

Case study

Open Access

Disease-Resistant Tomato Cultivars for High-Quality Production

Weichang Wu ¹, Kaiwen Liang ² ✉

¹ Cuixi Academy of Biotechnology, Zhuji, 311800, Zhejiang, China

² Agri-Products Application Center, Hainan Institute of Tropical Agricultural Resources, Sanya, 572025, Hainan, China

✉ Corresponding author: kaiwen.liang@hitar.org

Bioscience Evidence, 2026, Vol.16, No.2 doi: [10.5376/be.2026.16.0008](https://doi.org/10.5376/be.2026.16.0008)

Received: 07 Feb., 2026

Accepted: 13 Mar., 2026

Published: 05 Apr., 2026

Copyright © 2026 Wu and Liang, This is an open access article published under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Preferred citation for this article:

Wu W.C., and Liang K.W., 2026, Disease-resistant tomato cultivars for high-quality production, Bioscience Evidence, 16(2): 92-103 (doi: [10.5376/be.2026.16.0008](https://doi.org/10.5376/be.2026.16.0008))

Abstract Tomato (*Solanum lycopersicum* L.) is an important economic and nutritional crop worldwide, but its production has long been heavily constrained by various diseases. This study reviews the major types of diseases affecting tomato cultivation, with a focus on the genetic basis of disease resistance in tomato. It summarizes the main strategies currently used in resistance breeding. Through case analysis of typical resistant varieties and multi-resistant hybrids, it further shows that disease resistance, yield stability, and fruit quality can be improved together. The study also highlights the key role of resistant varieties in integrated disease management systems, as well as their potential value in improving postharvest quality and extending shelf life. Finally, in response to challenges such as pathogen evolution, climate change, and emerging diseases, it is suggested that future research should strengthen the integration of multi-omics, intelligent breeding, and high-throughput phenotyping technologies, so as to promote the coordinated development of disease resistance and high-quality tomato production and achieve sustainable agricultural goals.

Keywords Tomato (*Solanum lycopersicum* L.); Disease resistance breeding; Gene pyramiding; Molecular mechanisms; Quality traits

1 Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most widely cultivated and economically important horticultural crops in the world. In recent years, the global planting area has been about 5 million hectares, with total production close to or exceeding 180–190 million tons. As a high-value crop, tomato not only supports the livelihoods of smallholder farmers but also drives large-scale commercial agriculture. It also contributes to a broad processing industry, including sauces, juices, ketchup, and canned products (Akotowanou et al., 2022).

From a nutritional perspective, tomato is widely recognized as an important component of a healthy diet. It is rich in vitamins (especially vitamin C and provitamin A), minerals, dietary fiber, and various bioactive compounds, including carotenoids (particularly lycopene and β -carotene), tocopherols, and phenolic metabolites. Regular consumption of tomatoes and their products can significantly increase dietary levels of carotenoids, lycopene, vitamin C, and polyphenols, which are closely associated with a reduced risk of cardiovascular diseases, certain cancers, and other chronic conditions (Egea et al., 2022).

Despite its importance, tomato production is severely constrained by a wide range of diseases. These diseases are caused by fungi, oomycetes, bacteria, viruses, viroids, and nematodes, and can infect plants at all stages from seedling to postharvest, often leading to serious yield and quality losses. Major diseases include soil-borne diseases such as Fusarium wilt, Verticillium wilt, bacterial wilt, and root-knot nematodes; foliar and fruit diseases such as early blight, late blight, Septoria leaf spot, and gray mold; as well as viral diseases such as tomato yellow leaf curl virus, tomato spotted wilt virus, and tomato brown rugose fruit virus (Adhikari et al., 2017). These pathogens not only reduce yield but also lower market and processing quality by affecting fruit size, color, firmness, and storage ability, while increasing the risk of postharvest decay.

Traditional disease management mainly relies on chemical pesticides and intensive plant protection inputs. However, this approach brings environmental and health risks, increases production costs, and accelerates the development of pathogen resistance to pesticides. At the same time, climate change, soil degradation, and the

expansion of global trade have further intensified and redistributed disease pressure, promoting the spread of new or more aggressive pathogen strains. Under these conditions, the use of host resistance has become one of the key strategies for sustainable tomato production. With the help of molecular markers, genomics, and CRISPR/Cas gene editing technologies, breeding programs are now focusing on developing new varieties that combine durable resistance to major diseases with high yield, early maturity, and good fruit quality (Rane et al., 2024).

This study explores how to integrate genetic disease resistance with strict quality requirements to support stable, efficient, and nutritious tomato production. It clarifies the global economic and nutritional importance of tomato and the scale of yield and quality losses caused by diseases in major production systems. It also systematically summarizes current research progress on major and emerging tomato diseases and reviews breeding and biotechnological strategies for developing resistant varieties. By linking disease resistance with yield stability, market standards, and nutritional value, this study outlines the pathways and prospects for achieving sustainable tomato production under multiple stress conditions.

2 Major Diseases Affecting Tomato Cultivation

2.1 Fungal diseases

Early blight is mainly caused by *Alternaria solani* and is one of the most destructive leaf diseases in tomato. It forms brown necrotic spots with typical concentric rings on leaves. In severe cases, it leads to heavy defoliation, reduced photosynthetic area, and can cause yield losses of up to 80% under favorable conditions (Ivanović et al., 2022). All aboveground parts of the plant can be affected. The disease becomes serious under conditions of high temperature, heavy dew, and high humidity.

Late blight is caused by *Phytophthora infestans*, a highly infectious oomycete disease that attacks leaves and fruits. It can destroy an entire crop within a few days. Cool and humid conditions favor its outbreaks, and historically it has caused total crop failure in Solanaceae crops (Oladokun et al., 2019).

Fusarium wilt is caused by *Fusarium oxysporum* f. sp. *lycopersici*. It is a soil-borne vascular disease that blocks the xylem vessels, leading to unilateral yellowing, wilting, and eventually plant death. The pathogen can survive in soil for a long time, and yield losses in susceptible varieties can reach 10%~80% (Li et al., 2024).

2.2 Bacterial diseases

Among bacterial diseases, bacterial wilt caused by *Ralstonia solanacearum* is one of the most destructive soil-borne diseases. It infects the vascular system, causing rapid and often irreversible wilting, stunting, and even death of plants, especially under warm and humid conditions. Contaminated soil, irrigation water, and plant residues allow the pathogen to survive for long periods, making it difficult to continue tomato cultivation in affected fields.

Bacterial spot is mainly caused by bacteria of the genus *Xanthomonas*. It is an important disease of leaves and fruits in both open-field and greenhouse production. The disease forms small water-soaked spots that later turn dark and scab-like, leading to leaf drop, reduced photosynthesis, and visible lesions on fruit surfaces, which lower market quality (Panno et al., 2021).

