

combining ability (SCA) may contribute more to yield variation than general combining ability (GCA), indicating that identifying superior hybrid combinations is more important than selecting individual elite parents.

In practice, parental design should focus on NTrait-based complementarity, such as crossing high-biomass but moderate-sugar genotypes with high-sugar parents to develop ideotypes with strong source-large sink-optimal maturity. Successful cases demonstrate that systematic parental design combined with multi-trait selection can overcome traditional trade-offs and achieve simultaneous improvements in yield and sugar content (Wu et al., 2024; Liu et al., 2025). Additionally, a comprehensive multi-trait evaluation system should be established during progeny selection, integrating early-stage elimination with multi-environment validation in later stages, thereby shifting conventional breeding from experience-driven to target-oriented design.

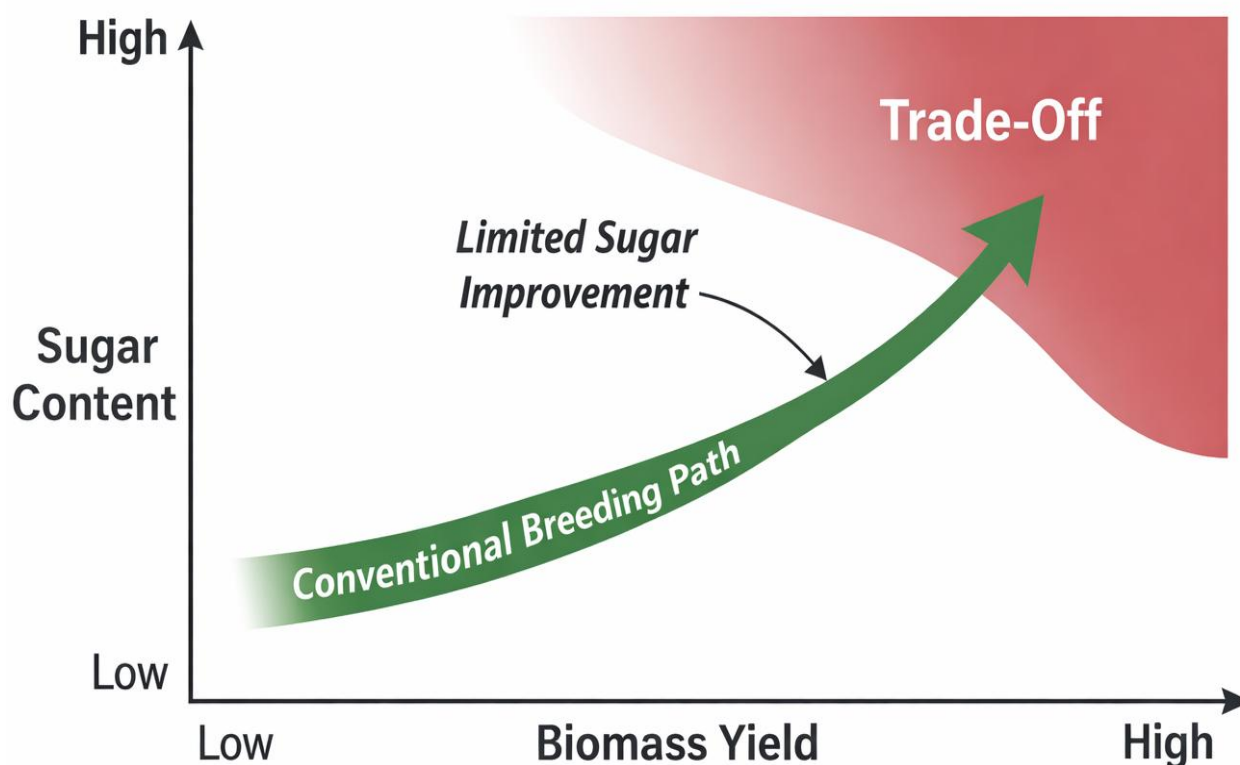


Figure 4 Conceptual relationship between biomass yield and sugar content in conventional breeding

Image caption: Limited improvement in sugar content despite yield gains

6.2 Applications of marker-assisted Selection, genomic selection, and gene editing

Advances in molecular breeding technologies have significantly improved sugarcane breeding efficiency. Marker-assisted selection (MAS) enables early-generation screening based on genotypic information and has been successfully applied to relatively simple traits such as disease resistance—for example, the use of Bru1-associated markers in rust resistance breeding (Lu et al., 2024). However, for complex quantitative traits such as yield and sugar content, which are controlled by multiple genes and environment interactions, the explanatory power of single markers is limited, and MAS is mainly used as a supplementary tool.

With the development of high-density SNP markers and GWAS, an increasing number of loci associated with yield and sugar traits have been identified, providing a foundation for pyramiding favorable alleles (Eltaher et al., 2025). In contrast, genomic selection (GS) is more suitable for complex traits, as it uses genome-wide markers to predict breeding values and capture the combined effects of numerous small-effect loci. Studies have shown that GS can improve selection accuracy, shorten breeding cycles, and provide stable predictions across environments, making it a key tool for future coordinated improvement in sugarcane.