

Sugarcane variety YZ05-51 with high yield and strong resistance: breeding and cultivation perspectives

Authors

Qibin Wu[#], Aomei Li[#], Jiayong Liu,
Yong Zhao, Peifang Zhao,
Yuebin Zhang^{*}, Youxiong Que^{*}

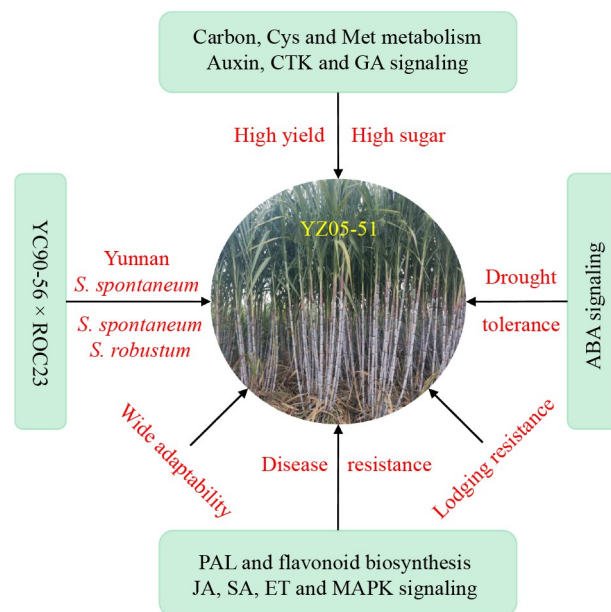
Correspondence

ynzyb@sohu.com;
queyouxiong@126.com

In Brief

This study delves into the breeding logic and genetic characteristics of YZ05-51 and explores the biological mechanisms that contribute to its high yield, high sugar, drought tolerance, and disease resistance. The challenges and prospects are also discussed, providing a foundation for the breeding and promotion of newly developed sugarcane varieties.

Graphical abstract



Highlights

- The breeding logic and agronomic features of YZ05-51 are described in detail.
- The biological basis of the elite traits of YZ05-51 is dissected.
- The challenges and prospects of sugarcane breeding are discussed.

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Sugarcane variety YZ05-51 with high yield and strong resistance: breeding and cultivation perspectives

Qibin Wu^{1#}, Aomei Li^{1,2#}, Jiayong Liu¹, Yong Zhao¹, Peifang Zhao¹, Yuebin Zhang^{1*} and Youxiong Que^{1,3*}

¹ National Key Laboratory for Tropical Crop Breeding, Institute of Tropical Bioscience and Biotechnology, Chinese Academy of Tropical Agricultural Sciences/Sugarcane Research Institute, Yunnan Academy of Agricultural Sciences, Sanya/Kaiyuan 572024/661600, China

² Key Laboratory of Sugarcane Biotechnology and Genetic Improvement (Guangxi), Ministry of Agriculture and Rural Affairs, Guangxi Academy of Agricultural Sciences, Nanning 530007, China

³ Key Laboratory of Sugarcane Biology and Genetic Breeding, Ministry of Agriculture and Rural Affairs, National Engineering Research Center for Sugarcane, College of Agriculture, Fujian Agriculture and Forestry University, Fuzhou 350002, China

Authors contributed equally: Qibin Wu, Aomei Li

* Corresponding authors, E-mail: ynzyb@sohu.com; queyouxiong@126.com

Abstract

Sugarcane (*Saccharum* spp), a significant cash crop in the tropics and subtropics, accounts for 80% of sugar and 40% of bioethanol in the world. In China, it is also a prominent sugar crop, with cane sugar contributing to over 85% of sugar production. In recent years, there has been a notable shift towards drier slopes in Chinese sugarcane cultivation, resulting in significant ecological changes. Over the past two decades, scientists have developed the theory of high-heterogeneous composite high-yield and high-sugar breeding, leading to the successful breeding of the fifth-generation sugarcane varieties, among which YZ05-51 is a representative one. It was developed by the Sugarcane Research Institute (YSRI) of Yunnan Academy of Agricultural Sciences. Originating from a cross between YC90-56 and ROC23, YZ05-51 demonstrates several excellent agronomic traits, such as high yield, high sugar, strong stress resistance, and wide adaptability, particularly thriving in dry slope conditions. By 2023, cultivation of YZ05-51 has reached approximately 31,947 hectare, constituting 12.13% of the total cultivated area in Yunnan province. This variety has even surpassed previous records for sugarcane yield in non-irrigated areas, achieving a remarkable yield of 138 tons per hectare (t/ha). To summarize experience and inspire innovation, here the insights into the breeding logic and genetic characteristics of YZ05-51 are detailed. Further, the biological mechanisms underlying its agronomic traits were investigated through the integration of transcriptomics and metabolomics analysis. The challenges and prospects were also discussed, setting up the basis for the breeding and promotion of newly bred sugarcane varieties.