Because bactericides are often less effective against bacterial diseases and the pathogens can spread through seeds or water, control of these diseases is relatively difficult. Therefore, breeding resistant varieties and maintaining strict sanitation measures are particularly important.

2.3 Viral diseases

Tomato yellow leaf curl virus (TYLCV) is a whitefly-transmitted begomovirus and one of the most damaging tomato viruses worldwide. Infected plants show severe leaf curling, shortened internodes, chlorosis, and stunted growth, resulting in a sharp decline in fruit set and yield. Yield loss in susceptible varieties can approach 100% (Mugao, 2023).

Tomato mosaic virus (ToMV) is a highly stable virus belonging to the genus Tobamovirus. It can spread through mechanical contact, contaminated tools, seeds, and workers. The disease causes mosaic patterns, mottling, and deformation of leaves, as well as fruit deformation, size reduction, and internal browning. These symptoms greatly reduce market value and processing quality, especially under greenhouse conditions (Ding et al., 2019).

Tomato hosts a very large range of viruses, with more than 300 viruses or viroids reported so far. Therefore, TYLCV and ToMV are only representative examples among many viral threats. In breeding for disease resistance, multiple viral factors need to be considered together.

3 Genetic Basis of Tomato Disease Resistance

3.1 Types of resistance

Tomato shows two main types of resistance: vertical resistance (species- or race-specific) and horizontal resistance (quantitative resistance). Vertical resistance is usually controlled by one or a few major R genes. These genes can recognize specific pathogen effectors and trigger strong defense responses. Typical examples include Ve genes for resistance to *Verticillium* wilt, I genes for *Fusarium* wilt, Mi genes for resistance to root-knot nematodes, and Ty genes for resistance to tomato yellow leaf curl disease. These genes often provide near-complete resistance, but they are easily broken by newly emerging pathogen races.

In contrast, horizontal resistance is usually controlled by multiple genes, with several QTL acting together. Each locus contributes a small effect, and this type of resistance often works against a wide range of pathogen strains. For example, resistance QTL for early blight, bacterial wilt, anthracnose, and tomato chlorosis virus (ToCV) have been widely reported (Khojasteh et al., 2024). This quantitative resistance is generally more durable, but it is relatively difficult to select and fix in breeding populations.

3.2 Resistance genes and QTL

Many key resistance genes in tomato have been cloned or mapped. The Ve locus contains Ve1 and Ve2, among which Ve1 encodes a receptor-like protein that provides resistance to race 1 of *Verticillium dahliae* and *V. albo-atrum*. The I gene family (such as I-2), located on chromosome 11, confers resistance to specific races of *Fusarium oxysporum* f. sp. *lycopersici* and has been widely used in commercial varieties (Orchard et al., 2023). The Mi gene provides resistance to root-knot nematodes and, in some genetic backgrounds, is also associated with resistance to other pests (Ercolano et al., 2012).

For virus resistance, several Ty genes (Ty-1 to Ty-6) derived from wild species can provide resistance or tolerance to tomato yellow leaf curl virus. Among them, Ty-2 encodes an NLR protein, and its locus has been widely used in breeding through gene pyramiding (Dhaliwal et al., 2020).

Besides major genes, meta-analysis of large-scale mapping studies has identified dozens of meta-QTL (MQTL) related to bacterial and fungal diseases. These MQTL significantly narrow down the genomic intervals and reveal candidate defense genes such as NDR1, PR proteins, and WRKY transcription factors. Individual studies have identified multiple QTL associated with resistance to early blight, bacterial wilt, anthracnose, and ToCV. These QTL usually explain moderate but significant phenotypic variation, indicating that quantitative resistance is widely present (Adhikari et al., 2023; Gebhardt, 2023).

3.3 Molecular mechanisms

At the molecular level, tomato disease resistance depends on a layered immune system. Pattern-triggered immunity (PTI) is activated when pattern recognition receptors on the cell surface detect pathogen-associated molecular patterns, leading to basic defense responses such as reactive oxygen species burst, cell wall reinforcement, and defense gene expression (Abbasi et al., 2021). Effector-triggered immunity (ETI) is mainly mediated by intracellular NLR-type R proteins, which recognize specific pathogen effectors and trigger faster and stronger responses, often accompanied by localized cell death (hypersensitive response). Genome-wide studies show that tomato contains hundreds of NLR genes, and their expression is induced during pathogen infection, highlighting their key role in ETI (Bashir et al., 2022).

These immune layers are tightly regulated by signaling pathways centered on salicylic acid (SA), jasmonic acid (JA), and ethylene (ET). In the interaction between *Alternaria* and tomato, JA and ET signaling pathways work together under the regulation of transcription factors to control defense responses against necrotrophic fungi (Tominello-Ramirez et al., 2024). SA-related genes, such as EDS1, NDR1, and NPR1-like regulators, are involved in Ve1-mediated signaling pathways and broader defense responses. Many resistance-related QTL and candidate genes encode components of these pathways, including WRKY transcription factors, PR proteins, and receptor-like kinases.

4 Breeding Strategies for Disease-Resistant Varieties

4.1 Conventional breeding methods

Traditional breeding for disease resistance in tomato mainly relies on selection and hybridization, often using wild relatives as sources of resistance genes. Under natural or artificial disease pressure, repeated cycles of backcrossing and phenotypic selection have produced lines resistant to begomoviruses, late blight, bacterial wilt, Fusarium wilt, and tomato mosaic virus. Among them, multi-resistant F7 lines can show relatively high yield under suitable conditions (Hanson et al., 2016).

Backcross breeding is widely used to introduce specific resistance genes into elite but susceptible genetic backgrounds while recovering the genome of the recurrent parent. This approach provides a foundation for further improvement of multi-resistant lines using molecular techniques.

However, relying only on conventional breeding usually takes a long time, and when using distant wild donors, it is often affected by linkage drag.

4.2 Marker-assisted selection (MAS)

Marker-assisted selection (MAS) tracks molecular markers tightly linked to resistance genes and QTLs, allowing early and accurate selection in segregating generations, which greatly speeds up the breeding process (Borrelli et al., 2018).

MAS has been widely used to introduce and combine Ty genes related to tomato yellow leaf curl disease, Ph genes related to late blight, the root-knot nematode resistance gene Mi, and many other resistance loci.

Marker-assisted backcrossing and gene-specific marker techniques make the pyramiding of multiple resistance traits more efficient. Lines carrying combinations such as Ty-1/Ty-2/Ty-3 with Ph-2/Ph-3 or Sw-5 and Tm-2² can be developed. These lines show strong overall resistance and good horticultural traits (Kaushal et al., 2024). Compared with relying only on phenotypic selection, MAS significantly improves the accuracy, efficiency, and reliability of disease-resistance breeding.

