

diversity in certain market types, thereby limiting further genetic gain in yield. For example, the yield improvement of processing cucumbers in the United States has shown little progress over the past 15 years despite long-term selection, suggesting that reliance solely on conventional selection may be insufficient to overcome yield plateaus.

The application of molecular breeding technologies to the improvement of complex yield traits still faces several bottlenecks. Because yield is generally controlled by multiple loci with small effects, the efficiency of marker-assisted selection (MAS) for complex yield traits remains limited, and the transferability of markers across different market types and genetic backgrounds is often inadequate. For example, background-selection SNP markers developed for Korean Baekdadagi-type cucumber exhibit reduced polymorphism in other materials, requiring the establishment of specialized marker systems. Even for major-effect traits, the lack of tightly linked and breeding-applicable markers can limit their practical use. Breeding for cucumber vein yellowing virus resistance was greatly constrained before the fine mapping of the CsCvy-1 gene and the development of KASP markers. Furthermore, candidate genes, QTLs, and regulatory mechanisms identified under laboratory or single-environment conditions still require validation across multiple locations, seasons, and cultivation systems to assess their stability and breeding value. This is particularly important under protected cultivation conditions, where temperature, light, CO<sub>2</sub> concentration, water and fertilizer supply, diseases, pests, and management practices interact strongly. Therefore, the translation of fundamental research findings into practical production systems remains a major challenge.

## 7.2 Future directions driven by emerging technologies

With the rapid development of modern biotechnology, information technology, and intelligent agriculture, research on cucumber yield formation mechanisms is shifting from single-gene and single-trait analyses toward multi-omics, multi-environment, and data-driven systematic investigations. High-quality reference genomes, saturated SNP genetic maps, and genotyping platforms based on SLAF-seq, GBS, and resequencing technologies have provided important tools for high-density QTL mapping of fruit size, branching, flowering traits, parthenocarp, and other yield-related traits. Some identified loci can explain a substantial proportion of phenotypic variation and provide important foundations for fine mapping and gene cloning (Wang et al., 2024). In the future, greater emphasis should be placed on comparisons among different genetic backgrounds, cultivation environments, and market types to improve the stability and breeding applicability of key loci.

Multi-omics technologies will further enhance the dissection of complex yield traits in cucumber. Next-generation sequencing, transcriptomics, metabolomics, and proteomics can generate large amounts of molecular marker, expression, and metabolic regulatory data, thereby supporting genome-wide association studies (GWAS), haplotype mapping, candidate gene mining, and stress adaptation research. Future studies should strengthen the integration of genomic, transcriptomic, proteomic, metabolomic, phenomic, and environmental data to construct association models linking “genes-regulatory networks-physiological processes-yield phenotypes-cultivation environments.” Such approaches will promote the transition from single candidate-gene analysis to comprehensive dissection of complex regulatory networks.

Gene editing, high-throughput phenotyping, and artificial intelligence technologies will become major driving forces in high-yield cucumber breeding. CRISPR/Cas systems enable precise modification of key functional genes. For example, targeted knockout of the cucumber eIF4E gene has produced non-transgenic materials with broad-spectrum resistance to multiple RNA viruses without causing significant negative effects on yield, demonstrating that precise gene editing can rapidly achieve durable disease resistance and indirectly stabilize yield. In the future, gene editing should be integrated with MAS, genomic selection (GS), and multi-omics-based candidate gene mining to pyramid superior alleles related to high yield, superior quality, disease resistance, stress tolerance, and adaptation to protected cultivation systems (Bhat et al., 2023; Kumar et al., 2024). Meanwhile, intelligent phenotyping systems based on image recognition, automated sensors, three-dimensional reconstruction, unmanned platforms, and machine learning can continuously monitor plant architecture, leaf area, flowering dynamics, fruit development, and stress responses, thereby providing important support for predicting gene-trait