

4.3 Application of transcriptomics, metabolomics, and multi-omics in trait dissection

With the advancement of omics technologies, transcriptomics, metabolomics, and multi-omics integration have become essential tools for dissecting complex quantitative traits in sugarcane. Due to the highly complex genome, traditional forward genetics faces significant limitations in gene identification and functional analysis. Therefore, approaches focusing on gene expression regulation and metabolic networks have become effective strategies for studying yield and sugar formation mechanisms. In particular, RNA-seq enables systematic comparisons of gene expression across tissues, developmental stages, and genotypes, facilitating the identification of key regulatory factors associated with yield and sucrose accumulation.

Transcriptomic studies comparing high- and low-sugar materials, as well as elite and control varieties, have identified numerous differentially expressed genes involved in carbon fixation, starch and sucrose metabolism, plant hormone signaling, secondary metabolism, and cell wall formation. Pan-transcriptome analyses have further distinguished core and variable gene clusters and identified important candidate genes (Li et al., 2024). In the study by Chen et al. (2025a), ScHCT has been proposed as a key regulator of lignin biosynthesis, showing a negative correlation with sugar content and a positive correlation with lignin content, indicating a genetic coupling between secondary cell wall formation and sugar accumulation. This provides molecular insight into the balance between high sugar-low fiber and high biomass-high fiber traits.

Metabolomics reveals the dynamic processes of carbon allocation and sugar formation at the metabolite level. High-sugar varieties are enriched in sugars and sugar-phosphate intermediates related to sucrose accumulation, while secondary metabolites such as phenylpropanoids and flavonoids can indirectly regulate sugar formation by influencing carbon allocation and stress responses. In recent years, multi-omics integration has combined genomic, transcriptomic, metabolomic, and phenotypic data to dissect regulatory networks of yield and sugar content at multiple levels. Such studies have identified over 18 000 differentially expressed genes and 175 differentially accumulated metabolites, and highlighted around 100 key genes that may significantly influence high-yield and high-sugar phenotypes (Li et al., 2024). Additionally, transcription factor families such as MYB, WRKY, bHLH, NAC, TIFY, and C2C2-Dof have been identified as key regulatory nodes coordinating sugar metabolism and secondary metabolism.

5 Key Constraints on the Coordinated Improvement of Sugarcane Yield and Sugar Content

5.1 Negative correlation or trade-off between yield and sugar content

In sugarcane breeding, yield and sugar content often exhibit a certain degree of negative correlation, which is a key constraint on their coordinated improvement. Cane yield is generally positively correlated with traits such as stalk length, stalk diameter, and single stalk weight, but negatively correlated with quality traits such as Brix, sucrose percentage, juice purity, and CCS%. This indicates that although yield and sugar content jointly determine final sugar yield, they do not always increase simultaneously during trait formation, and high yield does not necessarily correspond to high sugar content.

From a physiological perspective, this trade-off reflects competition in carbon allocation between structural growth and sugar storage. Yield mainly depends on biomass accumulation in the stalk, whereas sugar content depends on sucrose concentration and storage within the stem. During vigorous vegetative growth, assimilates are preferentially allocated to cell division, elongation, and cell wall synthesis to support stalk development. In contrast, during the maturation stage, carbon flow gradually shifts toward sucrose accumulation. Under limited carbon resources, biomass increase and sugar storage tend to compete with each other.

However, this negative relationship is not absolute. Long-term breeding results indicate that increases in sugar yield have mainly been driven by biomass improvement, while gains in sugar content have been relatively slower. Nevertheless, this does not imply a permanent antagonism. Mehdi et al. (2024) mentioned in their study that there is no fixed negative trend between biomass and sugar content; instead, their relationship is strongly influenced by environmental conditions. Under favorable environments, sugarcane can simultaneously achieve high biomass and high sugar content (Mehdi et al., 2024). Therefore, this trade-off should be regarded as a conditional constraint influenced by environment, maturity process, and genetic background.