

and GBS-based single-dose markers identified multiple QTLs associated with yield and quality traits, some of which showed stability across environments and crop cycles (Figure 2).

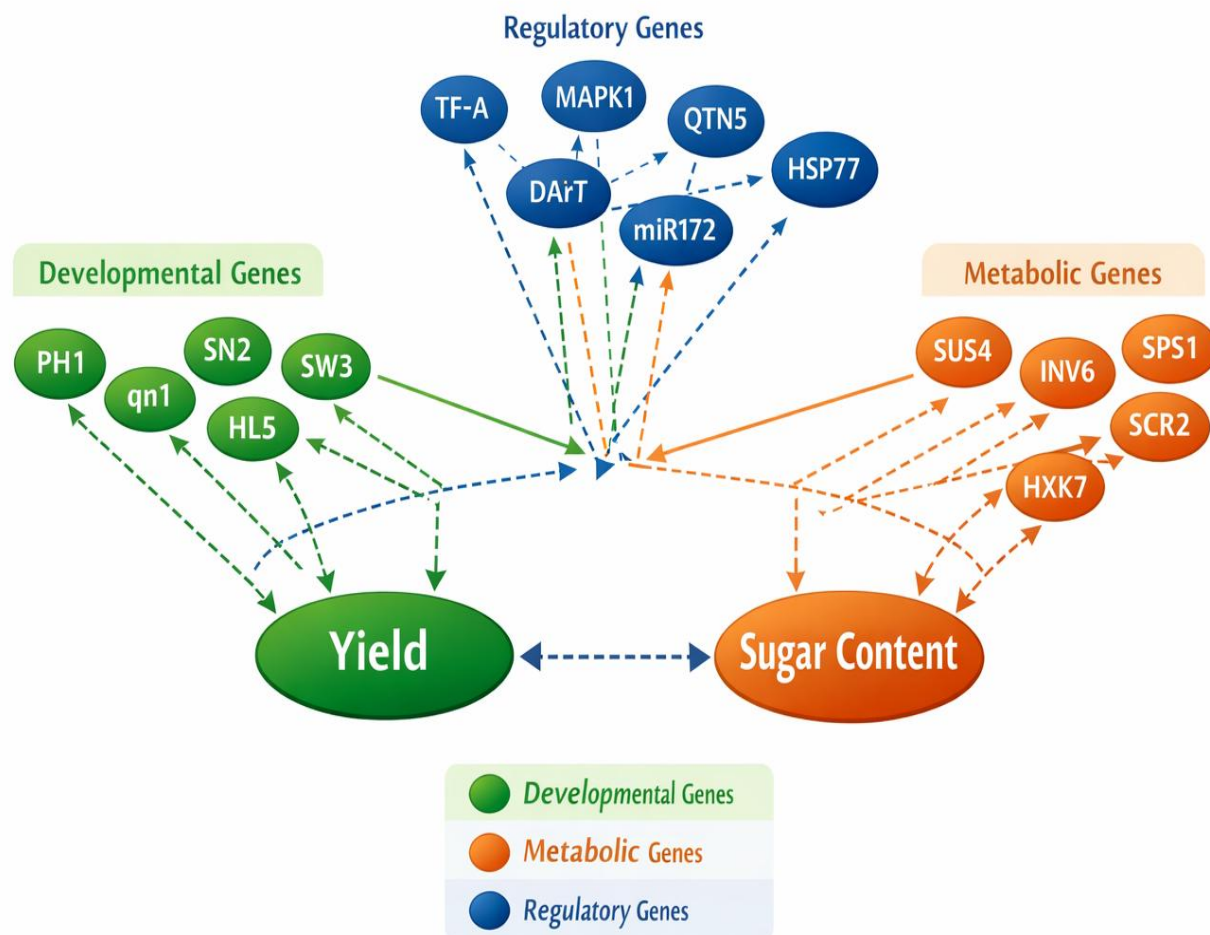


Figure 2 Conceptual model of the polygenic architecture underlying sugarcane yield and sugar content
Image caption: The interactions among multiple QTLs, QTNs, and regulatory networks

With the application of high-density SNP data, GWAS has greatly improved the resolution of genetic analysis. In Brazilian sugarcane germplasm populations, multiple marker-trait associations related to Brix, plant height, stalk number, stalk weight, and cane yield have been identified, and strong genotypic correlations among these traits suggest shared developmental and metabolic pathways (Barreto et al., 2019). In Zhang's (2023) study, more than 100 QTLs related to Brix and other yield traits were identified across the entire genome., including 35 candidate genes involved in internode development, cell wall formation, signal transduction, and carbon metabolism. These findings indicate that sugarcane yield formation is regulated by multiple developmental and metabolic processes.

For sugar content and quality traits, high-density GWAS and candidate gene analyses have identified numerous SNPs associated with Brix, Pol, CCS, sucrose content, and sugar yield (Li et al., 2024; Eltaher et al., 2025). Notably, a functional SNP in the sucrose synthase gene SoSUS1 (mSoSUS1_SNPCh10.T/C) shows significant associations with Pol, CCS, Brix, fiber content, and sugar yield across multiple environments, demonstrating clear pleiotropy and serving as an important candidate marker for selecting high-sugar genotypes with appropriate fiber content (Li et al., 2024). Meanwhile, studies on fiber-related QTLs further reveal the genetic trade-off between sugar accumulation and biomass formation (Chen et al., 2025b). With the transition to high-density SNP arrays and high-throughput sequencing platforms, QTL mapping, functional marker development, and genomic prediction are jointly driving sugarcane breeding from single-marker selection toward multi-locus integrated prediction.