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-2^2 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 SlSAMT 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).