

when low-cost strategies such as pooled DNA, crude DNA extraction, or multiplex PCR are used to reduce the unit sample cost, laboratory platform construction, quality control, and professional personnel allocation still constitute important barriers (Ru et al., 2015).

MAS is not simply “molecular detection replacing phenotypic evaluation”. Instead, it requires the highly integrated implementation of marker development, DNA extraction, genotyping, data management, and conventional hybridization and selection procedures, which places high demands on a team’s capabilities in molecular biology, statistical analysis, and bioinformatics (Chang-Brahim et al., 2024). In practical operation, differences among laboratories in DNA quality, marker platforms, interpretation standards, and data management may all affect result consistency and technical reproducibility. Meanwhile, some breeding teams lack a clear cost–benefit evaluation framework and are uncertain about the breeding stage at which MAS should be introduced, making it difficult for molecular markers to be truly embedded into routine breeding decision-making processes (Ru et al., 2015). In developing countries or emerging breeding systems, insufficient funding, limited testing services, and pressure from short-term production goals further intensify this problem, resulting in an obviously uneven pattern of global MAS application.

5.3 Limitations of MAS in complex traits

The limitations of MAS are most prominent in the improvement of complex traits, especially in polygenic traits such as yield, adaptability, and comprehensive stress resistance. Such traits are usually determined by a large number of minor-effect loci and are simultaneously influenced by gene–environment interactions (G×E) and epistatic effects. Therefore, the phenotypic variation explained by a single or a few QTLs is very limited, making it difficult to accurately predict final performance (Yáñez et al., 2023). Taking soybean yield as an example, it is essentially the combined result of multiple component traits such as pod number, seed weight, branch number, and growth period. If only a few molecular markers are tracked, it is insufficient to capture the complete genetic basis, and the improvement magnitude may also be difficult to justify the cost and operational complexity of MAS implementation (Yáñez et al., 2023; Oh et al., 2025).

Marker–trait associations in complex traits often show clear environmental dependence: a QTL that is significant in one population or environment may have a weakened effect or even disappear under another genetic background, management condition, or climatic context, thereby reducing the stability and transferability of MAS results (Chang-Brahim et al., 2024; Li and Lin, 2024). Increasing numbers of studies advocate limiting MAS to major genes and large-effect QTLs, while assigning the improvement of highly polygenic traits more to genomic selection (GS), because GS can use whole-genome marker information to integrate a large number of minor-effect loci and their interaction effects (Yáñez et al., 2023; Kumar et al., 2025).

6 MAS in the Genomic Era

6.1 High-throughput genotyping technologies

With the rapid development of genomics, high-throughput genotyping technologies have significantly expanded the marker resources and application boundaries of MAS. Due to their wide distribution, high stability, and ease of automated detection, SNPs have become the core marker type in modern molecular breeding. Commercial SNP chips can typically detect tens of thousands to hundreds of thousands of loci simultaneously and have been widely used for QTL mapping, routine MAS, genomic selection (GS), and breeding quality control (Kumar et al., 2024). In soybean, high-density platforms such as SoySNP50K have been used for constructing genetic maps and screening key loci, providing a basis for high-precision MAS (Bhat et al., 2016).

The popularization of NGS has further promoted the development of sequencing-based genotyping (GBS). GBS can simultaneously discover and genotype thousands of SNPs at a relatively low cost through reduced-representation genome sequencing, combining high throughput with considerable flexibility. Even at lower sequencing depths, it can support genetic analysis of complex traits and prediction of breeding values (Bhat et al., 2016; Sinha et al., 2023). New platforms such as GBTS and mSNP liquid-phase chips provide layered schemes with approximately 1K to over 40K markers, allowing the same system to simultaneously serve