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Introduction

Sugarcane (*Saccharum* spp) is a significant cash crop in the tropics and subtropics and accounts for 80% of sugar and 40% of bioethanol production in the world. It is a prominent sugar crop in China, with cane sugar contributing to over 85% of sugar production^[1, 2]. *Saccharum* is categorized into cultivated and wild species, encompassing six species, including *S. sinense*, *S. edule*, *S. barberi*, *S. officinarum*, *S. spontaneum*, and *S. robustum*. Notably, *S. spontaneum* and *S. robustum* are wild species, while the other four are cultivated^[3]. Sugarcane is cultivated in 18 provinces across China, with the primary areas in the tropical and subtropical regions below the latitude line 24° N. These regions are predominantly situated in the southern and southwestern parts of China, particularly in Guangxi, Yunnan, Guangdong, and Hainan provinces^[4]. In recent years, there has been a notable shift towards drier slopes in Chinese sugarcane cultivation, resulting in significant ecological changes. Surprisingly, from 2000 to 2013, approximately 85% of sugarcane cultivation was occupied by ROC series varieties, especially ROC22^[5]. This has raised concerns about the sustainable development of the sugarcane industry. There is thus a pressing need to prioritize the selection and adoption of new sugarcane varieties.

High yield and high sugar content are essential for a desirable sugarcane variety. As the economy continues to evolve and agricultural science advances, new standards are continually being established for sugarcane varieties. Ideally, they should possess favorable traits such as high yield, high sugar, drought tolerance, disease resistance, resistance to lodging, and wide adaptability^[4,6–8]. Recently, researchers have developed the concept of high-heterogeneous composite high-yield and high-sugar breeding, resulting in the breeding of fifth-generation (2013 to now) sugarcane varieties, mainly including Yunzhe 08-1609 (YZ08-1609), YZ05-51, Guitang 42 (GT42), GT44, and Liucheng 05-136 (LC05-136), now accumulatively accounting for over 83.4% of cultivation in China, mostly in Guangxi, Yunnan, Guangdong, and Hainan provinces^[4,6,9]. Among them, YZ05-51, developed by Sugarcane Research Institute (SRI) of Yunnan Academy of Agricultural Sciences, stands out as the one bred in China and first registered in the United States. This variety, arising from crossing Yacheng 90-56 (YC90-56) with ROC23, showcases high yield, high sugar, and strong stress resistance, particularly excelling in dry slope conditions^[4,10,11]. Notably, in the Gengma county of Yunnan province, YZ05-51 achieved a record-breaking yield of 138 t/ha in non-irrigated areas^[4]. Besides, Luo et al.^[7,8] utilized GGE

biplot to identify that YZ05-51 had relatively high yield and wide stability. In the present review, detailed insights into the breeding logic and genetic characteristics of YZ05-51 are provided. Furthermore, the biological mechanisms for the formation of desirable agronomic traits are explored. Finally, the challenges and prospects are addressed, laying the groundwork for cultivation and breeding of sugarcane.

What is the breeding logic of YZ05-51?

During sugarcane breeding, sexual hybridization, transgene, molecular marker-assisted selection and mutagenesis are frequently used^[3], with hybrid breeding being the most effective^[4,12,13]. Parental material is crucial for selecting and breeding elite sugarcane varieties. Furthermore, germplasm enhancement plays a key role in the development of breakthrough varieties. In sugarcane hybrid breeding, significant advancements have consistently emerged from the discovery and utilization of novel parental materials throughout the history.

In 1991, the National Sugarcane Germplasm Resource Nursery was established as a national-level gene bank managed by SRI of Yunnan Academy of Agricultural Sciences. At present, it houses more than 5,900 sugarcane germplasm resources, making it the largest one in the world^[4]. This nursery has exploited key parent varieties like YC71-374, YC90-56, Yunrui 05-292 (YR05-292), and YR05-770, known for their genetic impact on sugar content, resistance, and other elite agronomic traits. Three sugarcane varieties, namely, YZ05-51, YZ08-1609 and YZ01-1413, have been registered in the United States. Among them, YZ05-51, is an early-maturing variety resulting from the cross of YC90-56 and ROC23 (Fig. 1). The female parent YC90-56 contains the bloodline of Yunnan *S. spontaneum* (YN57-11-35), and the male parent ROC23 is an elite cultivar developed by Taiwan Sugar Research Institute (Fig. 1). YZ05-51, inheriting a pedigree from POJ, F, Co, and NCo series^[14,15] (Fig. 1), achieved a significant breakthrough in high yield on dry slopes, with a record yield of 138 t/ha in the

Gengma county of Yunnan province, surpassing the previous record for sugarcane yield in non-irrigated areas^[4,10,11]. In China, the introduction of specific bloodlines from the high yield of ROC-type and high resistance of *S. spontaneum*, along with the bloodlines fusion of large-stemmed wild *S. robustum*, has expanded the sugarcane breeding bloodlines from four to five. This has enabled the mixing of domestic and foreign parentage, leading to significant progress in sugarcane breeding^[4] (Fig. 1).