4.3 Genomic and biotechnological approaches

Genomic selection (GS) uses whole-genome markers and prediction models to select superior genotypes for complex quantitative resistance traits without phenotyping every generation. With the increasing availability of high-density genomic resources, this method is showing good application potential in tomato breeding (Anand et al., 2025).

Biotechnological approaches provide more options for disease-resistance breeding. CRISPR/Cas genome editing can precisely modify resistance (R) genes and susceptibility (S) genes, allowing rapid development of resistant materials without extensive crossing.

In tomato, CRISPR/Cas9 has been used to knock out susceptibility genes such as *Pelo* and *Mlo1* to obtain resistance to TYLCV and powdery mildew. Knocking out *DMR6-1* and *MYBS2* can enhance broad-spectrum resistance to bacterial, oomycete, and late blight pathogens. Editing *XSP10* and *SISAMT* improves tolerance to Fusarium wilt. Edited plants usually show enhanced resistance with minimal effects on growth (Pramanik et al., 2021; Debbarma et al., 2023) (Figure 1).

Deletion of the PMR4 genomic region led to the development of the non-transgenic powdery mildew-resistant variety “Tomelo” in less than 10 months, showing the high efficiency and precision of this technology. In addition, CRISPR can be used for rapid domestication of stress-resistant wild materials, keeping their resistance while introducing good agronomic traits.

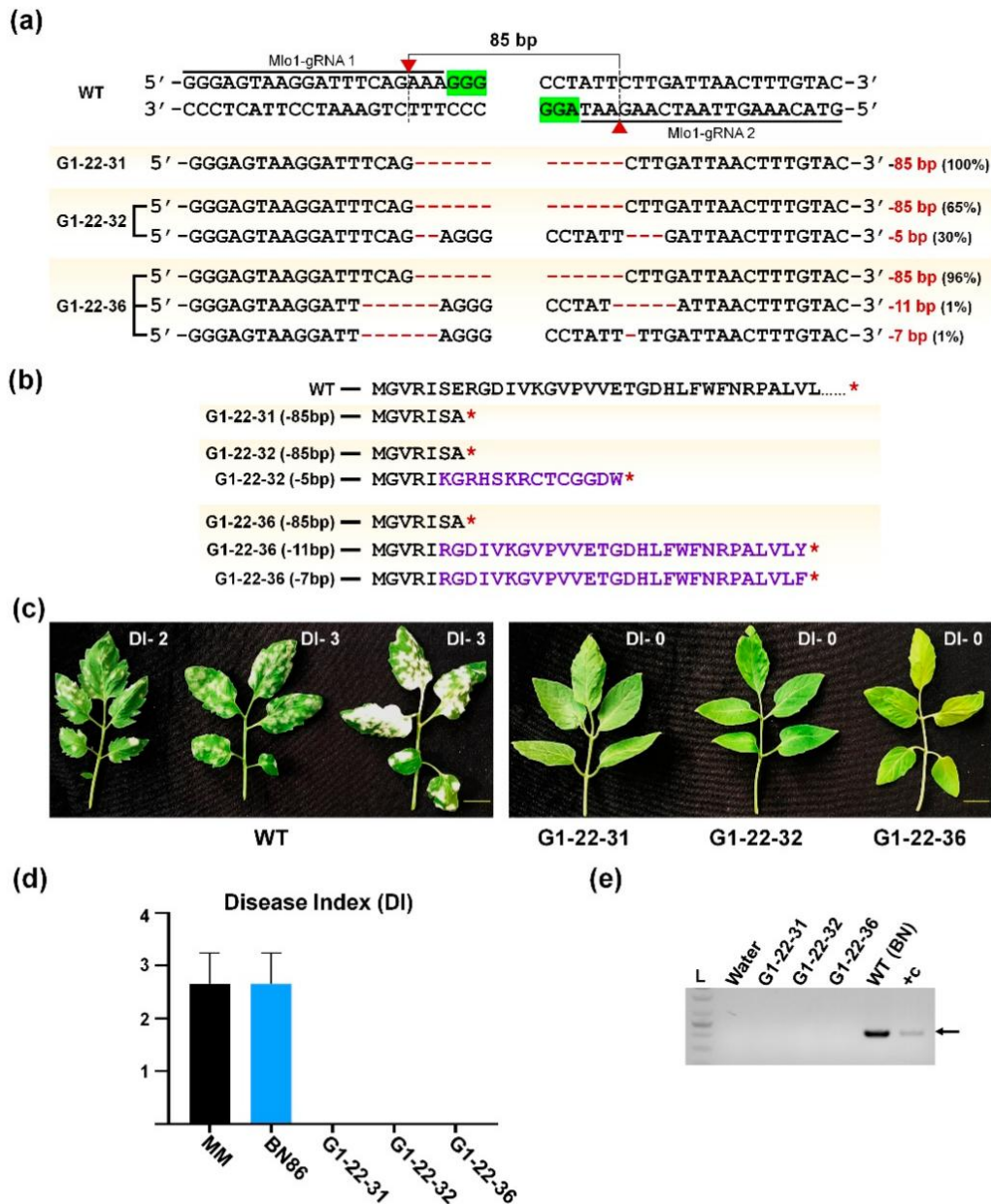


Figure 1 Characterization of CRISPR/Cas9-mediated *SIMlo1* genome-edited tomato lines for powdery mildew resistance. (a) Indel patterns of three *SIMlo1*-knockout plants showing the homozygous (G1-22-31), biallelic (G1-22-32), and chimeric (G1-22-36) genotype. The knockout efficiency (%) of individual lines evaluated using the ICE tool. Red dash indicates the deleted nucleotides; (b) Comparison of amino acid sequence between wild-type (WT) MLO1 protein and truncated region resulting from knockout alleles. Stop codon in red star symbol and altered amino acids in blue was indicated; (c) Analysis of *SIMlo1*-knockout mutant lines tested for resistance against powdery mildew-causing fungus *Oidium neolyopersici*. The phenotype of the mutant plants evaluated at 21 days post-infection (DPI). Referring to visual fungal growth symptoms, we calculated the disease index; (d) Powdery mildew disease index was calculated with WT (BN-86 and Moneymaker (MM)) and G1 *SIMlo1* mutant lines (G1-22-31, G1-22-32, G1-22-36). Error bars represent SE (three biological replicates); (e) Detection of *O. neolyopersici* by PCR method using strain-specific 16S ribosomal RNA (rRNA) primers. Non-infected plants used as mock control; fungal DNA used for PCR as a positive control (Adopted from Pramanik et al., 2021)

4.4 Resistance gene pyramiding

Resistance gene pyramiding combines multiple resistance genes and/or QTLs into a single variety to achieve broader and more durable resistance. Through marker-assisted pyramiding, genes such as Ty-1, Ty-2, and Ty-3 for tomato yellow leaf curl disease, Ph-2 and Ph-3 for late blight, and the Mi gene for root-knot nematode resistance have been integrated into the same genetic background. This has resulted in lines and hybrids with high overall resistance and stable yield under disease pressure (Prabhandakavi et al., 2021).

