

In terms of insect pests, Rag series genes associated with traits such as resistance to soybean aphid have also been mapped and used for molecular detection, indicating that MAS is applicable not only to disease resistance, but also to the rapid introgression and pyramiding of major pest-resistance loci.

2.2 Abiotic stress tolerance

Abiotic stresses such as drought, salinity-alkalinity, high temperature, low temperature, and waterlogging continue to limit stable and increased soybean production. Under the background of climate change, both their frequency and damage intensity are increasing. Therefore, stress-resistance breeding has become an important direction in soybean improvement (Manghwar et al., 2022). Although most stress-resistance traits have quantitative genetic characteristics, recent GWAS and QTL mapping studies have identified a group of loci with relatively large effects in soybean, enabling MAS to conduct effective selection for certain key tolerance traits. Taking drought resistance as an example, related QTLs are mostly associated with root architecture, osmotic regulation, and the maintenance of redox homeostasis, and are closely related to yield and yield stability under drought conditions (Amangeldiyeva et al., 2025; Gai et al., 2025) (Figure 1). In addition, the practice of introducing drought-resistance QTLs through MAS in rice, which achieved yield improvement under stress conditions without an obvious yield penalty under normal environments, also provides methodological reference for drought-resistance breeding in soybean (Ramayya et al., 2021; Hassan et al., 2023).

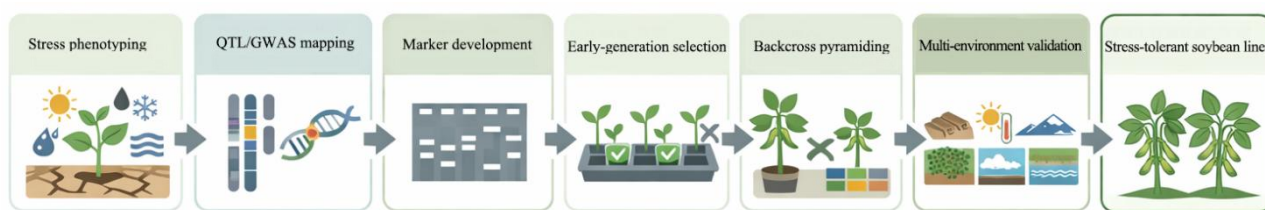


Figure 1 Molecular marker-assisted breeding workflow for soybean abiotic stress tolerance

Salinity-alkalinity stress is another key factor limiting regionalized soybean production. In addition to classical salt-tolerance loci, recent studies have further identified key genes such as *GmPM30*, whose favorable haplotypes can significantly improve survival and yield performance under salt stress by maintaining ion homeostasis and alleviating oxidative damage. The related haplotype-specific markers already have potential for application in MAS pipelines (Gai et al., 2025; Huang et al., 2025). In terms of waterlogging and heat tolerance, although their genetic bases are more complex, several major-effect QTLs or candidate regulatory genes associated with flooding survival rate, pollen viability, and flowering stability have been reported, such as *GmDREB*, *GmNAC*, *GmWRKY*, and *GmHSP*, indicating that MAS can still be used for targeted improvement around stable major-effect loci (Manghwar et al., 2022; Gai et al., 2025).

2.3 Agronomic trait improvement

Agronomic traits such as plant height, branching patterns, and growth habits directly affect light interception efficiency, lodging resistance, adaptability to mechanized harvesting, and final yield potential in soybean populations. Therefore, they are important targets for MAS of major-effect loci. GWAS and linkage analyses have identified multiple genomic regions associated with plant height and architecture in soybean, some of which overlap with determinate/indeterminate growth habit genes. The related SSR and SNP markers have been validated in breeding populations (Ravelombola et al., 2021; Podzorova et al., 2022). For example, SSR markers Satt244, Satt288, and Satt371 are significantly associated with plant height and related yield traits and can be used for early-generation selection of ideal plant-type materials, reducing lodging risk and improving population uniformity (Podzorova et al., 2022).

Flowering and maturity time are core traits determining regional adaptability of soybean, mainly regulated by photoperiod response genes such as *E1*, *E2*, *E3*, and *E4*. SNP markers closely linked to these loci have been used in breeding for adaptation to different ecological zones, allowing breeders to rapidly select genotypes with