What are the genetic characteristics of YZ05-51?

YZ05-51 is an early-maturing, high-yielding, and high-sugar variety with several other outstanding traits. It exhibits fast seedling emergence, strong tillering, uniform and neat stems, strong lodging, and easy defoliation. The plants are tall and erect, with medium to large stems, solid, medium-length, cylindrical internodes, thick wax powder, no water splitting, and no aerial roots. Its internodes are initially yellowish-green but turn purple upon exposure. The prismatic buds have medium bodies, shallow and inconspicuous grooves, medium wings, tips that extend beyond the growth zone, bases level with the leaf scars, and moderate root zones. This variety features drooping leaf tips, few or no group 57 hairs, triangular inner leaf auricle, and absent outer leaf auricle. Interestingly, it is highly resistant to smut disease, and highly tolerance to drought stress, but moderately susceptible to mosaic disease (Fig. 2). It demonstrates rapid growth in the initial and middle stages, requiring early fertilization in the seedling period and sufficient fertilization for stem boosting during growth.

Due to the strong growth potential, it is important to cultivate it in appropriately high soil to prevent late collapse. After harvest, it is necessary to promptly clean up the cane field, ensure early irrigation and root and stem loosening, and to use ground film cover to promote early plant development. It is also important to cover with sugarcane leaves or mulch to utilize soil moisture and promote plant sprouting on dry slopes.

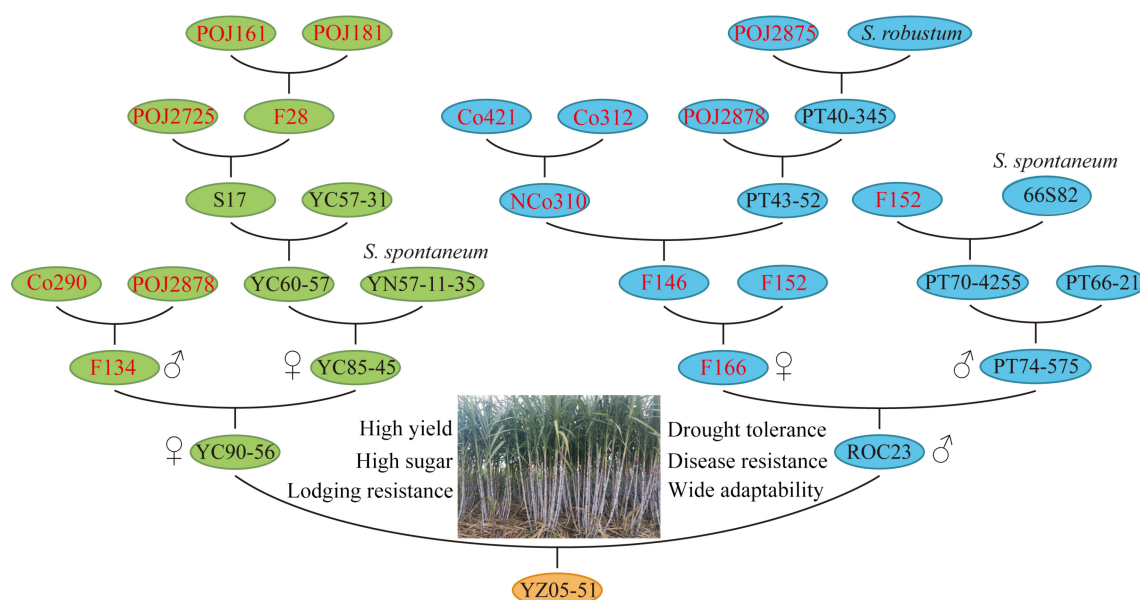


Fig. 1 Pedigree and elite traits of sugarcane variety YZ05-51.

