Three-chain empowered sugarcane bio-breeding in China

Peilin Wang,[1,2,8] Qibin Wu,[1,2,8] Wenzhi Wang,[1] Dongjiao Wang,[1] Jungang Wang,[1] Tingting Sun,[1] Yachun Su,[2] Hengbo Wang,[2] Liping Xu,[2] Dongliang Huang,[3] Aomei Li,[3] Baoqing Zhang,[3] Jie Zhang,[4] Jiayong Liu,[5] Prakash Lakshmanan,[3] Xingtan Zhang,[6] Shuzhen Zhang,[1] Yangrui Li,[3,*] Fei Chen,[7,*] Yuebin Zhang,[5,*] and Youxiong Que[1,2,*]

[1]State Key Laboratory of Tropical Crop Breeding, Sanya Research Institute, Chinese Academy of Tropical Agricultural Sciences, Sanya 572024, China
[2]National Engineering Research Center for Sugarcane, College of Agriculture, Fujian Agriculture and Forestry University, Fuzhou 350002, China
[3]Sugarcane Research Institute, Guangxi Academy of Agricultural Sciences, Nanning 530007, China
[4]State Key Laboratory of Plant Genomics, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China
[5]State Key Laboratory of Tropical Crop Breeding, Sugarcane Research Institute, Yunan Academy of Agricultural Sciences, Kaiyuan 661600, China
[6]State Key Laboratory of Tropical Crop Breeding, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen 518120, China
[7]State Key Laboratory of Tropical Crop Breeding, College of Breeding & Multiplication, Hainan University, Sanya 572025, China
[8]These authors contributed equally
*Correspondence: liyr@gxaas.net (Y.L.); feichen@hainanu.edu.cn (F.C.); ynzyb@sohu.com (Y.Z.); queyouxiong@126.com (Y.Q.)
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Sugarcane accounts for up to 80% of sugar production, yet breeding progress remains constrained by its complex genetic architecture, including allopolyploidy, high heterozygosity and extensive polymorphism. These features prolong breeding cycles and hinder trait pyramiding, limiting the development of breakthrough cultivars. Biobreeding technologies, particularly genetic transformation and gene-editing, enable precise improvement of key agronomic traits. Recently, Sugarcane Research Center of the Chinese Academy of Tropical Agricultural Sciences (CATAS-SRC), leveraging the State Key Laboratory of Tropical Crop Breeding (NBLTC), has established a Three-Chain empowered mechanism to accelerate translation from laboratory research to field application. This integrates the Innovation Chain for functional element discovery, the Industry Chain for platform construction and deployment, and the Support Chain for sustained funding and talent development. The resulting "government-industry-academia-research-application" model provides a practical and transferable framework for biobreeding in sugarcane and other crops with complex genomes.

