

relationships, optimizing hybrid combinations, and designing ideal plant architectures (Bhat et al., 2023; Farooq et al., 2024; Zhu et al., 2024).

7.3 Prospects for high-yield cucumber breeding

Future high-yield cucumber breeding will increasingly rely on the deep integration of conventional breeding, molecular breeding, intelligent phenotyping, and digital decision-making technologies. Existing gene and QTL databases, together with gradually standardized nomenclature systems, provide important foundations for constructing genome-wide resource libraries of yield-related loci, plant architecture loci, sex expression loci, and disease-resistance QTLs, thereby facilitating the pyramiding of superior genes through MAS and marker-assisted backcrossing (Dhall et al., 2023). Studies on multi-pistillate flowering QTLs, the parthenocarp locus Parth2.1, sex expression, and fruit diameter indicate that multiple genetic factors affecting fruit number and fruit size can be effectively pyramided through molecular breeding approaches, enabling the development of ideal high-yield plant architectures adapted to different market types and production systems (Wang et al., 2024).

Future breeding objectives will shift from the simple pursuit of high yield toward the coordinated improvement of high yield, superior quality, stable production, stress resistance, and resource-use efficiency. As consumer demands for fruit quality, nutritional value, and food safety continue to increase, new cucumber cultivars should not only possess high yield potential but also exhibit excellent marketability, enhanced nutritional quality, strong disease and stress resistance, and adaptability to water-saving, fertilizer-saving, low-pesticide-input, and intelligent greenhouse management systems. Particularly under the background of climate change, breeding cultivars resistant to low temperature, low light, high temperature, salinity, and multiple diseases will become an important strategy for ensuring stable vegetable supply in protected horticulture systems (Mirzwa-Mróz et al., 2024).

Accelerated breeding technologies will substantially shorten the breeding cycle of new cucumber cultivars and improve selection efficiency for complex yield traits. Doubled haploid (DH) technology, rapid generation advancement, speed breeding in greenhouses, high-throughput phenotyping, and artificial intelligence-assisted selection can be integrated with GS and molecular design breeding to improve prediction accuracy and breeding efficiency for complex traits (Bhat et al., 2023). At the same time, multi-omics studies will further elucidate the regulatory networks underlying yield formation and stress adaptation and guide precise gene editing and molecular marker design (Mirzwa-Mróz et al., 2024). It can be anticipated that with the integrated development of genomics, phenomics, artificial intelligence, gene editing, and intelligent protected agriculture, high-yield cucumber breeding will gradually enter a new stage characterized by precision, intelligence, and sustainability.

8 Concluding Remarks

Cucumber is one of the most important vegetable crops worldwide, with an annual global production reaching tens of millions of tons. It has extremely high market demand in major producing countries such as China; therefore, improving and stabilizing cucumber yield is of great economic and food-supply significance. Cucumber yield is determined by multiple interacting traits, including earliness, sex expression, fruit number and size, and resistance to biotic and abiotic stresses. The genetic basis of these traits is being progressively elucidated through QTL mapping, mutant analysis, and molecular characterization. Owing to its relatively small genome, diploid structure, short life cycle, and abundant natural and artificial genetic variation, cucumber has become an ideal model crop for dissecting yield-related traits and rapidly applying research findings to breeding practice.

To date, systematic studies have identified at least 81 simply inherited genes or major-effect QTLs, as well as 322 QTLs associated with 42 quantitative traits, many of which are directly or indirectly related to cucumber yield, fruit size and shape, flowering time, sex expression, and stress resistance. Wild ancestral species and diverse landraces provide rich allelic resources for flowering traits, fruit size, and yield components. Some QTLs exhibit clear signatures of domestication and improvement selection; however, positive transgressive segregation can still occur when favorable wild alleles are introgressed into elite cultivated backgrounds. Fine mapping and cloning studies of major fruit-size QTLs, such as FS5.2/CsCRC, and parthenocarp QTLs, such as Parth2.1, have demonstrated that their regulatory mechanisms mainly involve auxin, gibberellin, and cytokinin signaling