

major-effect gene MAS and whole-genome prediction (Guo et al., 2019; 2021). Therefore, high-throughput genotyping technologies have enabled MAS to transition from “few-locus detection” to a new stage of “high-density, customizable, and integrable” applications.

6.2 Integration with genomic selection

Methodologically, the core difference between MAS and genomic selection (GS) lies in how molecular marker information is utilized. MAS primarily relies on a few discovered and validated markers that are tightly linked to major genes or large-effect QTLs, making it suitable for targeted selection of Mendelian or oligogenic traits such as disease resistance, maturity, and specific quality loci. In contrast, GS assumes that all genome-wide markers may be linked to causal variants and predicts genomic estimated breeding values (GEBVs) by simultaneously estimating all marker effects, making it more suitable for complex quantitative traits controlled by a large number of minor-effect loci (Bhat et al., 2016; Nanthini et al., 2025). In crops such as soybean, with the development of high-throughput SNP chips and GBS platforms, the predictive potential of GS for complex traits such as yield, stress tolerance, and comprehensive quality has continuously improved, while MAS still maintains an advantage in managing major-effect loci.

For highly polygenic complex traits, GS generally offers higher prediction accuracy and genetic gain per unit time than MAS, because it can integrate a large number of minor-effect loci across the genome and their combined effects without requiring individual markers to reach significance thresholds (Budhlakoti et al., 2022). However, when major-effect loci that explain a substantial proportion of phenotypic variation exist for the target trait, MAS still retains strong competitiveness. Therefore, the currently more practical strategy is not to replace MAS with GS, but to integrate the two: use MAS to introgress or fix key major-effect genes, such as disease-resistance genes, maturity genes, or important quality loci; simultaneously utilize GS to optimize the genetic background composed of numerous minor-effect loci, thus improving both Mendelian and quantitative components (Sinha et al., 2023; Kumar et al., 2024; Jarallah et al., 2025). This complementary approach of “precise control of major-effect loci + whole-genome background prediction” is becoming an important direction in soybean molecular breeding in the genomic era.

7 Future Prospects of MAS in Soybean Breeding

7.1 Improving accuracy and validation of molecular markers

The key to further enhancing the application value of MAS in soybean lies in continuously improving the accuracy, stability, and cross-population transferability of molecular markers. Currently, many markers are still based on “tight linkage with target genes or QTLs” rather than directly corresponding to causal variants, and their predictive ability may be reduced in different genetic backgrounds or ecological environments due to recombination or haplotype differences. This is particularly evident for traits regulated by multiple loci, such as seed weight, sucrose content, and seed quality (Bhat and Yu, 2021; Hasan et al., 2021). In the future, fine mapping, candidate gene analysis, and haplotype analysis should be more extensively employed to gradually upgrade traditional linked markers to functional markers or high-resolution targeted SNP panels, enabling markers to more directly reflect causal variants and thereby improving stability and accuracy in routine breeding (Yang et al., 2023).

The practical breeding value of molecular markers does not depend on “significance” but on “sufficient validation”. Future validation systems should emphasize cross-validation, independent population testing, and multi-environment trials to systematically evaluate marker stability across different germplasms and stress conditions. For example, SNPs associated with soybean pod shattering resistance can maintain over 90% prediction accuracy across different breeding stages and environments, indicating that rigorous validation is a prerequisite for markers to enter routine MAS pipelines (Kim et al., 2020). Only sufficiently validated markers have large-scale application value for critical decisions such as parental selection, hybrid design, and release of gene-edited materials. For complex traits, validated key markers can further be integrated with GS models to improve prediction efficiency and decision reliability (Xue et al., 2025).