

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).

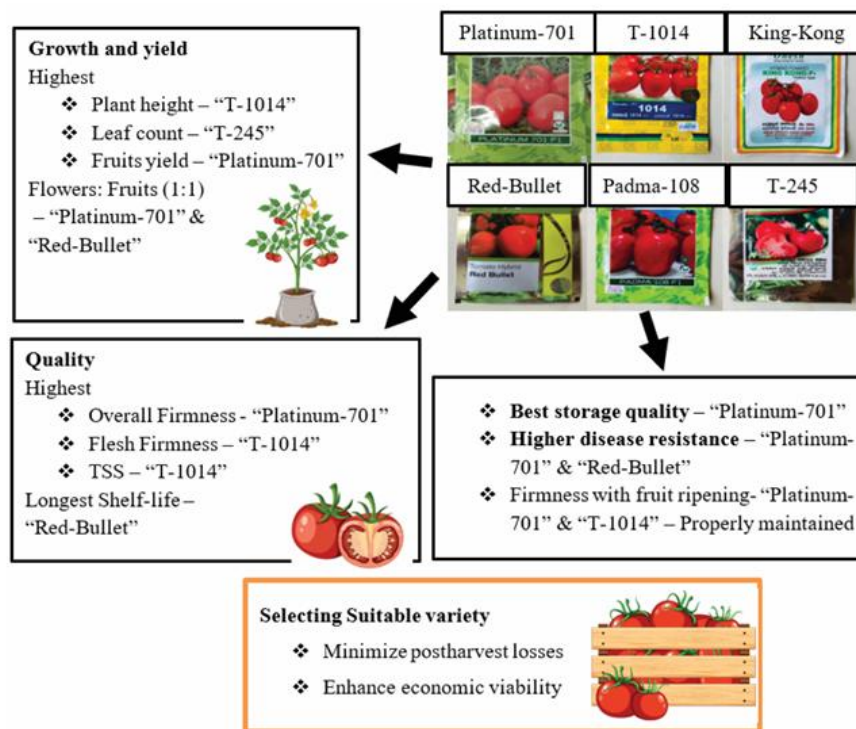


Figure 2 Comparative evaluation of tomato varieties based on growth, yield, quality, and postharvest performance (Adapted from Imali et al., 2025)

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).