

Aroma formation further enriches peach flavor quality. The characteristic aroma of peach is composed of volatile organic compounds such as lactones, esters, aldehydes, alcohols, and terpenes. These compounds are mainly derived from the fatty acid  $\beta$ -oxidation pathway, the lipoxygenase (LOX) pathway, amino acid metabolism, and terpene and carotenoid cleavage pathways. For example, lactones usually contribute to the typical sweet and ripe-fruit aroma of peach, esters are associated with floral and fruity notes, while aldehydes and alcohols contribute to freshness (Li et al., 2023). Studies have shown that these volatile compounds change dynamically during fruit development and storage. Different cultivation conditions, such as light, temperature, and exogenous treatments, can alter the types and proportions of aroma compounds by regulating enzyme activities and the intensity of metabolic pathways, thereby leading to differences in fruit flavor among regions and years (Cao et al., 2024).

#### 4.2 Molecular genetic mechanisms

Differences in peach fruit quality traits are fundamentally controlled by genetic factors. In recent years, with the development of genomics, transcriptomics, and multi-omics integration, a large number of key genes and regulatory networks related to sugar and acid accumulation, fruit coloration, texture formation, and aroma biosynthesis have been gradually elucidated, providing important support for understanding the molecular basis of quality traits. In terms of sugar and acid metabolism, QTL mapping and genome-wide association studies (GWAS) have identified multiple genomic regions associated with soluble solids content (SSC), titratable acidity (TA), and sugar-acid balance. For example, major QTLs associated with SSC and TA have been identified on linkage group 5, and epistatic interactions among acidity-related loci can further regulate sugar-acid balance. At the candidate gene level, the malate transport-related gene *PpALMT1* and the sugar transporter gene *PpERDL16* have been confirmed to be closely associated with malate and fructose accumulation, thereby contributing to flavor differences among cultivars (Yao et al., 2025). This indicates that peach internal quality is not determined by a single metabolic enzyme but is coordinately controlled by transport, synthesis, degradation, and compartmentation processes.

In fruit coloration, structural genes and regulatory genes in the anthocyanin pathway together constitute a complex molecular regulatory network. Studies have shown that structural genes such as *CHS*, *DFR*, and *UFGT* control key steps in anthocyanin biosynthesis, while transcription factors such as MYB and bHLH act as upstream regulators that respond to environmental signals and coordinate downstream gene expression (García-Gómez et al., 2020; Da Silva Linge et al., 2021). In addition, some NAC family transcription factors are also involved in regulating flesh or peel coloration. For example, *PpBL* can affect red flesh pigmentation by regulating *PpNAC1*, and is also associated with the formation of certain aroma compounds such as linalool and (Z)-3-hexenyl acetate, reflecting a cross-link between color and aroma metabolism (Rawandoozi et al., 2020a). Aroma biosynthesis is likewise under the coordinated regulation of multiple genes. Studies have reported that terpene synthase genes, lipoxygenase-related genes, and carotenoid cleavage dioxygenase genes are all closely associated with the formation of volatile aroma compounds in peach (Li et al., 2023). *PpCCD4* and other CCD family members are closely related to the production of norisoprenoid aroma compounds, while GWAS has also identified terpene synthase genes associated with linalool synthesis. Meanwhile, different haplotypes of the *PpAAT* gene cluster can lead to variation in ester content, thereby influencing fruit aroma intensity and flavor style among cultivars. This suggests that peach aroma quality is essentially controlled by multiple gene modules and different metabolic branches (Feng et al., 2024).

In recent years, multi-omics technologies have further advanced the systematic dissection of peach quality regulatory networks. Transcriptomic studies have shown that hundreds to thousands of genes change expression during fruit ripening, involving sugar and acid metabolism, cell wall remodeling, ethylene signaling, stress response, and flavor compound formation (Veerappan et al., 2021). By integrating transcriptomic and metabolomic data, gene expression changes can be linked to the levels of sugars, organic acids, anthocyanins, and volatile compounds, thereby enabling the construction of “gene-metabolite-quality trait” regulatory network models. These studies indicate that peach quality traits are influenced not only by a few key structural genes, but also by complex transcription factor networks, coupled metabolic pathways, and polygenic control (Cao et al., 2024; Feng et al., 2024).