

early-generation selection, marker-assisted backcrossing (MABC), and the pyramiding of favorable alleles (Li et al., 2024; Wang et al., 2024).

With the completion of soybean genome sequencing and the application of high-throughput genotyping platforms, such as SoySNP50K and BARCSoySNP6K, a large number of genes and QTLs controlling important agronomic traits, disease resistance, and seed quality have been gradually identified, laying a foundation for the application of MAS in soybean breeding (Ravelombola et al., 2021; Lin et al., 2022). For example, MAS for maturity E gene loci (E1-E4, etc.) has been successfully applied to the improvement of early-maturing adaptability in high-latitude regions (Yerzhebayeva et al., 2023); the prediction accuracy of SNP markers for pod shattering resistance, such as KSS-SNP5, can exceed 90% (Kim et al., 2020); and various SSR and KASP markers have also been developed to improve quality traits such as seed protein, oil content, and Kunitz trypsin inhibitor (Riaz et al., 2023; Li et al., 2024). Studies have shown that MAS has become an important conventional breeding strategy for introducing key genes into the genetic backgrounds of elite varieties.

Although MAS has made progress in soybean breeding, its application still faces certain limitations. Many important agronomic traits, especially yield-related traits, are usually controlled jointly by multiple loci with small effects and are influenced by gene–environment interactions. This limits the predictive ability of MAS based on a small number of marker loci (Zhang et al., 2016; Ravelombola et al., 2021). Recent studies have shown that, in the improvement of such complex traits, genomic selection (GS) based on whole-genome marker information has higher prediction accuracy. Therefore, modern breeding strategies are increasingly inclined to combine MAS with GS in order to fully exploit the complementary advantages of both approaches (Bhat and Yu, 2021; Miller et al., 2023).

This study systematically analyzes the research progress and practical application effects of MAS in the improvement of important soybean traits, with a focus on its application achievements in disease resistance, stress resistance, agronomic traits, and quality improvement. It also discusses the limitations of MAS in the improvement of complex quantitative traits and its potential integration with emerging technologies such as genomic selection, with the aim of providing a reference for optimizing future molecular breeding strategies in soybean.

2 Application of MAS in Major-Effect Traits

2.1 Disease and pest resistance

Disease and pest resistance is one of the categories of major-effect traits in soybean that is most suitable for marker-assisted selection (MAS). Soybean cyst nematode (SCN) is one of the most destructive diseases and pests worldwide, and breeding resistant varieties is considered the most economical and environmentally friendly control strategy. At present, *rhg1* and *Rhg4* have been successfully identified and have become core loci for SCN resistance improvement. SSR, SNP, CAPS, and KASP markers developed around these loci have been widely used for early-generation screening of breeding populations and pyramiding of resistance genes, thereby improving resistance durability and reducing dependence on a single resistance source (Lin et al., 2022; Qu et al., 2025).

In addition to SCN, *Phytophthora* root rot and soybean rust are also among the most mature disease types for MAS application. *Phytophthora* root rot, caused by *Phytophthora sojae*, is mainly controlled by the *Rps* gene series. Map-based cloning of *Rps11* has shown that major-effect disease-resistance genes can provide direct targets for the deployment of broad-spectrum resistance. Therefore, foreground selection and marker-assisted backcrossing using markers closely linked to *Rps1*, *Rps3*, *Rps6*, *Rps11*, and other genes have become effective strategies for introducing disease-resistance genes into elite genetic backgrounds (Lin et al., 2022). For soybean rust, pyramiding of the *Rpp* gene series has also been applied in breeding. However, because the pathogen *Phakopsora pachyrhizi* evolves rapidly and has complex pathotypes, relying only on a single major-effect gene makes it difficult to maintain long-term stable resistance. Therefore, a combined strategy of “major-effect genes + minor-effect QTLs” is more suitable.