

MYB, NAC, WRKY, bHLH, and ERF/AP2 can maintain fruit-setting ability and yield stability by regulating photosynthetic stability, hormonal balance, and stress responses.

## 5.2 Signal transduction and regulatory networks

Cucumber yield formation depends not only on the effects of individual functional genes but also on the coordinated regulation of complex signal transduction and transcriptional regulatory networks. Plant hormone signaling serves as an important bridge linking functional genes, cellular development, and yield phenotypes. Hormones such as ethylene, auxin, gibberellins, cytokinins, and abscisic acid participate in sex differentiation, floral organ formation, parthenocarpy, fruit elongation, and organ size regulation through synergistic or antagonistic interactions. The dynamic balance among different hormonal pathways determines fruit set stability, fruit development efficiency, and final yield level in cucumber. Therefore, shifting from single-gene effects to integrated regulatory networks is an important direction for understanding the molecular mechanisms of cucumber yield formation.

Within the fruit morphology regulatory network, CsCRC acts as an important hub connecting transcriptional regulation, hormone signaling, and cellular development. FS5.2/CsCRC regulates auxin content and the expression of auxin-responsive genes, linking YABBY-mediated transcriptional regulation with auxin-regulated cell division and cell expansion processes. Meanwhile, gibberellin signaling also participates in CsCRC-dependent fruit elongation regulation. Further studies have shown that CsPIF1 can directly activate CsCRC transcription, whereas the YABBY protein CsINO and the bHLH protein CsSPT1 physically interact with CsCRC, thereby integrating light signaling, reproductive development, and auxin regulation into the fruit elongation process (Xie et al., 2023). Transcriptome analyses of near-isogenic lines with long and short fruits further revealed significant activation of microtubule-, cell cycle-, and hormone-related genes, while multiple transcription factor families, including MYB, bHLH, NAC, and ERF/AP2, were involved in fruit length regulation (Che et al., 2023; Xing et al., 2023).

Parthenocarpy is an important mechanism enabling greenhouse cucumber to maintain stable yield under insufficient pollination, low-light conditions, or environmental stresses, and its formation also depends on precise hormonal network regulation. Materials with strong parthenocarpic ability generally exhibit higher cytokinin and gibberellin levels and lower ABA levels, accompanied by upregulated expression of cytokinin biosynthesis and response genes as well as auxin signaling components. Exogenous application of cytokinins, auxin, or GA<sub>4+7</sub> can induce parthenocarpic fruit formation in weakly parthenocarpic materials. The GA biosynthesis gene CsGA20OX1 is considered a positive regulator of parthenocarpy, and both its expression level and related hormone contents are significantly increased in induced parthenocarpic fruits (Meng et al., 2026). In addition, LL-mediated organ size regulation is associated with auxin and cytokinin pathways, whereas CsTRM5-mediated fruit shape variation involves ABA accumulation and changes in the expression of genes related to cell wall formation and ABA signaling. Exogenous ABA can reduce fruit elongation by inhibiting cell expansion (Figure 2) (Xie et al., 2023; Xu et al., 2023). These findings indicate that cucumber yield formation results from the combined action of multi-level regulatory networks involving hormone signaling, transcriptional regulation, cell division, and cell expansion.

## 5.3 Multi-omics studies and molecular breeding

The development of multi-omics technologies has provided important tools for systematically elucidating the mechanisms underlying cucumber yield formation. Genomics can reveal genetic variation, structural variation, and candidate genomic regions among different materials; transcriptomics can analyze dynamic gene expression under different developmental stages and environmental conditions; and proteomics and metabolomics help clarify the relationships between yield formation and processes such as signal transduction, hormone metabolism, cell wall formation, sugar metabolism, and amino acid metabolism. Through integrated multi-omics analyses, researchers can construct molecular regulatory networks underlying high-yield formation in cucumber at multiple levels, including “gene-transcript-protein-metabolite-phenotype”.