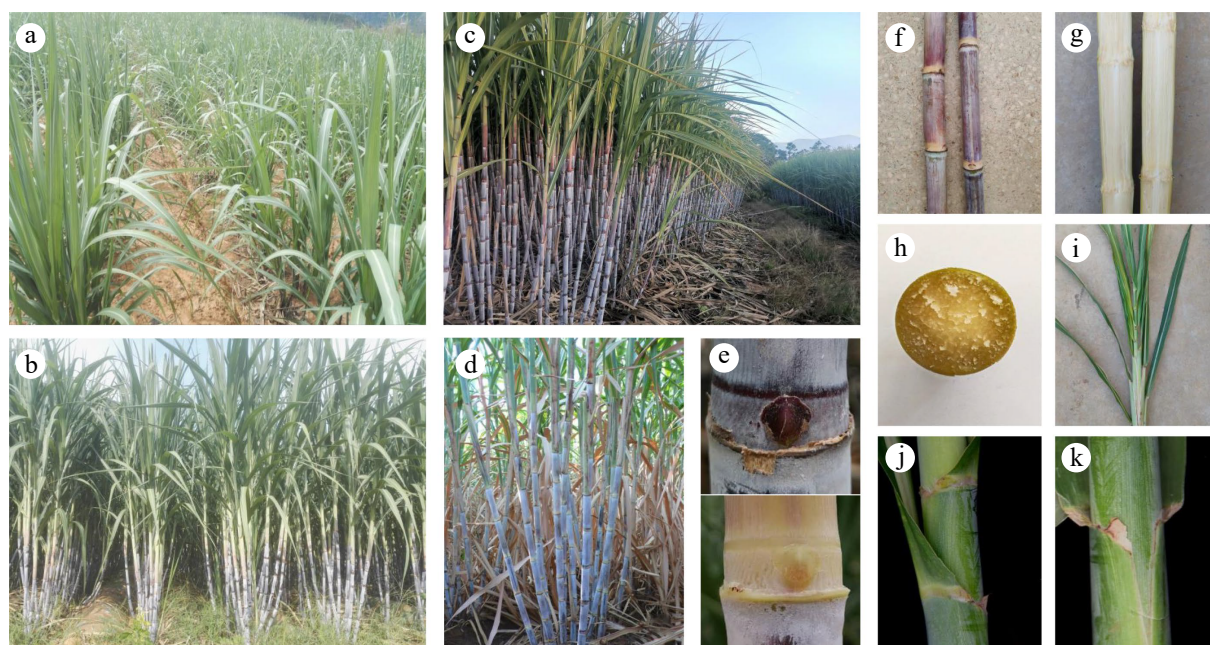


Fig. 2 Genetic characteristics of sugarcane variety YZ05-51. (a) seedling stage, (b) elongation stage, (c) maturity stage, (d) plant type, (e) bud, (f) stem, (g) stem longitudinal section, (h) stem transverse section, (i) leaf, (j) leaf sheath, (k) leaf auricle. The original photos were provided by the co-author Dr. Jiayong Liu.

Additionally, it is crucial to strengthen pest, disease, and weed control measures. During the growth stage, attention should be given to preventing withered heart in the seedling stage and controlling thrips^[10]. In a national regional trial, the average yield is 100.8 t/ha, with a sucrose content of 14.10% in November to December, 15.67% in January to March, and an overall average of 15.00%^[11]. YZ05-51 is recommended for row spacing of 1.1~1.2 m, suitable for planting in autumn, winter, and spring, with an ideal density of 112,500~135,000 buds per hectare. It is particularly well-suited for cultivation in Yunnan, Guangxi, Guangdong, and Fujian, especially in locations with ample water and fertilizer resources, offering potential for increased production and raised sucrose content^[10]. Since 2017, the planting acreage of YZ05-51 has been rising each year in Yunnan province. Notably, in 2023, the cultivation of this variety reached a nominal value of 31,947 hectare, accounting for 12.13% of the total cultivated area in Yunnan province (Table 1).

Why is YZ05-51 high-yield and high-sugar?

During the eighth national sugarcane regional trial at 14 locations in China (2011-2011, two plant-cane crops and one ratoon crop), except for Zhanjiang (ZJ) of Guangdong and Lingao (LG) of Hainan, YZ05-51 exhibited a higher average cane yield than the control ROC22 (Fig. 3a). Specifically, at Chongzuo (CZ) of Guangxi, Kaiyuan (KY) and Lincang (LC) of Yunnan, the