Double PCR and linked marker techniques allow efficient stacking of resistance genes for viruses and soil-borne diseases through backcrossing, enabling predictable recovery of elite genetic backgrounds with fewer plants.

Gene editing further expands the ability of gene pyramiding. Using multiplex CRISPR/Cas systems, multiple S or R genes can be edited at the same time, producing broad-spectrum resistance in a single generation and avoiding linkage drag (Tiwari et al., 2023). Combining resistance genes with different mechanisms and integrating good agronomic management practices is key to achieving long-term stable resistance in high-quality tomato varieties.

5 Disease-Resistant Varieties and Their Performance

5.1 Commercialized disease-resistant varieties

Widely used cultivars and hybrids usually carry resistance to key diseases such as Fusarium wilt, Tomato yellow leaf curl disease (TYLCD), Tomato spotted wilt virus (TSWV), and bacterial wilt. These resistances may exist individually or be combined through gene pyramiding. In Mexico, commercial Saladette-type hybrids carrying resistance genes to Fol races 1-3, TYLCV, and TSWV not only meet strict quality standards in both the United States and domestic markets, but also show early maturity (Lafrance et al., 2024). In India and other regions, F1 hybrids with resistance to multiple diseases (such as early blight, bacterial wilt, and leaf curl disease) have been widely used for both fresh consumption and processing purposes (Kaushal et al., 2020).

5.2 Yield stability and adaptability

The performance of disease-resistant varieties is influenced by season, production system, and disease pressure. In Mali, AVTO1710 can still maintain a relatively high yield (40.9 t/ha) during the rainy season, when many local varieties perform poorly, while VIO43614 performs best under drier conditions with high TYLCD incidence, showing good adaptability to different environments (Bihon et al., 2022). In Honduras, the line AVTO1903 shows high marketable yield under both open-field (101.3 t/ha) and greenhouse conditions (62.1 t/ha), indicating stable performance across cultivation systems (Flores et al., 2024). Late blight-resistant varieties such as “Mountain Gem” also show yield differences across regions, with clear yield improvement under grafting conditions, highlighting the importance of multi-location trials for resistant materials (Reeves et al., 2023).

5.3 Quality traits of disease-resistant varieties

Studies show that disease resistance can be combined with good fruit quality. In the Sinaloa region, hybrids resistant to Fol, TYLCV, and TSWV usually meet international standards in fruit firmness, color, pH, total soluble solids (TSS), acidity, and TSS/acid ratio, and some of them also have early maturity and good market quality (Lafrance et al., 2024). Differences exist among resistant materials in traits such as firmness, TSS, pH, dry matter content, and fruit shape index, allowing breeders to select lines that match local consumer preferences. Research on late blight-resistant families shows that strongly resistant genotypes can also approach the ideal type (ideotype), with good performance in fruit size, color, firmness, acidity, and soluble solids content (Copati et al., 2024). In addition, phenotypic analysis of diverse germplasm indicates that some resistant lines are not only high-yielding, but also have higher vitamin C content, antioxidant activity, and polyphenol levels, suggesting good potential for breeding varieties with both disease resistance and enhanced nutritional quality (Grozeva et al., 2020).

6 Integration of Disease Resistance and High-Quality Production

6.1 Balance between resistance and fruit quality

Breeding studies show that disease resistance and quality can be improved together, but there is still a certain trade-off between them. Materials carrying multiple Ty genes to enhance resistance to TYLCV usually show strong resistance. However, when selecting for low disease index and high yield, they are often accompanied by a

decrease in vitamin C content and locule number, while fruit firmness, Brix value, and β -carotene content tend to increase (Mahmoud et al., 2025).

Dual resistance to ToLCV and bacterial wilt can be combined with good processing traits, but it is necessary to maintain a balance of lycopene, total soluble solids (TSS), and acidity during parent selection (Acharya et al., 2018). In addition, hybrids with multiple resistance to Fol, TYLCV, and TSWV can meet market standards in terms of fruit firmness, TSS/acid ratio, and color. This indicates that if quality traits are included simultaneously in breeding selection, disease resistance does not significantly reduce fresh fruit quality.

Evaluation of diverse germplasm resources also found that some materials possess both ToMV resistance, high soluble solids content, and strong antioxidant activity. These can be used as important parental resources for simultaneous improvement of resistance and quality.

6.2 Agronomic measures supporting resistant varieties

Resistant varieties perform best under integrated disease management (IDM) systems. The IDM model that combines resistant or grafted plants with biological agents, pheromone traps, and need-based pesticide application not only increases yield but also significantly reduces pesticide use.

In areas with high incidence of bacterial wilt, integrated measures such as soil improvement, application of *Bacillus subtilis*, and intercropping systems can effectively reduce disease occurrence and improve input-output efficiency (Sheneka et al., 2025). In addition, studies on *Fusarium* wilt and late blight indicate that a single control method is not enough for long-term management. Instead, soil health management, crop rotation, and biological control should work together with resistant varieties to achieve sustainable control (Jehani et al., 2025).

6.3 Postharvest quality and shelf life

Disease resistance can also indirectly improve postharvest quality by reducing disease incidence, since healthy plants and fruits are less prone to decay. Breeding strategies that combine ToLCV resistance with delayed ripening traits have successfully developed hybrids with extended shelf life and stable yield (Manjunath et al., 2025).

Studies show that genotypes with higher fruit firmness have lower disease incidence during storage and can maintain a longer shelf life, thereby reducing market losses (Imali et al., 2025) (Figure 2). In addition, molecular improvement of gene loci related to fruit firmness and shelf life can delay fruit softening and enhance resistance to pathogens during transportation and storage.