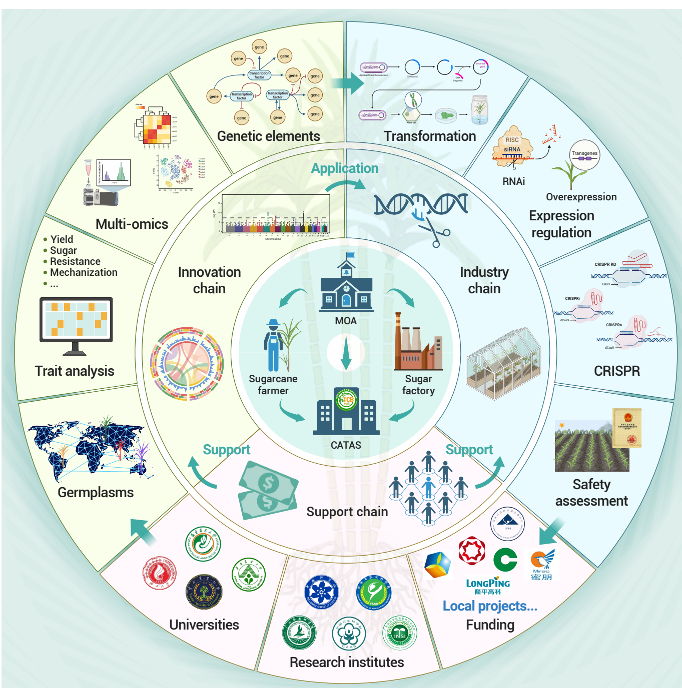

Figure 1. Three-chain collaborative framework for sugarcane biotechnological breeding innovation and industrial application This framework is centered on the Ministry of Agriculture and RuralAffairs (MOA), Chinese Academy of Tropical Agricultural Sciences (CATAS) and State Key Laboratory of Tropical Crop Breeding (NBLTC), sugar factories, and sugarcane growers, and illustrates the coordinated integration of the Innovation Chain, the Industry Chain, and the Support Chain. The Innovation Chain is supported by universities—Fujian Agriculture and Forestry University, South China Agricultural University, Yunnan Agricultural University, and Guangxi University—and research institutes including Chinese Academy of Sciences, Chinese Academy of Agricultural Sciences (Biotechnology Research Institute, Agricultural Genomics Institute), Guangxi Academy of Agricultural Sciences, Nanfan Seed Industry Research Institute, and Yunnan Academy of Agricultural Sciences. The Support Chain is reinforced by funding from the National Natural Science Foundation of China (NSFC) and regional foundations in Guangxi, Guangdong, Yunnan, Fujian, and Hainan. The Industry Chain is driven by leading domestic sugar enterprises, including COFCO Sugar, East Asia Sugar, Nanhua Sugar, Nanning Sugar, and Shanghai Sugar Tobacco and Alcohol, as well as biobreeding companies such as Bella-Gen, Longping High-tech and KingAgroot CropScience. Through the joint application of biotechnological tools—including genomics, CRISPR-based gene-editing, genetic transformation, and multi-omics analyses—the mechanism enables a seamless pipeline from germplasm resource identification and trait dissection to genetic element mining, technology development, biosafety evaluation of transgenic or gene-edited materials, and large-scale industrial application. Image elements are from BioRender (https://www.biorender.com).

INTRODUCTION

Under the combined pressures of diminishing arable land and climate change, the stable production of major cash crops is a key objective worldwide. As a cornerstone crop for sugar-producing countries, sugarcane is critical for sugar supply, bioethanol production, and livelihoods. Sugarcane has an extraordinarily large genome, with high chromosome numbers and repetitive sequences.[1] Although sustained efforts have released numerous elite cultivars, the genetic complexity is still a double-edged sword: it supports adaptability and biomass potential but severely constrains breeding efficiency.

Conventional hybrid breeding faces inherent limits. The cycles often exceed 10-12 years, progenies show strong trait segregation, and ideal genotypes are rare. Consequently, released varieties often involve trade-offs like "yield increase without sugar improvement." These constraints form a persistent genetic bottleneck for the sugarcane sector. Fortunately, genetic transformation enables precise introduction of exogenous genes.[2] By directly manipulating key agronomic loci, biotechnological breeding could shorten cycles and enable rational design of multiple traits when integrated with conventional breeding.

Up to now, in sugarcane, efficient transformation is still technically demanding; regulatory networks for complex traits are unresolved; identifying valuable genetic elements is challenging; and biosafety evaluation is extended. In recent years, Sugarcane Research Center of the Chinese Academy of Tropical Agricultural Sciences (CATAS-SRC) has utilized the State Key Laboratory of Tropical Crop Breeding (NBLTC) to establish a large-scale collaborative framework for sugarcane biotechnological breeding. This integrates universities, research institutes, and enterprises. This paper analyzes the rationale, implementation, and implications of this coordinated mechanism, proposing it as a replicable paradigm for breeding crops with complex genomes.

Three-chain fusion: A large-scale collaboration for sugarcane biobreeding

Traditional linear research models are insufficient for the systemic challenges of sugarcane biobreeding. Guided by relevant authorities, a large-scale collaborative mechanism integrating government, industry, academia, research, and application has been established under the leadership of the CATAS-SRC. The framework aims to dismantle institutional barriers, align dispersed resources, and achieve deep coordination across the innovation chain, the industry chain, and the support chain, forming a powerful engine for sustained innovation (Figure 1).

Innovation chain: An advancement from basic research to genetic element discovery

In sugarcane, dissecting complex agronomic traits requires a large-scale collaborative effort mobilizing expertise in genomics, bioinformatics, and related disciplines.[3] Within this framework, the laboratory has made efforts to generate high-quality reference genomes and construct integrated multi-omics databases from core germplasm and wild relatives. All units operate on this unified platform, enabling efficient sharing of germplasm and data while minimizing redundancy. Building on this foundation, the network systematically decomposes industry-prioritized complex traits according to each institution's expertise. Through defined divisions of labor, the consortium inves tigates the genetic networks underlying key targets, including yield, sucrose metabolism, disease resistance, stress tolerance, and ideal architecture.[4] This coordinated approach has identified and validated a suite of genetic elements with independent intellectual property and clear breeding potential.

