

Research Perspective

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Marker-assisted Selection in Soybean Breeding: Achievements and LimitationsHangming Lin ¹ ✉, Xiaoxi Zhou ²¹ Tropical Legume Research Center, Hainan Institute of Tropical Agricultural Resources, Sanya, 572025, Hainan, China² Institute of Life Sciences, Jiyang College of Zhejiang A&F University, Zhuji, 311800, Zhejiang, China✉ Corresponding author: hangming.lin@hitar.orgInternational Journal of Horticulture, 2026, Vol.16, No.3 doi: [10.5376/ijh.2026.16.0014](https://doi.org/10.5376/ijh.2026.16.0014)

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Abstract Soybean is a globally important crop for both food and oil production. However, traditional breeding relies heavily on phenotypic selection, which is time-consuming, inefficient, and highly influenced by environmental factors, making it difficult to achieve the coordinated improvement of high yield, superior quality, and stress resistance. This study systematically reviews the application progress of marker-assisted selection (MAS) in soybean breeding, including resistance to diseases and pests, tolerance to abiotic stresses, optimization of agronomic traits, and improvement of seed quality. It also analyzes the practical value of MAS in gene pyramiding and backcross breeding. The results indicate that MAS has clear advantages in tracking, introgressing, and pyramiding major genes and large-effect quantitative trait loci (QTL), thereby improving selection efficiency and shortening breeding cycles. However, for complex quantitative traits such as yield and wide adaptability, its effectiveness is still constrained by factors including minor-effect QTL, gene–environment interactions, and cost inputs. MAS serves as a fundamental technology for precision breeding in soybean. In the future, it should be integrated with genomic selection, multi-omics approaches, and gene editing technologies to enhance the improvement of complex traits and support the development of climate-resilient soybean varieties.

Keywords Soybean; Marker-assisted selection; Gene pyramiding; Quality improvement; Genomic selection

1 Introduction

Soybean (*Glycine max* (L.) Merr.) is an important crop used for both grain and oil production. It provides plant protein and oil for human food, animal feed, and industrial uses, and holds a highly important position in global agricultural production (Bhat and Yu, 2021; Xue et al., 2025). In recent years, with population growth, changes in dietary structure, and the expansion of animal husbandry and bio-based industries, global demand for soybean yield and quality has continued to increase (Vargas-Almendra et al., 2024). Climate change, emerging diseases, and limited arable land resources have also placed greater pressure on soybean production. Therefore, more efficient breeding methods are needed to develop new varieties with higher yield, better quality, and stronger stress resistance as soon as possible.

Traditional soybean breeding mainly relies on phenotypic selection and long-term field evaluation, and has achieved many results in genetic improvement. However, the overall breeding cycle is long, the labor demand is high, and the process is easily affected by the environment. These limitations are particularly evident in the improvement of complex quantitative traits such as yield, quality, and stress resistance (Ma et al., 2016; Bhat and Yu, 2021). With the development of molecular biology and genomics, introducing molecular genetic information into the breeding process has become an important approach to improving efficiency and shortening the breeding cycle.

Marker-assisted selection (MAS) has developed under this background. It uses DNA markers closely linked to target genes or quantitative trait loci (QTLs) to conduct indirect selection in breeding populations (Bhat and Yu, 2021). Compared with traditional phenotypic selection, MAS can complete genotypic identification at the seed or seedling stage, reduce repeated phenotypic evaluations, and improve screening efficiency (Lin et al., 2022). Commonly used markers currently include SSR, SNP, InDel, and KASP, which have been widely applied in