7 Case Studies of Disease-Resistant Tomato Varieties

7.1 Breeding progress of TYLCV-resistant tomato varieties

Resistance to TYLCV (Tomato yellow leaf curl virus) is mainly achieved by introgressing Ty genes from wild relatives and combining gene-specific markers with linked markers for gene pyramiding. For example, commercial F1 hybrids such as 'Brivio', 'Dania', 'SV8320', and 'Tyrmes' commonly contain combinations of multiple resistance genes, including Ty-1/Ty-3, Ty-2, Ty-4, and ty-5. Under field TYLCV pressure, these varieties may show moderate or mild symptoms, but they can still maintain relatively good yield and fruit quality (Mahmoud et al., 2023). Studies have shown that pyramiding Ty-1/Ty-3 with Ty-2 using marker-assisted selection can significantly enhance resistance, confirming the synergistic effect of stacking multiple loci (Lee et al., 2020). In variety trials under natural TYLCV pressure in Georgia, USA, cultivars carrying Ty-1 or Ty-3/Ty-6 showed lower disease incidence and higher yield compared with susceptible controls, indicating good field resistance (Acharya et al., 2025). However, resistance based on Ty-1 may break down under high-temperature conditions, suggesting limitations in environmental adaptability of the current resistance system (Koeda and Kitawaki, 2024).

7.2 *Fusarium* wilt-resistant tomato hybrids

Resistance to tomato *Fusarium* wilt mainly comes from the I gene family introgressed from wild species (Chitwood-Brown et al., 2021). By crossing lines carrying the I-3 gene with commercial cultivars containing I-1 and I-2, the FOX hybrid series has been developed. Some of these materials show resistance to different physiological races of *Fusarium oxysporum* f. sp. *lycopersici* (Fol), but their agronomic traits still need

improvement. When used as rootstocks, FOX4 can effectively suppress wilt occurrence while maintaining yield and fruit quality, whereas FOX1 may have some negative effects on certain quality traits (Fernandes et al., 2022). In addition, germplasm screening in different regions has identified various resistant or moderately resistant materials. These can be used as resistance donors or directly promoted varieties to reduce yield losses. Meanwhile, new resistance loci identified in the wild species *Solanum pennellii* further expand the genetic base for commercial hybrid breeding (Li et al., 2022).

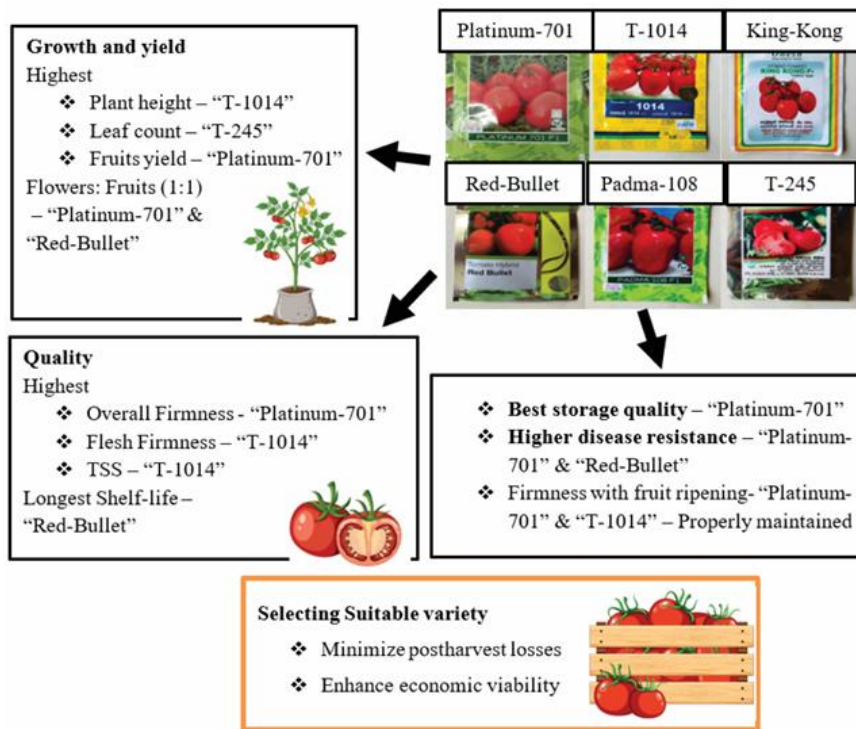


Figure 2 Comparative evaluation of tomato varieties based on growth, yield, quality, and postharvest performance (Adapted from Imali et al., 2025)

7.3 Multi-resistant varieties under protected cultivation conditions

In protected cultivation systems, tomatoes are often exposed to combined pressure from soil-borne pathogens and viruses. Grafting susceptible scions onto *Fusarium* wilt-resistant rootstocks can effectively reduce disease occurrence under naturally infested soil conditions, while maintaining plant growth and yield (Kawicha et al., 2025). For viral diseases such as TYLCV, efficient inoculation systems allow rapid screening of breeding materials, which speeds up the development of multi-resistant varieties (Bian et al., 2024). At present, F1 hybrids combining TYLCV resistance with resistance to other diseases are widely used in greenhouse production systems. These resistant varieties not only help stabilize yield but also reduce reliance on chemical pesticides.

8 Challenges and Future Prospects

8.1 Evolution of pathogen virulence

Many tomato pathogens evolve rapidly and can easily weaken resistance based on single major-effect genes. The loss or mutation of avirulence genes and effectors, as observed in *Cladosporium fulvum* and its Avr genes, allows pathogens to evade Cf gene-mediated resistance (De La Rosa et al., 2024; Zaccaron and Stergiopoulos, 2024). Experimental evolution studies of *Ralstonia solanacearum* on quantitatively resistant tomato lines show that the pathogen adapts through convergent rewiring of virulence regulatory networks, rather than completely overcoming resistance. This highlights its strong adaptive potential even under quantitative resistance (Gopalan-Nair et al., 2021). For viruses such as ToBRFV and similar threats, new strains have already broken traditional ToMV/TMV resistance genes, creating an urgent need for new resistance resources and gene-editing strategies (Panno et al., 2021).

8.2 Climate change and disease dynamics

Climate change is expected to increase disease pressure by altering temperature, humidity, and rainfall patterns, thereby shifting pathogen distributions and promoting outbreaks. Studies predict that many plant pathogens will expand their geographic ranges and occur more frequently, which could significantly impact tomato production and food security (de Almeida et al., 2020). Field evidence from Nepal shows that changes in temperature and precipitation are closely associated with increased incidence of late blight, leaf curl disease, and black spot in tomato, forcing farmers to use more pesticides to maintain yields (Bhandari et al., 2021). In addition, emerging viruses such as ToBRFV are spreading into new regions, a process partly driven by both climate change and global trade.

8.3 Future breeding directions

Future breeding will increasingly rely on multi-omics integration and advanced analytical approaches. The combined application of transcriptomics, ionomics, and other omics technologies in tomato has identified candidate genes and SNPs associated with resistance to late blight and ToBRFV, providing a basis for developing more precise molecular markers and functional targets (Deb et al., 2023). Further studies emphasize the need to integrate genomics, transcriptomics, metabolomics, and effectomics to better understand resistance mechanisms and guide the design of durable resistance (Adhikari et al., 2020).

