridae*), is transmitted by the whitefly (*Bemisia tabaci*) and induces characteristic symptoms such as leaf curling, vein thickening, reduced leaf size, stunted growth, and poor fruit set. Early-stage infection can result in severe yield losses, whereas late infection adversely affects fruit size and quality, with reported yield reductions ranging from 30 to 90% depending on genotype susceptibility and stage of infection (Czosnek and Laterrot, 1997; Lapidot and Friedmann, 2002; Navas-Castillo *et al.*, 2011) [4, 5, 2].

Chemical management of the whitefly vector has proved largely ineffective due to rapid development of insecticide resistance, high cost, and environmental concerns. Consequently, host plant resistance is widely recognized as the most economical, environmentally safe, and sustainable strategy for managing TLCV (Pico *et al.*, 1996; Hanssen *et al.*, 2010; Prasanna *et al.*, 2015) [7, 3, 8]. Identification and utilization of resistant genotypes therefore constitute a major objective of tomato improvement programmes. However, resistance alone does not ensure varietal adoption, as resistant genotypes may exhibit inferior yield or undesirable agronomic traits. Hence, simultaneous evaluation of TLCV resistance along with yield and yield-related traits is essential to identify genotypes combining stable resistance with acceptable productivity (Lapidot *et al*., 2006; Vidavski *et al*., 2008) [9, 10].

Field-based screening under natural epiphytotic conditions provides reliable information on disease reaction and yield stability across diverse genotypes. In view of these considerations, the present investigation was undertaken to screen tomato genotypes for resistance to TLCV, to classify genotypes based on disease incidence and severity, to assess the impact of TLCV on yield performance, and to identify promising genotypes suitable for cultivation and resistance breeding programmes.

## Materials and Method

The present investigation was conducted to evaluate tomato genotypes for resistance to Tomato Leaf Curl Virus (TLCV) under open field conditions. A total of 74 tomato genotypes, comprising advanced breeding lines and hybrids, were evaluated during the Kharif -2023 at IARI-New Delhi.

### Experimental design

The experiment was laid out in a Randomized Block Design (RBD) with three replications. No insecticides were applied for whitefly control to ensure natural epiphytotic development of TLCV.

### Assessment of Tomato Leaf Curl Virus (TLCV)

Disease observations were recorded under natural field conditions at the stage of peak symptom expression. TLCV infection was identified based on typical symptoms such as upward curling of leaves, vein thickening, reduction in leaf size, and stunted plant growth.

### Disease incidence (%)

Disease incidence was calculated using the following formula:

Disease incidence (%) = Number of infected plants/ Total number of plants observed × 100

### Percent Disease Index (PDI)

Disease severity was assessed using a standard disease rating scale, and Percent Disease Index (PDI) was calculated to quantify the intensity of TLCV infection.

**Table 1:** Based on PDI values, genotypes were categorized as:

| Category | Range |
|---|---|
| Resistant (R) | 0-5% |
| Moderately resistant (MR) | 5.1-20% |
| Susceptible (S) | >20% |

### Recording of yield parameters

At crop maturity, yield-related traits were recorded from each genotype in all replications. The parameters included:

- Number of fruits per plant
- Yield per plant (kg)
- Average fruit weight (g)

Mean values were computed using data obtained from three replications to ensure accuracy and reliability. Yield-related traits were subjected to analysis of variance (ANOVA) to test the significance of differences among genotypes. Correlation analysis was performed to determine the association between percent disease index (PDI) and yield per plant.

### Statistical analysis

The experimental data were subjected to statistical analysis to assess variability among genotypes for TLCV resistance and yield-related traits. Mean performance of genotypes was calculated, and descriptive statistical parameters were used to interpret disease incidence, disease severity, and yield variation. Frequency distribution and graphical analyses were employed to visualize the distribution pattern of TLCV incidence and PDI among genotypes.

## Results

A total of 74 tomato genotypes were evaluated for their reaction to Tomato Leaf Curl Virus (TLCV) under natural epiphytotic field conditions using disease incidence (%) and percent disease index (PDI). The genotypes exhibited considerable variability for both parameters, indicating substantial genetic diversity for resistance to TLCV.