average cane yield of YZ05-51 was significantly higher than that of ROC22, with an increasing of 6.65%, 8.51%, and 34.35%, respectively (Fig. 3a). Except for ZJ, Baise (BS) and Laibin (LB) of Guangxi, and LG, the average sucrose content of YZ05-51 was higher than ROC22 (Fig. 3b), while at Fuzhou (FZ) of Fujian, KY, and LC, the average cane yield of YZ05-51 was 4.80%, 15.39%, and 38.76% higher than ROC22, respectively^[9,10] (Fig. 3b). Previous studies revealed that tillering ability and well development, controlled by cysteine and methionine metabolism, have a significant impact on sugarcane yield^[16, 17]. In the present study, transcriptomics integrated with metabolomics (unpublished) identified three differential accumulated metabolites (DAM; L-aspartic acid, L-homocystine, and 3P-D-glycerate) and six differentially expressed genes (DEGs) including *cysE*, *hom*, *TAT*, *MTAN*, *mtnA*, and *mtnD* (Fig. 3c). Carbon fixation and starch/sucrose metabolism provides energy for plant growth and dry matter accumulation are vital for plant development and biomass accumulation^[18–20]. In the present study, L-aspartic acid was also discovered, along with eight DEGs such as *Rubisco*^[21], *PGK*, *GAPDH*, *MDH2*, β -*Glu*, *endo-Glu*, *TPS*, and *BAM* (Fig. 3d). Phytohormones are acknowledged for their impact on plant growth and development^[22]. In the present study, six DEGs including *AUX/IAA*, *ARF*, *GH3*, *SAUR*, *A-ARR*, and *GID1* involved in Auxin^[23], CTK^[24] and GA^[25,26] signaling pathways, were identified (Fig. 3e). These above DEGs and DAMs jointly contributed to the high yield and high sugar for YZ05-51.

Table 1. Information on the trend in promotion acreage for YZ05-51 in Yunnan province.

YZ05-51	2017	2018	2019	2020	2021	2022	2023
Planting area (hectare)	1,380	3,047	5,673	14,640	24,333	27,513	5,673
Percentage of total area (%)	0.48	1.05	1.96	5.08	8.91	10.20	12.13
Percentage of plant-cane area (%)	/	/	/	10.71	17.25	13.67	12.13

The data was provided by the Yunnan Provincial Department of Agriculture and Rural Development.

