8 Concluding Remarks

Sugar–acid balance in kiwifruit is regulated by a coordinated developmental program in which sugar accumulationand acid remodeling proceed together rather than independently. Across development and ripening, metabolome–transcriptome studies show that flavor formation reflects linked changes in soluble sugars, organic acids, and their regulatory genes, with network organization becoming clearer when fruit are sampled across many developmental stages. During postharvest ripening, starch reserves are converted into sucrose, glucose, and fructose while titratable acidity declines mainly through citrate degradation, producing the sensory shift from sour, firm fruit to sweet, edible fruit. This coordination is stage specific: early fruit development emphasizes starch and acid accumulation, whereas ripening activates starch breakdown, sugar release, respiratory carbon reallocation, and acid decline. Recent work also shows that this transition is not governed by ethylene alone, because cool temperature can directly activate AcBAM-centered starch degradation through the AcPUB11–AcCTS1–AcBAM3 module, linking environmental sensing to flavor formation.

Substantial progress has been made in identifying the structural genes, transcription factors, and hormonal cues involved in this process, but the regulatory architecture remains incomplete. Network studies in ‘Hongyang’ and red-fleshed kiwifruit have uncovered modules linking sugar metabolism, organic acid metabolism, and ripening-related transcription factors, yet these studies also emphasize that earlier work relied heavily on single-omics designs or limited metabolite coverage. Cultivar and species differences remain a major gap. ‘Hongyang’ and ‘Jinyan’ differ in their dominant sugar composition, *A. eriantha* shows distinctive high-acid behavior, early-maturing germplasm exhibits faster starch conversion under lower endogenous hormone levels, and species-level comparisons reveal divergent carbon allocation strategies between sweetness and other quality traits. Even postharvest flavor regulation can be strongly genotype dependent, as shown by varietal specificity in ‘Cuixiang’, *A. melanandra*, and CPPU-treated red-fleshed fruit.

Another unresolved issue is the still limited integration of metabolism, transport, and signaling across tissues and scales. Existing studies have largely succeeded in mapping changes in metabolites and candidate transcripts, but fewer have connected these data to tissue-specific transport, chromatin state, alternative splicing, long noncoding RNAs, or epigenetic regulation. This matters because flavor balance likely emerges from cross-compartment and cross-pathway coordination, not from enzyme abundance alone. Spatiotemporal networks already show that regulatory relationships differ among fruit skin, outer pericarp, inner pericarp, and core, while m6A studies show that epigenetic modifiers such as AcALKBH10 can simultaneously increase glucose, fructose, and sucrose and decrease citrate. More broadly, studies in other fruit systems indicate that integrated transcriptomic, chromatin, hormonal, and metabolomic analyses are effective for uncovering regulators of sugar and acid accumulation, suggesting a clear path forward for kiwifruit.

Future research should therefore move toward multi-omics dissection of sugar–acid regulatory networks across diverse *Actinidia germplasm*, tissues, environments, and postharvest conditions. Dense time-series sampling remains essential because regulatory peaks for transcripts, enzymes, and metabolites are stage dependent and may be missed by single-time-point studies. At the applied level, the field is now positioned to translate candidate genes, metabolite markers, and trait-linked SNPs into molecular breeding for flavor-balanced cultivars and into precision cultivation strategies that better align orchard climate, ripening management, and harvest timing with desired sugar–acid outcomes. Because consumers perceive flavor through the combined balance of sugars, acids, and other metabolites, breeding targets should shift from single traits such as SSC toward integrated flavor phenotypes supported by metabolomic and genetic markers.

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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.