### TLCV incidence (%)

TLCV incidence among the evaluated genotypes ranged from 0 to 74%. A large proportion of the genotypes recorded zero disease incidence, indicating a high level of resistance under natural field conditions. More than half of the genotypes remained completely free from infection, confirming the predominance of resistant genetic material.

A few genotypes showed low to moderate incidence (1-25%), while only a limited number of genotypes exhibited high incidence (>25%), indicating susceptibility (Table 1). Genotypes such as K-20 (74%), K-131 (44%), K-38 (32%), K-412 (31%) and K-98 (25%) recorded comparatively higher disease incidence and were categorized as susceptible.

**Table 2:** Classification of tomato genotypes based on reaction to Tomato Leaf Curl Virus

| Disease reaction | TLCV incidence (%) | PDI (%) |
|---|---|---|
| Resistant (R) | 0 | 0-5 |
| Moderately resistant (MR) | 1-25 | 5.1-20 |
| Susceptible (S) | >25 | >20 |

The frequency distribution of TLCV incidence showed a highly skewed pattern towards zero incidence, with most genotypes clustered under the resistant class, confirming effective disease pressure and clear differentiation among genotypes.

**Table 3:** Frequency distribution of tomato genotypes based on TLCV incidence

| Incidence class (%) | Disease reaction |
|---|---|
| 0 | Resistant |
| 1-10 | Highly resistant |
| 10.1-25 | Moderately resistant |
| >25 | Susceptible |

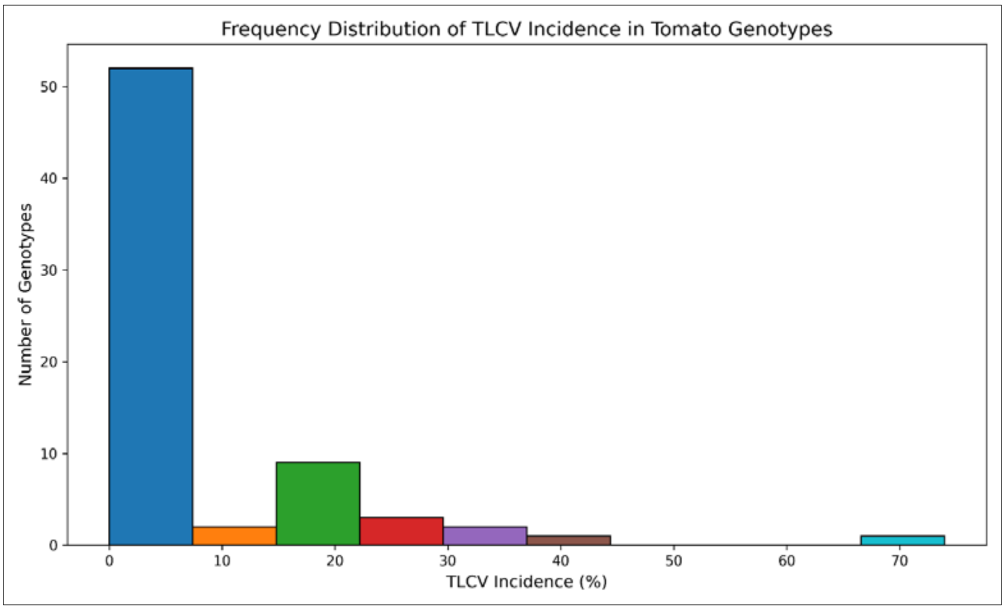

**Fig 1:** Frequency Distribution of Tomato Leaf Curl Virus (TLCV) Incidence in Tomato Genotypes

Fig1. The frequency distribution of TLCV incidence revealed a highly skewed pattern with maximum genotypes falling under zero disease incidence, indicating the predominance of resistant genotypes. A small proportion of genotypes showed moderate to high incidence, confirming sufficient disease pressure under natural epiphytotic conditions.