Industry chain: Empowering the industry-oriented applied transformants

This collaborative mechanism consistently adheres to industry demand guiding R&D, aiming to construct a seamless pathway for elite transformants to progress from laboratory to field.

To overcome industrialization bottlenecks, a full-process integrated platform has been established. First, a high-efficiency, genotype-independent transformation system breaks long-standing technical barriers,[5] enabling scalable generation of transformants. Second, a pilot-scale testing and propagation platform supports preliminary evaluation under isolated conditions. Concurrently, a comprehensive biosafety evaluation platform integrates expertise in molecular characterization, environmental and food safety. Following biosafety assessment, leading enterprises establish multi-location testing stations across ecological regions. Superior transformants are then evaluated for agronomic performance and sugar yield under realistic conditions. Research institutions focus on core innovation, while enterprises engage early—co-designing trials, sharing evaluation costs, and planning downstream promotion. This collaborative approach establishes an end-to-end platform linking efficient transformation, pilot trials, environmental release, biosafety evaluation, and final variety registration.

Support chain: Strengthening the integrated funding and talent development

To address sustain the long cycles and high uncertainty of biobreeding, a three-dimensional funding system has been established: "stable support, competitive incentives, and market feedback." Stable support comes from national basic research programs, safeguarding exploratory work and shared platforms. Market feedback complements this by guiding enterprises and venture capital toward product development, creating a cycle where "national investment supports the front end, and market forces drive the back end." Within this framework, the NBLTC serves as a key national platform for tropical crop biobreeding.

The mechanism also cultivates a sustainable talent ecosystem. Plans include establishing a "Sugarcane Biobreeding" graduate program jointly supervised by universities, research institutes, and enterprises, aimed at producing professionals with strong theoretical foundations, interdisciplinary skills, and industrial awareness. To enhance knowledge integration, a "revolving door" system promotes personnel exchange: public researchers serve as enterprise consultants, while enterprise R&D personnel become visiting scholars. This mobility framework accelerates knowledge flow and bridges academia-industry divides.

CHALLENGES AND PROSPECTS

The establishment of this large-scale collaborative mechanism for sugarcane biobreeding is an innovation in Chinese agricultural research organization, transitioning from isolated breakthroughs toward systematic integration. Its strengths include integrating fragmented resources into a unified force; reducing redundancy through task sharing; shortening the pipeline from gene discovery to variety release via integrated platforms; and enhancing translational efficiency through early industry involvement. Significant challenges remain. Technically, improving the efficiency and stability of transformation and establishing robust gene-editing platforms are still needed, alongside multiplex editing and precise regulation. In governance, clarifying cross-institutional intellectual property ownership and designing equitable benefit-sharing mechanisms. Societally, necessitating proactive science communication, transparent data, and open dialogue. To accelerate Breeding 3.0, precision molecular design should be positioned as the technical core that links the Three Chains, with priorities placed on (i) a stable, genotype-independent transformation and gene-editing, (ii) multiplex editing and regulated expression for rational trait stacking, and (iii) multi-omics-enabled dissection of regulatory networks to refine target selection for complex traits. On this basis, progression toward Breeding 4.0 should emphasize intelligent breeding, integrating data-driven modeling and artificial intelligence-assisted design with multi-location phenotyping to form rapid feedback loops from field performance to molecular optimization.

Looking ahead, the collaboration has a broader vision. In the short term (3-5 years), it aims to produce one to two landmark outcomes, notably completing biosafety evaluations for transgenic or edited lines with agronomic performance exceeding current leading cultivars—a critical "zero-to-one" industrial breakthrough. In the medium to long term (5–10 years), the goal is to refine this "Chinese large-scale collaboration model" into a replicable paradigm, establishing a sustained national mechanism for biobreeding integration.

CONCLUSIONS

Biotechnological breeding offers powerful solutions. This paper articulates a practical pathway for a large-scale collaborative mechanism—guided by national strategy—that integrates innovation, empowers industry, and activates support chains. It is expected to transcend genetic constraints to cultivate elite sugarcane varieties, through this deeply integrated government-industry-academia-research-application network.

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AUTHOR CONTRIBUTIONS

All authors contributed to the manuscript and approved the final version.

DECLARATION OF INTERESTS

The authors declare no competing interests.