

the stem and enhance sucrose accumulation at specific stages. Ethylene is often associated with maturation promotion and increased sink strength, improving sugar storage capacity in some low-sugar genotypes (Lu et al., 2025). In contrast, sustained high levels of defense-related hormones such as JA and salicylic acid may redirect resources toward defense metabolism, inhibiting growth and sugar accumulation (Lu et al., 2025). Therefore, from the perspective of coordinated improvement, the key lies in balancing growth promotion, maturation initiation, and defense responses, rather than enhancing a single hormonal pathway.

Environmental stresses further influence yield and sugar formation through hormonal signaling and redox regulation. Drought, high temperature, nutrient deficiency, and biotic stresses can reduce photosynthesis, disrupt reactive oxygen species (ROS) balance, and alter carbon metabolism and sugar partitioning via ABA, ethylene, JA, and calcium signaling pathways (Mehdi et al., 2024). Moderate water deficit during certain maturation stages may promote sucrose accumulation, but excessive or premature stress can lead to stomatal closure, impaired electron transport, and reduced net photosynthesis, thereby decreasing both biomass and sugar accumulation (Mehdi et al., 2024). Additionally, exogenous regulators such as ethylene, seaweed extracts, and indole-3-butyric acid can improve high-yield and high-sugar performance by enhancing sink strength, promoting root development, and improving photosynthesis and antioxidant capacity (Zhang et al., 2025). Overall, the formation of high yield and high sugar content in sugarcane results from the coordinated interaction of hormonal balance, stress adaptation, and carbon allocation, and can only be fully realized under suitable environmental conditions and proper management.

4 Genetic Basis of Sugarcane Yield and Sugar Content

4.1 Characteristics of the complex sugarcane genome and its impact on trait studies

Sugarcane is a typical complex polyploid crop. Modern cultivars are mainly derived from hybridization and backcrossing between the high-sugar species *Saccharum officinarum* and the wild species *S. spontaneum*, resulting in a genome that combines high sugar content with strong adaptability but is also highly complex and mosaic in nature (Healey et al., 2024; Brant et al., 2025). Compared with most diploid crops, sugarcane exhibits higher ploidy levels, strong heterozygosity, and pronounced aneuploidy. Each chromosome often has multiple homologous copies and is accompanied by extensive structural variations, copy number variations, and large-scale rearrangements (Healey et al., 2024). This makes sugarcane one of the most genetically complex cultivated crops.

In terms of genome size, elite sugarcane hybrids typically possess genomes of approximately 8-10 Gb, rich in repetitive sequences and structurally complex regions. Although sugarcane shares partial micro-collinearity with sorghum, the relationship is not strictly one-to-one, making it difficult to directly use the sorghum genome to precisely dissect complex sugarcane traits (Healey et al., 2024). The combination of high ploidy, high repetition, and high heterozygosity has long posed major challenges for genetic map construction, allele dosage estimation, variant detection, and reference genome assembly, leading to slower progress in sugarcane genetic research compared with crops such as rice, maize, and sorghum.

This complex genomic background directly affects the study of quantitative traits such as yield and sugar content. These traits are typically controlled by numerous minor-effect loci, allele dosage effects, and non-additive genetic interactions rather than a few major genes. Ignoring ploidy variation and dosage effects in linkage analysis, GWAS, or genomic prediction can reduce the accuracy of effect estimation. In recent years, advances in high-throughput sequencing, whole-genome resequencing, and reference genome assembly—such as the release of R570 and *S. spontaneum* reference genomes—have greatly improved variant detection and candidate gene identification, providing a solid foundation for dissecting complex traits and advancing molecular breeding in sugarcane (Healey et al., 2024; Brant et al., 2025).

4.2 Advances in genes, QTLs, and molecular markers related to yield and sugar content

Sugarcane yield and sugar content are typical polygenic traits, whose genetic basis is determined by multiple QTLs, QTNs, and complex regulatory networks. In recent years, significant progress has been made in QTL mapping, association analysis, and molecular marker development for traits such as plant height, stalk number, single stalk weight, cane yield, Brix, and fiber content. Early linkage maps constructed using TRAP, DArT, SSR,