: Genomic selection; Phenomic pro ling; Marker-assisted breeding; High-throughput phenotyping; Quantitative trait loci (QTL); Gene editing

In contemporary agricultural research, the eld of molecular plant breeding has revolutionized traditional breeding practices by integrating molecular biology with classical breeding methods [1-3]. is interdisciplinary approach leverages advancements in genomics, phenomics, and bioinformatics to expedite the development of improved crop varieties with desirable traits. By utilizing genomic tools such as marker-assisted selection and genomic selection, breeders can identify and manipulate genes associated with key agronomic traits more precisely and e ciently than conventional breeding methods allowed.

Moreover, the emergence of high-throughput phenotyping technologies has enabled comprehensive characterization of plant phenotypes at various scales, from molecular to organismal levels [4]. is capability not only enhances the accuracy of trait evaluation but also facilitates the identi cation of genotype-phenotype associations crucial for targeted breeding e orts. Additionally, the advent of gene editing technologies like CRISPR/Cas9 has provided unprecedented opportunities for precise genome modi cations, enabling breeders to introduce bene cial genetic variations directly into plant genomes. is approach holds promise for accelerating breeding cycles and addressing complex traits that were previously challenging to improve through conventional methods [5-7]. is introduction sets the stage for

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