

flower number, fruit dry matter accumulation, and total yield (Koo et al., 2024). Furthermore, optimization of greenhouse light environments based on cucumber light response characteristics can further improve canopy light-use efficiency and greenhouse production efficiency.

Water availability and root-zone environment also significantly affect cucumber yield formation. Cucumber possesses a relatively shallow root system and is highly sensitive to changes in soil moisture. Water deficit inhibits photosynthesis and cell turgor, thereby restricting fruit enlargement, whereas excessive water accumulation can cause root hypoxia and disease occurrence, reducing CO₂ assimilation efficiency and PSII photochemical activity. Under protected cultivation conditions, coordinated management of CO₂ concentration, temperature, light, water, and fertilizer can effectively improve dry matter accumulation and fruit quality. Studies have shown that the combination of elevated CO₂ and appropriate temperature not only promotes the accumulation of sugars, organic acids, and amino acids but also enhances fruit heat tolerance under high-temperature conditions while maintaining yield stability (Du et al., 2024). Therefore, under climate change scenarios, combining precise environmental regulation in protected cultivation systems with the breeding of stress-resistant genotypes is an important strategy for improving cucumber yield stability and resource-use efficiency.

5 Molecular Mechanisms of Cucumber Yield Formation

5.1 Yield-related functional genes

Cucumber yield formation is a complex process jointly determined by multiple genes, loci, and regulatory pathways, involving vegetative growth, sex differentiation, floral organ formation, fruit set, fruit enlargement, organ size regulation, and stress responses. With the continuous advancement of cucumber genomics, fine QTL mapping, and functional genomics studies, an increasing number of functional genes and major-effect QTLs closely associated with yield component traits have been identified, providing an important foundation for elucidating the mechanisms underlying high-yield formation and for conducting molecular design breeding in cucumber. Yield-related functional genes in cucumber mainly affect final yield through the regulation of fruit morphology, organ size, source-sink relationships, and stress adaptability.

Fruit length, fruit diameter, fruit shape index, and single fruit weight are core traits constituting cucumber yield and are also the major focus of current functional gene studies. The major fruit shape QTL FS5.2 has been finely mapped to a 95.5-kb interval, and its candidate gene, CsCRC, encodes a YABBY transcription factor that influences fruit morphology by regulating cell length and cell layer number, resulting in the short and thick fruit phenotype of Xishuangbanna cucumber. CsTRM5, a homolog of tomato TRM5, controls the round-fruit locus FS2.1, and loss of its function alters the direction of cell division and weakens cell expansion, thereby producing spherical fruits (Xie et al., 2023). In addition, CsSUN, located at the FS1.2 locus, is a homolog of the SUN gene and contains a 161-bp deletion in round-fruit types, significantly affecting the fruit length-to-diameter ratio. These studies indicate that cell division orientation, cell layer number, and cell expansion processes are important cytological bases determining cucumber fruit morphology and single fruit weight.

In addition to fruit morphology-related genes, some functional genes can influence yield by regulating leaf size, photosynthetic source strength, organ development, and continuous fruiting ability. The R2R3-MYB transcription factor CsRAXs suppresses leaf size and continuous fruiting ability by promoting auxin glycosylation. Its triple mutants exhibit larger leaves, higher fruit number per plant, and higher yield, whereas overexpression lines display reduced leaf area and fruit number (Chen et al., 2024). The littleleaf (LL) gene encodes a WD40 protein that restricts cucumber organ size and is closely associated with the expression of organ size regulators and hormone-related genes (Xu et al., 2023). SF1 encodes a RING-type E3 ubiquitin ligase that regulates fruit elongation through ethylene-dependent cell division processes (Xie et al., 2023). To date, 81 simply inherited genes or major-effect QTLs and 322 QTLs associated with 42 quantitative traits have been systematically identified in cucumber, many of which are related to fruit size, fruit shape, fruit number, and other yield component traits, and diagnostic markers applicable to breeding have been developed. In addition, heat shock proteins, antioxidant enzymes, hormone signaling factors, and members of transcription factor families such as