

7.2 Integrating MAS with multi-omics data

Future soybean MAS will no longer be limited to DNA-level linked markers, but will rely more on the coordinated integration of genomic, transcriptomic, proteomic, metabolomic, and high-throughput phenotypic data to systematically reveal the causal chains between “genotype–regulatory network–phenotype” (Hasan et al., 2021; Vargas-Almendra et al., 2024). For example, combining SNP information obtained from GWAS with transcriptomic expression patterns can more accurately distinguish truly functional candidate genes from markers that are merely in linkage. Further overlaying metabolomic data helps to pinpoint key pathways directly involved in seed component formation, stress responses, or developmental regulation, thereby improving the precision of functional marker development (Budhlakoti et al., 2022).

The value of multi-omics integration lies not only in improving marker development accuracy but also in enhancing the biological interpretability of MAS and its ability to improve complex traits. Studies have shown that incorporating a small number of metabolite markers obtained from metabolome association analysis into prediction models can increase the prediction accuracy of heterosis or complex traits by 4%-14%, sometimes even exceeding that of full genome–metabolome models (Xu et al., 2025). Applying similar strategies to soybean allows breeders to prioritize markers from transcripts, proteins, or metabolites with clear functional links to sucrose, isoflavones, protein, oil, or stress responses, making MAS not just “tracking loci” but “fixing favorable alleles within regulatory networks” (Riaz et al., 2023; Xue et al., 2025). In the future, multi-omics-driven MAS can also synergize with GS and gene editing to provide more interpretable and precise molecular breeding strategies for complex traits.

7.3 Developing climate-adapted soybean varieties

Climate change continues to intensify the combined stresses of high temperature, drought, flooding, and emerging pests and diseases on soybean production. Therefore, developing climate-adapted varieties with high yield, stable yield, stress resistance, and superior quality has become one of the core goals of future molecular breeding in soybean (Budhlakoti et al., 2022; Vargas-Almendra et al., 2024). In this process, MAS still plays an irreplaceable role, particularly suitable for tracking and pyramiding major disease-resistance genes, maturity-related genes, and certain stable stress-resistance loci. For highly polygenic traits such as drought tolerance, heat tolerance, and broad adaptability, MAS is best combined with GS to simultaneously capture the contributions of numerous minor-effect loci to complex stress responses (Budhlakoti et al., 2022). Therefore, future climate-adapted soybean breeding should not focus solely on single-stress tolerance but should prioritize fixing key adaptive alleles through MAS, and then optimize the whole-genome background using GS to maintain yield and quality stability under complex environments.

The future climate-adapted soybean breeding system is likely to adopt a comprehensive “MAS + GS + gene editing + rapid breeding” model: MAS is used to identify and fix key alleles, GS predicts combined breeding values under different environments, CRISPR/Cas is used to precisely introduce superior allelic variants when natural variation is insufficient, and rapid breeding shortens generation time to accelerate fixation of target genotypes (Fang et al., 2021; Vargas-Almendra et al., 2024). Studies have shown that optimizing hybrid combinations using genomic prediction can significantly improve the efficiency of soybean genetic improvement. This strategy can also be extended to prioritize the selection of hybrid combinations that combine stress resistance, disease resistance, suitable maturity, and superior quality (Miller et al., 2023). Therefore, MAS in the future will not be applied in isolation but will serve as a “key-locus anchoring tool” in climate-adapted breeding, embedded within a more systematic molecular design breeding framework to support global food and feed security.

8 Concluding Remarks

Marker-assisted selection (MAS) has become an important technical foundation of modern soybean molecular breeding and has profoundly changed the way genetic variation is discovered, tracked, and utilized. With the development of molecular marker systems from RFLP and SSR to high-density SNP chips and NGS-based detection platforms, breeders are able to more efficiently associate genomic regions with disease resistance, adaptability, quality, and some yield-related traits. In soybean, MAS is particularly effective for traits controlled