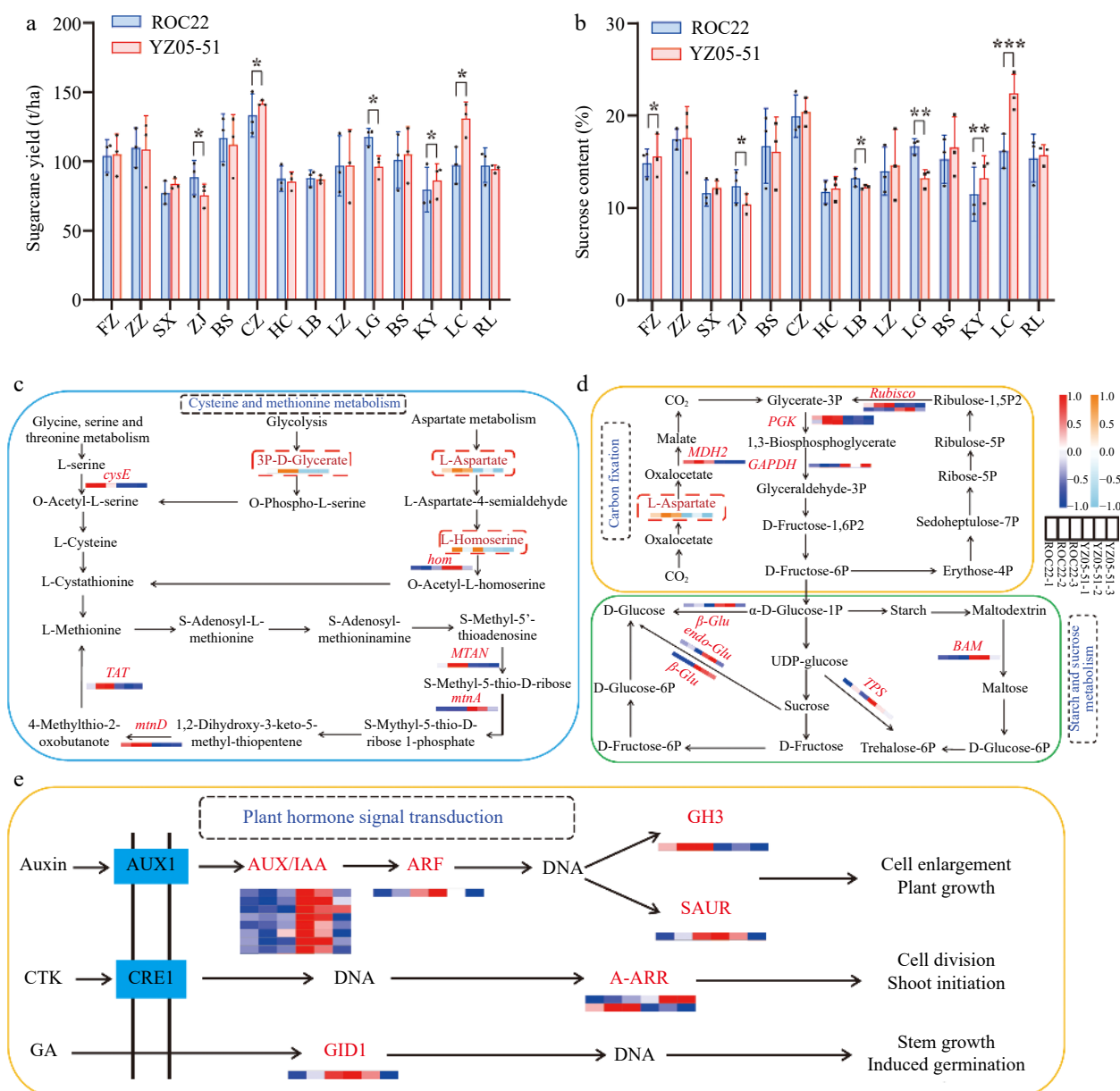


Fig. 3 Biological basis of high yield and high sugar in YZ05-51. (a), (b) Cane yield and sucrose content of YZ05-51 and ROC22 in the eighth national sugarcane regional trial (2011–2012, two plant-cane crops and one ratoon crop)^[10,11]. t/ha: tons per hectare. Significance (* for $p < 0.05$, ** for $p < 0.01$, and *** for $p < 0.001$) and standard deviation (SD) were calculated using two-way analysis of variance (ANOVA) followed by Duncan's new multiple range test of GraphPad Prism 8.0 software. FZ, Fuzhou of Fujian; ZZ, Zhangzhou of Fujian; SX, Suixi of Guangdong; ZJ, Zhanjiang of Guangdong; BS, Baise of Guangxi; CZ, Chongzuo of Guangxi; HC, Hechi of Guangxi; LB, Laibin of Guangxi; LZ, Liuzhou of Guangxi; LG, Lingao of Hainan; BS, Baoshan of Yunnan; KY, Kaiyuan of Yunnan; LC, Lincang of Yunnan; RL, Ruili of Yunnan. (c) Cysteine and methionine metabolism. (d) Carbon fixation and starch/sucrose metabolism. (e) Plant hormone signal transduction. The heat maps represent the expression of DEGs and DAMs in YZ05-51 compared to ROC22. Red/orange and blue/sky-blue colors indicate up-regulated and down-regulated DEGs/DAMs, respectively. *cysE*, serine O-acetyltransferase; *hom*, homoserine dehydrogenase; *TAT*, tyrosine aminotransferase; *MTAN*, 5'-methylthioadenosine nucleosidase; *mtnA*, methylthioribose-1-phosphate isomerase; *mtnD*, 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase; *Rubisco*, ribulose-bisphosphate carboxylase; *PGK*, phosphoglycerate kinase; *GAPDH*, glyceraldehyde 3-phosphate dehydrogenase (phosphorylating); *MDH2*, malate dehydrogenase 2; β -Glu, beta-glucosidase; *endo-Glu*, endoglucanase; *TPS*, trehalose 6-phosphate synthase. *BAM*, beta-amylase; *AUX/IAA*, auxin; *ARF*, auxin response factor; *GH3*, gretchen hagen 3; *SAUR*, small auxin up-regulated RNA; *A-ARR*, type-A *Arabidopsis* response regulator; *GID1*, GIBBERELLIN-INSENSITIVE DWARF1.

Why is YZ05-51 drought-tolerant and disease-resistant?

Since the 1950s, the global temperature has been increasing by approximately 0.13 °C every decade, causing global water

scarcity due to rising temperatures and declining precipitation^[27]. The frequent occurrence of droughts in agricultural areas has significantly jeopardized agricultural production, resulting in substantial reductions in crop yields and severe impacts on its quality. In plants, abscisic acid (ABA)

