

pathways, as well as the regulation of cell division and expansion, thereby revealing how genetic variation is translated into different yield architectures. Meanwhile, studies on sex expression, multi-pistillate flowering, and parthenocarp have identified multiple key loci and marker-trait associations, further clarifying the genetic networks underlying increased female flower production and enhanced fruit set and their contributions to yield formation.

Future breeding for high-yield cucumber cultivars will increasingly rely on the integrated application of genomic resources, multi-omics data, and advanced selection technologies. Comprehensive gene/QTL databases, high-density SNP molecular markers, and background-selection marker systems provide powerful tools for the precise pyramiding of favorable alleles related to yield, quality, and stress resistance. Genomic selection (GS), genome-wide association studies (GWAS), and gene-editing technologies, combined with rapid generation advancement and efficient phenotyping approaches, are expected to accelerate the development of ideal cucumber plant types possessing desirable fruit size, high female flower ratio, multi-pistillate flowering ability, stable parthenocarp, and broad stress resistance. At the same time, continuous exploration of wild resources and underutilized germplasm, as well as further dissection of domestication-related QTLs and heterosis-associated loci, will broaden the allelic resource pool for high-yield and stable-yield cucumber breeding. Overall, the integration of conventional breeding approaches with genomics and molecular biology technologies has made cucumber an important crop in which high and stable yield can be achieved through the rational design and targeted pyramiding of yield-related traits.

Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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