Artificial intelligence-assisted breeding and phenotyping are becoming key tools. Image-based high-throughput phenotyping in tomato bacterial wilt research can detect subtle quantitative differences and identify new QTLs earlier than manual scoring. In addition, integrating multi-omics data with machine learning to predict resistance phenotypes is considered an important future direction, highlighting the potential of intelligent breeding platforms to accelerate the development of disease-resistant crops (Cembrowska-Lech et al., 2023).

Author Contributions

The authors appreciate Dr Fang from the Hainan Institution of Biotechnology for her assistance in references collection and discussion for this work completion.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- Abbasi S., Sadeghi A., Omidvari M., and Tahan V., 2021, The stimulators and responsive genes to induce systemic resistance against pathogens: An exclusive focus on tomato as a model plant, *Biocatalysis and Agricultural Biotechnology*, 33: 101993.
<https://doi.org/10.1016/j.bcab.2021.101993>
- Acharya B., Dutta S., Dutta S., and Chattopadhyay A., 2018, Breeding tomato for simultaneous improvement of processing quality, fruit yield, and dual disease tolerance, *International Journal of Vegetable Science*, 24(5): 407-423.
<https://doi.org/10.1080/19315260.2018.1427648>
- Acharya N., Kumar M., Bag S., Cloud C., Torrance T., Simmons A., Kumari M., Romero E., and McAvoy T., 2025, Performance of tomato cultivars under natural tomato yellow leaf curl disease (TYLCD) pressure in Georgia, USA, *Plant Disease*, online ahead of print.
<https://doi.org/10.1094/PDIS-03-25-0469-RE>
- Adhikari P., Adhikari T.B., Louws F.J., and Panthee D.R., 2020, Advances and challenges in bacterial spot resistance breeding in tomato (*Solanum lycopersicum* L.), *International Journal of Molecular Sciences*, 21(5): 1734.
<https://doi.org/10.3390/ijms21051734>
- Adhikari P., Oh Y., and Panthee D.R., 2017, Current status of early blight resistance in tomato: An update, *International Journal of Molecular Sciences*, 18(10): 2019.
<https://doi.org/10.3390/ijms18102019>
- Adhikari T.B., Siddique M.I., Louws F.J., Sim S.C., and Panthee D.R., 2023, Molecular mapping of quantitative trait loci for resistance to early blight in tomatoes, *Frontiers in Plant Science*, 14: 1135884.
<https://doi.org/10.3389/fpls.2023.1135884>
- Akotowanou O.C.A., Adjou E.S., Olubi A.B., Kouglbenou S.D., Ahoussi E.D., and Sohounhloué D.C., 2022, The tomato (*Solanum lycopersicum* L.) in community development: An overview focused on nutritional properties, agronomic constraints, recent achievements and future prospective, *International Journal of Frontiers in Biology and Pharmacy Research*, 3(2): 008-016.
<https://doi.org/10.53294/ijfbpr.2022.3.2.0061>

- Anand S., Visakh R.L., Bhalaji B.K.S., Parvathy, Reddy N.R.S., and Rajasekharan A., 2025, Current trends in CRISPR-Cas system based genome editing in tomato (*Solanum lycopersicum*), Plant Breeding, e70023.
<https://doi.org/10.1111/pbr.70023>
- Bashir S., Rehman N., Zaman F., Naem M., Jamal A., Tellier A., Ilyas M., Arias G., and Khan M., 2022, Genome-wide characterization of the NLR gene family in tomato (*Solanum lycopersicum*) and their relatedness to disease resistance, Frontiers in Genetics, 13: 931580.
<https://doi.org/10.3389/fgene.2022.931580>
- Bhandari R., Neupane N., and Adhikari D.P., 2021, Climatic change and its impact on tomato (*Lycopersicon esculentum* L.) production in plain area of Nepal, Environmental Challenges, 4: 100129.
<https://doi.org/10.1016/j.envc.2021.100129>
- Bian Y., Zhang X., Chen C., Wang G., Zhang P., Liu G., Ma F., and Bao Z., 2024, Establish an efficient inoculation system of tomato yellow leaf curl virus to assist tomato resistance breeding, Scientia Horticulturae, 324: 112567.
<https://doi.org/10.1016/j.scienta.2023.112567>
- Bihon W., Ognakossan K.E., Tignegre J.B., Hanson P., Ndiaye K., and Srinivasan R., 2022, Evaluation of different tomato (*Solanum lycopersicum* L.) entries and varieties for performance and adaptation in Mali, West Africa, Horticulturae, 8(7): 579.
<https://doi.org/10.3390/horticulturae8070579>
- Borrelli V.M., Brambilla V., Rogowsky P., Marocco A., and Lanubile A., 2018, The enhancement of plant disease resistance using CRISPR/Cas9 technology, Frontiers in Plant Science, 9: 1245.
<https://doi.org/10.3389/fpls.2018.01245>
- Cembrowska-Lech D., Krzemińska A., Miller T., Nowakowska A., Adamski C., Radaczyńska M., Mikiciuk G., and Mikiciuk M., 2023, An integrated multi-omics and artificial intelligence framework for advanced plant phenotyping in horticulture, Biology, 12(10): 1298.
<https://doi.org/10.3390/biology12101298>
- Chitwood-Brown J., Vallad G.E., Lee T.G., and Hutton S.F., 2021, Breeding for resistance to Fusarium wilt of tomato: A review, Genes, 12(11): 1673.
<https://doi.org/10.3390/genes12111673>
- Copati M.G.F., Pessoa H.P., Dariva F.D., Castro Filho M.N.D., and Nick C., 2024, Tomato families possessing resistance to late blight also display high-quality fruit, Acta Scientiarum. Agronomy, 46: e66790.
<https://doi.org/10.4025/actasciagron.v46i1.66790>
- de Almeida G.Q., de Oliveira Silva J., Copati M.G.F., de Oliveira Dias F., and dos Santos M.C., 2020, Tomato breeding for disease resistance, Multi-Science Journal, 3(3): 8-16.
<https://doi.org/10.33837/msj.v3i3.1287>
- De La Rosa S., Schol C., Peregrina Á., Winter D., Hilgers A., Maeda K., Iida Y., Tarallo M., Jia R., Beenen H., Rocafort M., De Wit P., Bowen J., Bradshaw R., Joosten M., Bai Y., and Mesarich C., 2024, Sequential breakdown of the Cf-9 leaf mould resistance locus in tomato by *Fulvia fulva*, New Phytologist, 243(4): 1522-1538.
<https://doi.org/10.1111/nph.19925>
- Deb S., Della Lucia M.C., Ravi S., Bertoldo G., and Stevanato P., 2023, Transcriptome-assisted SNP marker discovery for *Phytophthora infestans* resistance in *Solanum lycopersicum* L., International Journal of Molecular Sciences, 24(7): 6798.
<https://doi.org/10.3390/ijms24076798>
- Debbarma J., Saikia B., Singha D., Das D., Keot A., Maharana J., Velmurugan N., Arunkumar K., Reddy P., and Chikkaputtaiah C., 2023, CRISPR/Cas9-mediated mutation in XSP10 and SISAMT genes impart genetic tolerance to fusarium wilt disease of tomato (*Solanum lycopersicum* L.), Genes, 14(2): 488.
<https://doi.org/10.3390/genes14020488>
- Dhaliwal M.S., Jindal S.K., Sharma A., and Prasanna H.C., 2020, Tomato yellow leaf curl virus disease of tomato and its management through resistance breeding: A review, The Journal of Horticultural Science and Biotechnology, 95(4): 425-444.
<https://doi.org/10.1080/14620316.2019.1691060>
- Ding S., Meinholz K., Cleveland K., Jordan S.A., and Gevens A.J., 2019, Diversity and virulence of *Alternaria* spp. causing potato early blight and brown spot in Wisconsin, Phytopathology, 109(3): 436-445.
<https://doi.org/10.1094/PHYTO-06-18-0181-R>
- Egea I., Estrada Y., Flores F.B., and Bolarín M.C., 2022, Improving production and fruit quality of tomato under abiotic stress: Genes for the future of tomato breeding for a sustainable agriculture, Environmental and Experimental Botany, 204: 105086.
<https://doi.org/10.1016/j.envexpbot.2022.105086>
- Ercolano M.R., Sanseverino W., Carli P., Ferriello F., and Frusciant L., 2012, Genetic and genomic approaches for R-gene mediated disease resistance in tomato: Retrospects and prospects, Plant Cell Reports, 31(6): 973-985.
<https://doi.org/10.1007/s00299-012-1234-z>
- Fernandes R.H., Silva D.J.H.D., Delazari F.T., and Lopes E.A., 2022, Screening of tomato hybrids for resistance to Fusarium wilt, Crop Breeding and Applied Biotechnology, 22: e43352248.
<https://doi.org/10.1590/1984-70332022v22n4a43>
- Flores F., Ramirez-Guerrero H.O., Maxwell L., Eybshitz A., Barchenger D.W., and Avellaneda M.C., 2024, Adaptability and yield performance of introduced tomato lines under greenhouse and open field conditions in Honduras, HortScience, 59(8): 1041-1048.
<https://doi.org/10.21273/HORTSCI17753-24>