### Percent Disease Index (PDI)

Percent disease index (PDI) values ranged from 0.00 to 50.00, reflecting wide variation in disease severity among genotypes. The majority of genotypes exhibited negligible disease severity (PDI ≤ 5), indicating strong resistance to TLCV. Several genotypes including K-55, K-54, K-63, K-73, K-125, K-64, K-83, K-192, K-220 and K-516 consistently recorded zero PDI, indicating complete resistance under field conditions. Moderate disease severity (PDI 5.1-20) was observed in a few genotypes such as K-61, K-70, K-132, K-69 and K-46. Severe disease expression (PDI > 20) was recorded only in a limited number of genotypes. The genotype H-81 recorded the highest disease severity with a PDI of 50.00, followed by K-51 and K-61 (19.35), indicating high susceptibility.

**Table 4:** Descriptive statistics for TLCV incidence and percent disease index (PDI)

| Parameter | Minimum | Maximum | Range | Distribution pattern |
|---|---|---|---|---|
| TLCV incidence (%) | 0 | 74 | 74 | Highly skewed |
| Percent disease index (PDI) | 0.00 | 50.00 | 50.00 | Right skewed |

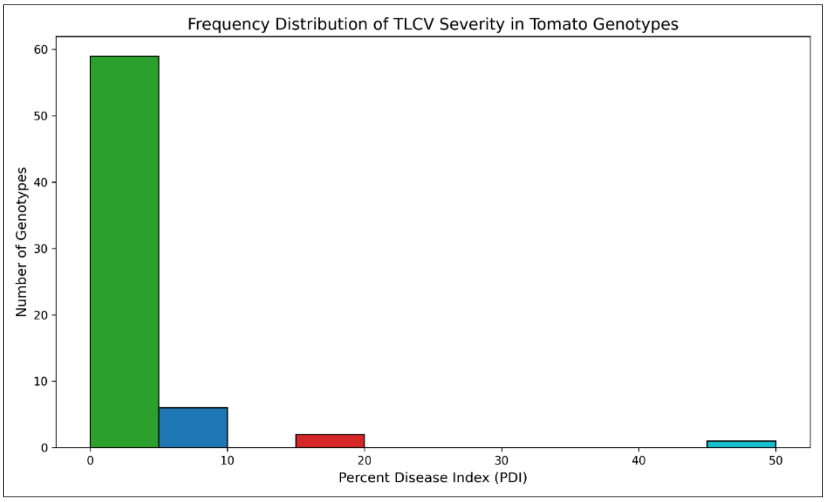

Fig 2: Frequency Distribution of Tomato Leaf Curl Virus (TLCV) Severity in Tomato Genotypes (Percent Disease Index, PDI)

Fig 2. The distribution of percent disease index (PDI) showed that most genotypes exhibited negligible to low disease severity, while a few genotypes expressed high PDI values, indicating susceptibility. This wide variation demonstrates substantial genetic diversity for TLCV resistance.

### Relationship between TLCV incidence and disease severity

Scatter plot analysis revealed a positive association between TLCV incidence and percent disease index. Genotypes with higher disease incidence generally showed increased disease severity, whereas genotypes with zero incidence consistently recorded zero PDI. However, some genotypes exhibited moderate incidence but low PDI, suggesting the presence of tolerance or partial resistance mechanisms that restrict disease severity despite infection. This highlights the importance of using both incidence and PDI for accurate disease characterization.