signaling pathway is the most studied signaling pathway involved in plant drought stress response^[28]. In the present study, several ABA-related DEGs including *PYR/PYL*, *PP2C*, *SnRK2* and *ABF* were identified, most of which had a higher expression level in YZ05-51 compared to ROC22 (Fig. 4a). Besides, six ABA-related genes (*PYL8*, two *PP2C9*, *SAPK8*, *SAPK4*, and *ABF9*) were up-regulated under drought stress in sugarcane (Fig. 4c). Plants frequently generate high levels of reactive oxygen species (ROS) in response to stress. To mitigate this, they utilize enzymes like ascorbate peroxidase (APX), catalase (CAT), peroxidase (POD) and superoxide dismutase (SOD) to remove excess toxic ROS^[29]. In the current dataset, five ROS-related DEGs (three *APX*, *CAT*, and *SOD*) were detected (Fig. 4b), among which four were up-regulated under drought stress (Fig. 4c). Transcription factors (TFs), including MYB, WRKY, ERF, NAC, and bZIP, have been confirmed as key players in drought stress tolerance^[30–34]. Here, it was observed that the expression of several *DREB* (2), *WRKY* (7), and *bZIP* (8) were induced by drought stress (Fig. 4b, c). We can thus deduce that, those DEGs involved in ABA signaling pathways, ROS-related enzymes and *DREB*, *WRKY*, and *bZIP* TFs collectively enhanced the tolerance to drought stress in sugarcane.

In plants, phenylpropanoid and flavonoid effectively regulate the accumulation of ROS in cells. They serve as the primary source of plant defensive secondary metabolites^[37–39]. Here in

our study, one DAM (Vitamin) and 10 DEGs (*PAL*, *4CL*, *COMT*, *POD*, *CYP98A*, *CYP75A*, *HCT*, *F3H*, *ANR*, and *CCoAOMT*) were determined in the phenylpropanoid and flavonoid biosynthesis pathways (Fig. 4d). As shown in Fig. 4e, *JAZ*, *TGA*, *MKK9*, and *XR4* involved in the jasmonate acid (JA)^[40,41], salicylic acid (SA)^[42], and ethylene (ET)^[43] signaling pathways, were identified. When the plant is infected with pathogens, to promote resistance, pathogen-associated molecular proteins (PAMPs) bind to receptor-like proteins (RLKs) or disease resistance proteins such as Cf9, CNGCs, and FLS2 to activate MAPK cascade signaling and pathogen secretion system^[44]. Based on our RNA-Seq data, *MEKK1*, *MKS1*, *WRKY33*, and *RbohD* enriched in MAPK pathways, were also discovered (Fig. 4f). Collectively, the DEGs and DAMs involved in phenylpropanoid and flavonoid biosynthesis, JA, SA, ET, and MAPK signaling pathways improved the resistance of sugarcane to pathogen infection, which is the potential reason why YZ05-51 is highly disease-resistance.

Challenges and prospects

Currently, sugarcane breeding faces several challenges, including a limited genetic pool, low breeding efficiency, and the struggle to develop innovative sugarcane varieties. Besides, resource sharing between different breeding units is challenging, information exchange, and communication are lacking,