- Gebhardt C., 2023, A physical map of traits of agronomic importance based on potato and tomato genome sequences, *Frontiers in Genetics*, 14: 1197206.
<https://doi.org/10.3389/fgene.2023.1197206>
- Gopalan-Nair R., Jardinaud M., Legrand L., Landry D., Barlet X., Lopez-Roques C., Vandecasteele C., Bouchez O., Genin S., and Guidot A., 2021, Convergent rewiring of the virulence regulatory network promotes adaptation of *Ralstonia solanacearum* on resistant tomato, *Molecular Biology and Evolution*, 38(5): 1792-1808.
<https://doi.org/10.1093/molbev/msaa320>
- Grozeva S., Nankar A.N., Ganeva D., Tringovska I., Pasev G., and Kostova D., 2020, Characterization of tomato accessions for morphological, agronomic, fruit quality, and virus resistance traits, *Canadian Journal of Plant Science*, 101(4): 476-489.
<https://doi.org/10.1139/cjps-2020-0030>
- Imali H.L.J., Weerahewa H.L.D., and Rajapakse R.P.S.S., 2025, The influence of tomato varietal selection on the postharvest quality of tomatoes (*Solanum lycopersicum* L.) grown under protected houses, *Ceylon Journal of Science*, 54(2).
<https://doi.org/10.4038/cjs.v54i2.8456>
- Ivanović Ž., Blagojević J., Jovanović G., Ivanović B., and Žeželj D., 2022, New insight in the occurrence of early blight disease on potato reveals high distribution of *Alternaria solani* and *Alternaria protenta* in Serbia, *Frontiers in Microbiology*, 13: 856898.
<https://doi.org/10.3389/fmicb.2022.856898>
- Jehani M.D., Mohamed J.M., Cheemala S., Nath B.C., Chonzik E.K., and Srivastava S., 2025, From pathogen to protection: Integrated disease management strategies for tomato late blight, *Journal of Pure and Applied Microbiology*, 19(3): 1686.
<https://doi.org/10.22207/JPAM.19.3.33>
- Kaushal A., Sadashiva A.T., Ravishankar K.V., Singh T.H., Prasanna H.C., Rai A.K., and Jatav V.K., 2020, A rapid disease resistance breeding in tomato (*Solanum lycopersicum* L.), In: *Accelerated Plant Breeding, Volume 2: Vegetable Crops*, Springer International Publishing, Cham, pp. 17-55.
https://doi.org/10.1007/978-3-030-47298-6_2
- Kaushal A., Sadashiva A.T., Ravishankar K.V., Sriram S., and Reddy M.K., 2024, Marker-assisted pyramiding of Ty-2, Ty-3, Ph-2, and Ph-3 genes for combined resistance to tomato leaf curl and late blight diseases in tomato (*Solanum lycopersicum* L.), *European Journal of Plant Pathology*, 168(3): 557-570.
<https://doi.org/10.1007/s10658-023-02784-y>
- Kawicha P., Saman P., Suwannachairob P., Ponpang-Nga P., Saengprajak J., Sangdee A., and Thanyasiriwat T., 2025, Intraspecific grafting of tomatoes: Impact of disease-resistant rootstocks on Fusarium wilt prevention, plant growth, and fruit quality under naturally infested field conditions, *The Plant Pathology Journal*, 41(5): 566.
<https://doi.org/10.5423/PPJ.OA.05.2025.0064>
- Khojasteh M., Ramandi H., Taghavi S., Taheri A., Rahmanzadeh A., Chen G., Foolad M., and Osdaghi E., 2024, Unraveling the genetic basis of quantitative resistance to diseases in tomato: A meta-QTL analysis and mining of transcript profiles, *Plant Cell Reports*, 43(7): 184.
<https://doi.org/10.1007/s00299-024-03268-x>
- Koeda S., and Kitawaki A., 2024, Breakdown of Ty-1-based resistance to tomato yellow leaf curl virus in tomato plants at high temperatures, *Phytopathology*, 114(1): 294-303.
<https://doi.org/10.1094/PHTO-04-23-0119-R>
- Lafrance R., Villicaña C., Valdéz-Torres J.B., García-Estrada R.S., Báez Sañudo M.A., Esparza-Araiza M.J., and León-Félix J., 2024, Selection of tomato (*Solanum lycopersicum*) hybrids resistant to Fol, TYLCV, and TSWV with early maturity and good fruit quality, *Horticulturae*, 10(8): 839.
<https://doi.org/10.3390/horticulturae10080839>
- Lee J.H., Chung D.J., Lee J.M., and Yeom I., 2020, Development and application of gene-specific markers for tomato yellow leaf curl virus resistance in both field and artificial infections, *Plants*, 10(1): 9.
<https://doi.org/10.3390/plants10010009>
- Li J., Chitwood-Brown J., Kaur G., Labate J.A., Vallad G.E., Lee T.G., and Hutton S.F., 2022, Novel sources of resistance to *Fusarium oxysporum* f. sp. *lycopersici* race 3 among *Solanum pennellii* accessions, *Journal of the American Society for Horticultural Science*, 147(1): 35-44.
<https://doi.org/10.21273/JASHS05080-21>
- Li Q., Feng Y., Li J., Hai Y., Si L., Tan C., Peng J., Hu Z., Li Z., Li C., Hao D., and Tang W., 2024, Multi-omics approaches to understand pathogenicity during potato early blight disease caused by *Alternaria solani*, *Frontiers in Microbiology*, 15: 1357579.
<https://doi.org/10.3389/fmicb.2024.1357579>
- Mahmoud A.M., Hassan A.A., Abdel-Ati K.E., Osman N.H., and Mohamed H.A., 2025, Exploring Ty resistance genes and genetic diversity in improved tomato lines selected from commercial hybrids, *BMC Plant Biology*, 25(1): 1213.
<https://doi.org/10.1186/s12870-025-07344-6>
- Mahmoud A.M., Osman N.H., and Mohamed H.A., 2023, Characterization of tomato yellow leaf curl virus resistance genes and genetic variability in commercial tomato F1 hybrids, *Scientia Horticulturae*, 318: 112088.
<https://doi.org/10.1016/j.scienta.2023.112088>
- Manjunath K.V., Das S., Mallick R.G., Hazra P., Chattopadhyay A., and Maji A., 2025, Combining ability and gene action for fruit yield components, quality, shelf life and reaction to tomato leaf curl virus disease, *Heliyon*, 11(3): e42040.
<https://doi.org/10.1016/j.heliyon.2025.e42040>

