

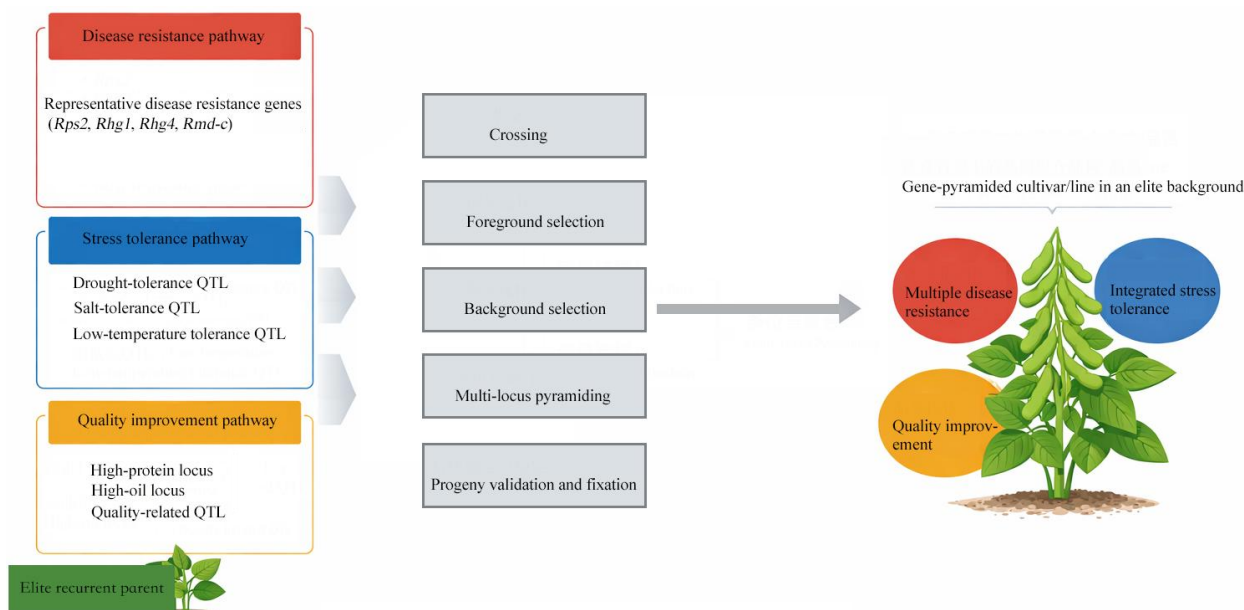


Figure 3 Representative applications of MAS-based gene pyramiding in soybean breeding

5 Limitations of MAS

5.1 Minor-effect QTLs

Although MAS has achieved significant results in the utilization of major genes and large-effect QTLs, its application is often clearly limited by the complex genetic architecture of minor-effect QTLs for typical quantitative traits such as yield, stress resistance, and certain quality traits. Such traits are usually jointly controlled by a large number of small-effect loci, with each individual locus explaining only a very low proportion of phenotypic variation. The remaining variation is also jointly influenced by undetected loci, environmental noise, and epistatic interactions. Therefore, relying only on a small number of markers makes it difficult to fully capture the complete genetic basis (Yáñez et al., 2023; Oh et al., 2025). When the target phenotype is jointly formed by multiple minor-effect QTLs through additive or interactive effects, the advantage of traditional MAS in “targeted selection of a few loci” is significantly weakened. This is also one of the important reasons why MAS is often inferior to genomic selection in the improvement of complex quantitative traits (Yáñez et al., 2023; Li and Lin, 2024).

Another key limitation lies in the poor environmental stability and transferability of minor-effect QTLs. Many minor-effect loci detected in specific populations and environments are often difficult to repeatedly validate under different genetic backgrounds, climatic conditions, or cultivation management practices, reflecting significant genotype $\times$ environment interactions and background-dependent marker–trait associations (Chang-Brahim et al., 2024; Li and Lin, 2024). Precise mapping of such loci usually requires large populations, high-density markers, and repeated validation across multiple environments in order to effectively distinguish true minor-effect QTLs from statistical false positives and reduce the risk of recombination between markers and causal variants (Song et al., 2023). In practical breeding, minor-effect QTLs are often difficult to stably convert into routine MAS tools in the same way as major genes.

5.2 Cost and operational challenges

Although MAS can theoretically significantly improve breeding efficiency, its routine promotion is still constrained by both cost and operational conditions, especially in resource-limited breeding programs. First, high-throughput genotyping, SNP chips, and sequencing-based detection platforms still involve relatively high costs when applied to large-scale populations, and often require dedicated instruments, reagents, and data processing software. As a result, although the testing cost per sample may decrease, the initial infrastructure investment and continuous operating expenses remain high (Song et al., 2023; Chang-Brahim et al., 2024). Even