and citrate while increasing AcPNAD-MDH1 expression (Qi et al., 2025). Broader kiwifruit studies on MYB and bZIP factors, although centered on ascorbate metabolism, show that these families form cooperative transcriptional complexes and are hormone responsive, making them plausible components of wider flavor-regulatory networks (Liu et al., 2022).

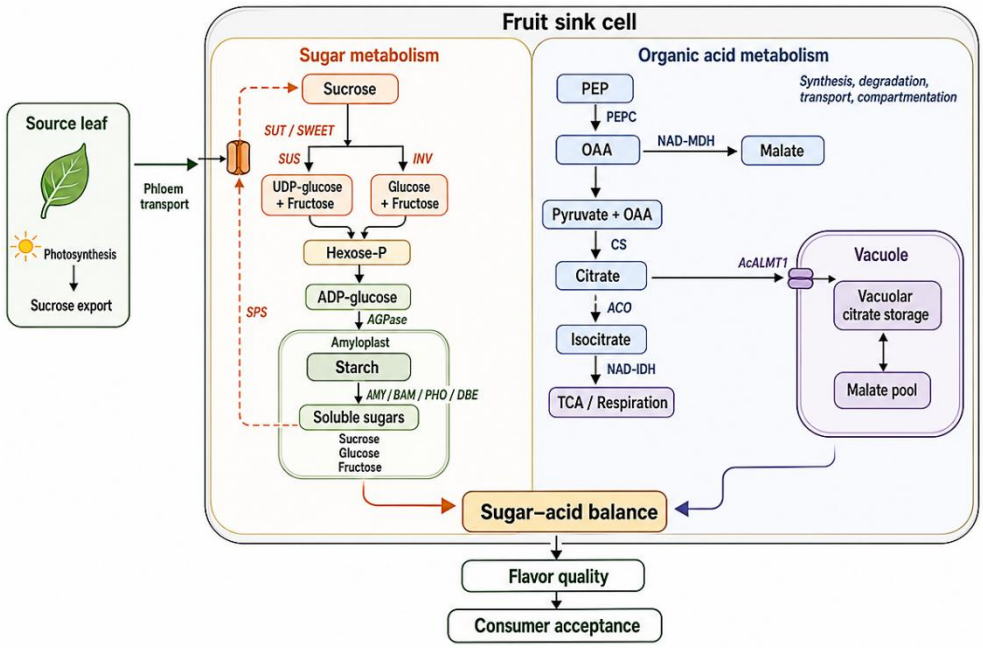


Figure 2 Integrated metabolic framework of sugar and organic acid metabolism underlying sugar – acid balance in kiwifruit
Image caption: Imported sucrose is unloaded into fruit tissues and enters sucrose cleavage, hexose metabolism, and starch biosynthesis pathways. During maturation and ripening, stored starch is remobilized through amylolytic pathways to support sucrose, glucose, and fructose accumulation. Organic acids are linked to central carbon metabolism through the TCA cycle, with citrate and malate levels determined by coordinated biosynthesis, degradation, transport, and vacuolar compartmentation. Key enzymes and transporters include AGPase, AMY, BAM, SUS, SPS, INV, PEPC, NAD-MDH, citrate synthase, aconitase, NAD-IDH, and AcALMT1

5.3 Hormonal regulation during kiwifruit ripening

Ethylene is the dominant hormonal regulator of sugar–acid conversion during postharvest ripening, but its effects are selective across traits and can interact with temperature. In climacteric kiwifruit, ethylene strongly accelerates ripening-associated transcriptional programs and starch degradation (Tipu and Sherif, 2024; Yang et al., 2025). Ethylene promotes sugar accumulation partly by inducing BAM-centered pathways: AdDof3–AdBAM3L, AcERF182–AcBAM3.5, and ethylene-upregulated AdBAM3-family genes all support faster starch loss and higher soluble solids (Zhang et al., 2018). Ethylene treatment also accelerates starch degradation and TSS accumulation, whereas 1-MCP suppresses these responses (Yang et al., 2025). However, Li et al. (2026) found that cool temperature can activate a partly ethylene-independent route, because AcCTS1 drives AcBAM3.3/3.5 expression and starch degradation under 5 °C–10 °C even when ethylene perception is blocked.

ABA and auxin appear to modulate maturation timing and flavor formation mainly through crosstalk with sugar and ethylene pathways rather than by replacing them. Across fruit systems, ABA usually rises during ripening and promotes flavor development, softening, and color, often in interaction with ethylene (Wu et al., 2023). In yellow-fleshed kiwifruit, ABA peaks early in postharvest ripening and participates with cytokinins and ethylene in a coordinated ripening model (Lin et al., 2024). Gong et al. (2025) reported that ABA also connects directly to sugar metabolism because AcBAM5 and AcBAM13 are strongly ABA induced, and their promoters contain ABRE elements. By contrast, auxin appears more associated with developmental timing: early-maturing *A. eriantha* germplasm has lower IAA, ABA, and ZR contents together with faster starch conversion and higher sucrose, glucose, and fructose at harvest (Liao et al., 2021). More generally, sugar signaling, ABA, and auxin are