- Mugao L., 2023, Morphological and molecular variability of *Alternaria solani* and *Phytophthora infestans* causing tomato blights, *International Journal of Microbiology*, 2023: 8951351.
<https://doi.org/10.1155/2023/8951351>
- Oladokun J.O., Halabi M.H., Barua P., and Nath P.D., 2019, Tomato brown rugose fruit disease: Current distribution, knowledge and future prospects, *Plant Pathology*, 68(9): 1579-1586.
<https://doi.org/10.1111/ppa.13096>
- Orchard C., Kressin J., Chompookam S., Chuapong J., Onmanee N., Van Leeuwen K., Struss D., Balatero C., and Francis D., 2023, Marker-assisted selection to combine alleles for four disease resistance genes of tomato collocated on chromosome 11, *HortScience*, 58(5): 495-501.
<https://doi.org/10.21273/HORTSCI16982-22>
- Panno S., Davino S., Caruso A., Bertacca S., Crnogorac A., Mandić A., Noris E., and Matic S., 2021, A review of the most common and economically important diseases that undermine the cultivation of tomato crop in the Mediterranean Basin, *Agronomy*, 11(11): 2188.
<https://doi.org/10.3390/agronomy11112188>
- Prabhandakavi P., Pogiri R., Kumar R., Acharya S., Esakky R., Chakraborty M., Pinnamaneni R., and Palicherla S., 2021, Pyramiding Ty-1/Ty-3, Ty-2, ty-5 and ty-6 genes into tomato hybrid to develop resistance against tomato leaf curl viruses and recurrent parent genome recovery by ddRAD sequencing method, *Journal of Plant Biochemistry and Biotechnology*, 30(3): 462-476.
<https://doi.org/10.1007/s13562-020-00633-1>
- Pramanik D., Shelake R.M., Park J., Kim M.J., Hwang I., Park Y., and Kim J.Y., 2021, CRISPR/Cas9-mediated generation of pathogen-resistant tomato against tomato yellow leaf curl virus and powdery mildew, *International Journal of Molecular Sciences*, 22(4): 1878.
<https://doi.org/10.3390/ijms22041878>
- Rane O., Jindal S.K., Dhaliwal M.S., Sharma A., Kaur S., and Gill R., 2024, Appraisal for multiple disease resistance in advanced breeding lines of tomato (*Solanum lycopersicum* L.), *Genetic Resources and Crop Evolution*, 71(1): 239-251.
<https://doi.org/10.1007/s10722-023-01618-4>
- Reeves E.R., Strayer-Scherer A., Panthee D.R., Gardner R., and Meadows I.M., 2023, Variable yield responses among grafted and nongrafted late blight-resistant tomato (*Solanum lycopersicum* L.) hybrids in North Carolina, *HortScience*, 58(8): 943-948.
<https://doi.org/10.21273/HORTSCI17145-23>
- Sheneka R., Angappan K., Karthikeyan M., Thiribhuvanamala G., Karthikeyan S., and Kumar K.K., 2025, Integrated disease management strategies for sustainable tomato cultivation in bacterial wilt-endemic region of Tamil Nadu, *Plant Science Today*, 12(1): 1-8.
<https://doi.org/10.14719/pst.7316>
- Tiwari J.K., Singh A.K., and Behera T.K., 2023, CRISPR/Cas genome editing in tomato improvement: Advances and applications, *Frontiers in Plant Science*, 14: 1121209.
<https://doi.org/10.3389/fpls.2023.1121209>
- Tominello-Ramirez C.S., Muñoz Hoyos L., Oubounyt M., and Stam R., 2024, Network analyses predict major regulators of resistance to early blight disease complex in tomato, *BMC Plant Biology*, 24(1): 641.
<https://doi.org/10.1186/s12870-024-05366-0>
- Zaccaron A.Z., and Stergiopoulos I., 2024, Analysis of five near-complete genome assemblies of the tomato pathogen *Cladosporium fulvum* uncovers additional accessory chromosomes and structural variations induced by transposable elements effecting the loss of avirulence genes, *BMC Biology*, 22(1): 25.
<https://doi.org/10.1186/s12915-024-01818-z>



Disclaimer/Publisher's Note

The statements, opinions, and data contained in all publications are solely those of the individual authors and contributors and do not represent the views of the publishing house and/or its editors. The publisher and/or its editors disclaim all responsibility for any harm or damage to persons or property that may result from the application of ideas, methods, instructions, or products discussed in the content. Publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.
