

by single genes or a small number of major-effect genes. It has achieved stable results in resistance to soybean cyst nematode, resistance to *Phytophthora* root rot, regulation of maturity, and improvement of certain seed quality traits, and has significantly shortened the breeding cycle through marker-assisted backcrossing and gene pyramiding.

However, the advantages of MAS are mainly concentrated in the management of major-effect loci, and clear limitations remain in the improvement of complex quantitative traits. Traits such as yield stability, climate adaptability, and multiple-stress tolerance are usually jointly affected by numerous minor-effect QTLs, gene–environment interactions, and genetic background effects. A small number of markers are difficult to fully explain their phenotypic variation, and therefore their predictive ability is usually weaker than that of genomic selection (GS). MAS is also constrained by the accuracy of phenotypic evaluation, marker stability across populations, environmental dependence of QTLs, and continuous genotyping costs. These problems are particularly prominent in resource-limited breeding systems.

In the future, MAS will not be replaced, but will be repositioned within an integrated genomic breeding framework. A more efficient strategy is to use MAS to precisely track key disease-resistance genes, major adaptive loci, and functional markers, while using GS to optimize polygenic backgrounds. At the same time, multi-omics analysis, high-throughput phenotyping, and artificial intelligence prediction should be integrated to improve the efficiency of candidate locus discovery and cross-environment prediction ability. On this basis, gene-editing technologies such as CRISPR/Cas will enable breeding to gradually move from “indirect selection based on linked markers” toward “direct modification or regulation of causal alleles.”

The development trajectory of MAS in soybean shows that it has evolved from a single molecular tool into a key component of modern precision breeding systems. As long as molecular markers are fully validated and applied synergistically with GS, gene editing, and multi-omics technologies, MAS will remain an important bridge connecting key genes with breeding practice, and will continue to play a central role in developing new soybean varieties with high yield, superior quality, stress resistance, and adaptation to climate change.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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