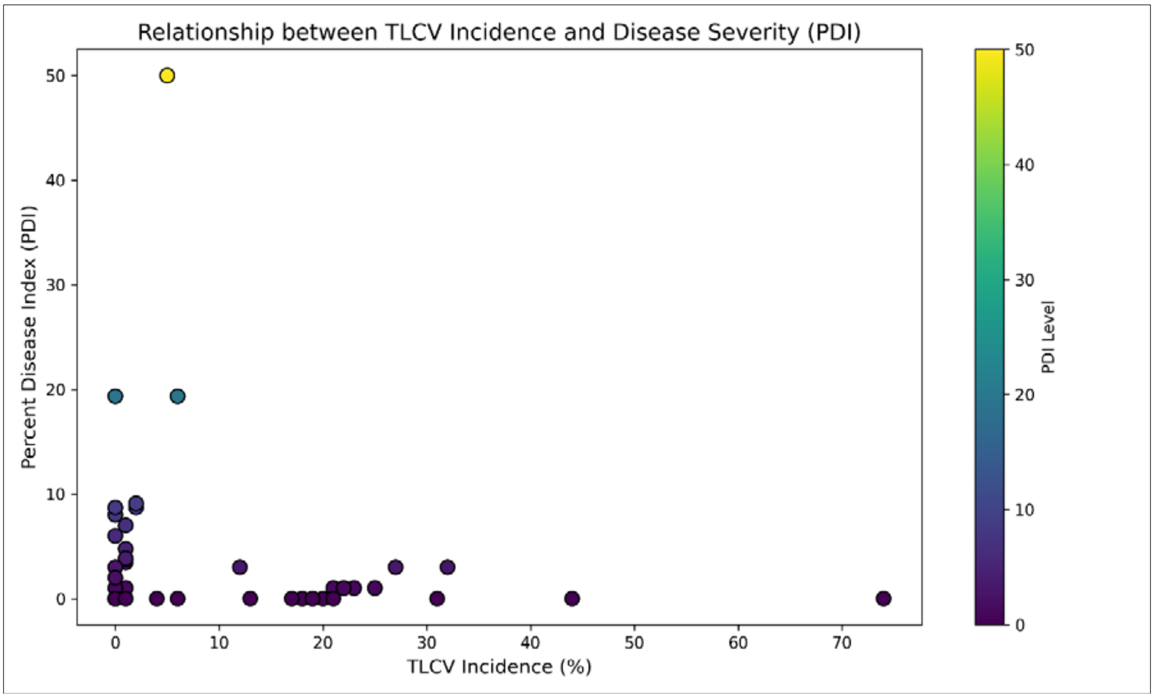

**Fig 3:** Relationship between Tomato Leaf Curl Virus (TLCV) Incidence and Disease Severity (Percent Disease Index, PDI)

Fig 3. Scatter plot analysis revealed a positive relationship between TLCV incidence and percent disease index. However, certain genotypes exhibited lower disease severity despite moderate incidence, suggesting partial resistance or tolerance mechanisms.

Analysis of variance revealed significant differences among tomato genotypes for yield per plant, number of fruits per plant, and average fruit weight, indicating substantial genetic variability for yield-related traits. Genotypes exhibiting low or negligible disease severity generally recorded superior yield performance compared to those with higher disease severity.

Correlation analysis indicated a negative association between percent disease index (PDI) and yield per plant, suggesting that increased TLCV severity resulted in reduced yield. Genotypes with zero or low PDI maintained comparatively higher yield levels, whereas susceptible genotypes showing higher PDI values exhibited noticeable yield reduction.

### Classification of tomato genotypes based on TLCV reaction

Based on disease incidence and percent disease index, the tomato genotypes were classified into resistant, moderately resistant and susceptible categories. A majority of the genotypes were classified as resistant, followed by a smaller proportion of moderately resistant genotypes, while only a few genotypes were categorized as susceptible. The presence of both highly resistant and highly susceptible genotypes validated the effectiveness of natural disease pressure and confirmed the reliability of the screening process.

**Table 5:** Tomato genotypes showing extreme reaction to Tomato Leaf Curl Virus

| Category | Genotypes |
|---|---|
| Highly resistant | K-55, K-54, K-63, K-73, K-125, K-64, K-83, K-192, K-220, K-516 |
| Moderately resistant | K-61, K-70, K-132, K-69, K-46, K-98 |
| Highly susceptible | K-20, K-131, K-38, K-412, H-81 |

The results clearly demonstrated significant variability among tomato genotypes for TLCV resistance. The predominance of resistant genotypes, coupled with the presence of a few highly susceptible genotypes, enabled effective discrimination of disease response. The skewed distribution of disease incidence and PDI towards lower classes confirmed strong resistance in the evaluated germplasm. Genotypes exhibiting zero disease incidence and negligible PDI under natural epiphytotic conditions represent valuable genetic resources and can be directly utilized in TLCV-prone areas or exploited as donor parents in tomato resistance breeding programmes.

## Discussion

The present study revealed substantial variability among tomato genotypes for resistance to Tomato Leaf Curl Virus (TLCV), as evidenced by wide differences in disease incidence and percent disease index (PDI). The predominance of genotypes exhibiting zero or negligible disease expression under natural epiphytotic conditions indicates the availability of strong genetic resistance within the evaluated germplasm. Similar wide variability for TLCV resistance has also been reported earlier in tomato collections evaluated under field conditions (Saikia and Muniyappa, 1989; Lapidot and Friedmann, 2002) [1, 5].

The skewed distribution of disease incidence and PDI towards lower classes suggests that resistance to TLCV is quantitatively inherited and widely distributed among the genotypes. Such skewness towards resistance has been commonly observed in host-virus interaction studies, where multiple minor genes contribute to reduced symptom expression rather than complete immunity (Pico *et al*., 1996; Vidavski *et al*., 2008) [7, 10]. The clustering of most genotypes at zero incidence and low PDI further confirms that the disease pressure was sufficient to discriminate resistant and susceptible reactions, validating the reliability of field screening. A positive association between TLCV incidence and disease severity observed in the present study indicates that increased infection generally results in enhanced symptom expression. However, the occurrence of genotypes showing moderate incidence but low PDI suggests the presence of tolerance or partial resistance mechanisms that restrict symptom development despite infection. Such tolerance has been previously reported in tomato, where virus multiplication occurs without severe physiological damage to the host plant (Lapidot *et al*., 2006) [9].

Genotypes exhibiting complete resistance, characterized by zero disease incidence and negligible PDI, are of particular importance. These entries represent valuable genetic resources that can be directly exploited in TLCV-prone regions or utilized as donor parents in resistance breeding programmes. The use of resistant cultivars is widely regarded as the most economical and environmentally safe strategy for managing TLCV, especially given the limited effectiveness of chemical control against the whitefly vector (*Bemisia tabaci*) (Czosnek and Laterrot, 1997; Hanssen *et al*., 2010) [4, 3]. The significant differences observed among genotypes for yield-related traits further emphasize the presence of genetic variability for productivity. The negative association between disease severity and yield confirms the detrimental impact of TLCV on tomato productivity and highlights the importance of selecting genotypes combining resistance with stable yield performance. The identification of a few highly susceptible genotypes alongside resistant ones further strengthens the conclusions of the study, as the presence of susceptible checks confirms adequate disease pressure during the evaluation. Such contrasting reactions are essential for effective selection and for understanding the genetic basis of resistance (Moriones and Navas-Castillo, 2000) [2].

Overall, the findings of the present investigation highlight the significant potential of host plant resistance in mitigating TLCV-associated yield losses. The resistant genotypes identified in this study can serve as promising candidates for future breeding programmes aimed at developing stable, high-yielding tomato cultivars with durable resistance to Tomato Leaf Curl Virus.

## Conclusion

The present investigation demonstrated substantial genetic variability among tomato genotypes for resistance to Tomato Leaf Curl Virus (TLCV) under natural epiphytotic field conditions. The predominance of genotypes exhibiting zero or negligible disease incidence and low percent disease index (PDI) clearly indicated the presence of strong and stable resistance within the evaluated germplasm. The skewed distribution of disease incidence and severity towards lower classes, along with the clear separation of resistant and susceptible genotypes, confirmed the effectiveness and reliability of field-based screening for TLCV resistance.

Genotypes showing complete resistance, characterized by absence of disease symptoms, represent valuable genetic resources and can be directly recommended for cultivation in TLCV-prone regions. Moreover, these resistant entries hold significant potential as donor parents in tomato breeding programmes aimed at developing high-yielding cultivars with durable resistance to TLCV. The identification of a few highly susceptible genotypes further validated the disease pressure and provided suitable checks for future screening studies. Overall, the findings underscore the importance of host plant resistance as a sustainable and environmentally safe strategy for managing Tomato Leaf Curl Virus in tomato.

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