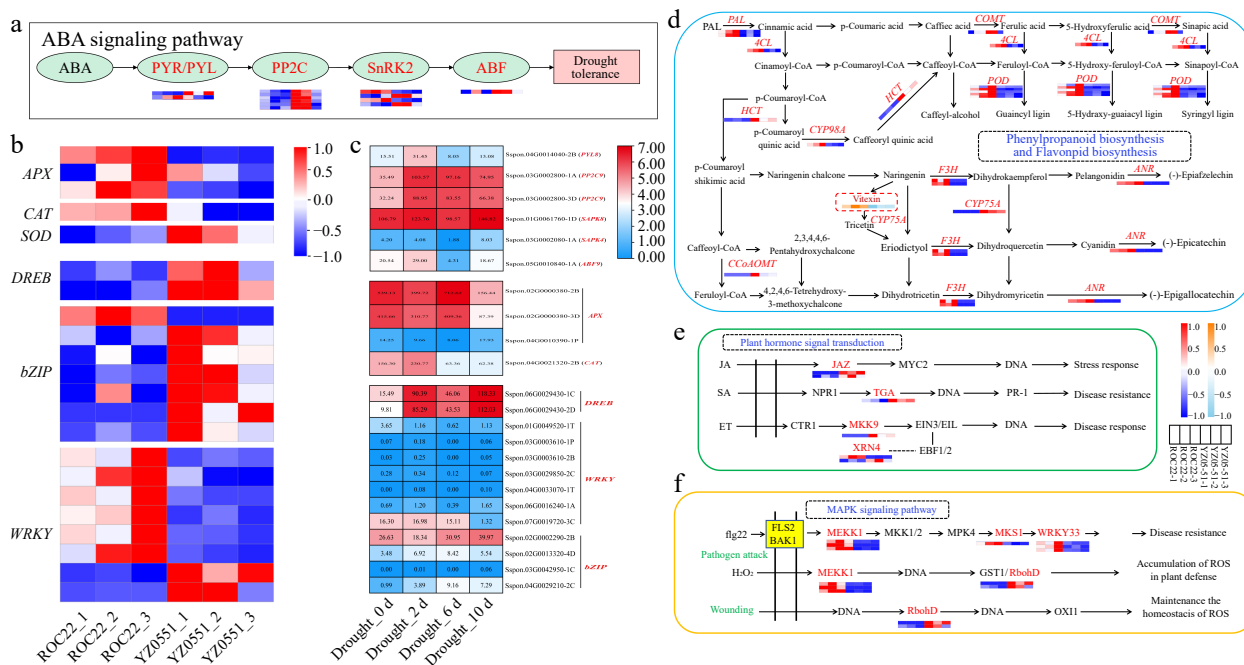


Fig. 4 Biological basis of drought tolerance and disease resistance in YZ05-51. (a) ABA signaling pathway. (b) ROS-related genes and transcription factors (TFs) in YZ05-51 compared to ROC22. (c) Expression patterns of ABA-related, ROS-related, *DREB*, *WRKY*, and *bZIP* genes. (d) Phenylpropanoid and flavonoid biosynthesis. (e) JA, SA, and ET signaling pathways. (f) MAPK signaling pathway. Red/orange and blue/sky-blue colors indicate up-regulated and down-regulated DEGs/DAMs, respectively. The source data of *S. spontaneum* subjected to drought treatment was obtained from NCBI website under project PRJNA636260^[35,36]. PYR/PYL, abscisic acid receptor PYR/PYL family; PP2C, protein phosphatase 2C; SnRK2, serine/threonine-protein kinase 2; ABF, ABRE binding factors; APX, ascorbate peroxidase; CAT, catalase, SOD, superoxide dismutase. PAL, phenylalanine ammonia-lyase; 4CL, 4-coumarate-CoA ligase; COMT, caffeic acid 3-O-methyltransferase; POD, peroxidase; HCT, shikimate O-hydroxycinnamoyltransferase; CYP98A, 5-O-(4-coumaroyl)-D-quinic acid 3'-monooxygenase; F3H, naringenin 3-dioxygenase; ANR, anthocyanidin reductase; CYP75A, flavonoid 3',5'-hydroxylase; CCoAOMT, caffeoyl-CoA O-methyltransferase; JAZ, jasmonate ZIM domain-containing protein; TGA, transcription factor TGA; MKK9, mitogen-activated protein kinase kinase 9; XR4, 5'-3' exonuclease 4; MEKK1, mitogen-activated protein kinase kinase kinase 1; MKS1, MAP kinase substrate 1; WRKY33, WRKY transcription factor 33; RbohD, respiratory burst oxidase D.

and collaboration between industry and academia is not as robust as needed. Additionally, mutagenic and transgenic breeding have not seen adequate advancement, and sugar industry enterprises are considered to be more actively involved in sugarcane breeding. To address these challenges, it is essential to enhance the introduction of sugarcane varieties and germplasm resources to broaden the genetic diversity. This involves identifying and selecting superior germplasm through rigorous testing and evaluation. Efforts should also be made to collect, study, and utilize wild sugarcane germplasm resources to generate innovative germplasm for further crossbreeding initiatives, with a focus on crossbreeding and backcrossing *S. spontaneum* and *S. arundinaceum*. Furthermore, research on sugarcane hybridization needs to be intensified, especially flowering induction for difficult-to-flowering parents. Moreover, refinement of variety selection and breeding procedures, along with comprehensive evaluation for disease and drought resistance in hybrid progeny, is indispensable. Continued efforts in gene cloning, transgenic breeding, and gene editing are urgently needed to cultivate superior sugarcane lines with huge potential. Lastly, the industrialization of healthy seedlings is imperative for expediting the dissemination of a sugarcane variety, which facilitates the adoption of sugarcane varieties and enhances the standards for seed production, leading to cost reduction and increased profitability.

Taken together, YZ05-51, resulting from a cross between YC90-56 and ROC23, demonstrate high yield, high sugar, strong stress resistance, and wide adaptability, particularly thriving in dry slope conditions. With a combination of high-yield characteristics from ROC-type and high-resistance traits from *S. spontaneum*, along with a pedigree from POJ, F, Co, and NCo series, it represents a significant advancement in sugarcane production. This variety has surpassed previous records for cane yield in non-irrigated areas, achieving a remarkable yield of 138 t/ha in Yunnan province. We can reasonably deduce that the widespread use of healthy seedlings has contributed to the promotion of YZ05-51, approximately 31,947 hectare, constituting 12.13% of the total cultivated area in Yunnan province. Hopefully, the successful breeding and widespread adoption of YZ05-51 establish a solid foundation for the development of sugarcane varieties with desirable agronomic traits.

Author contributions

The authors confirm contribution to the paper as follows: formal analysis, methodology: Wu Q; visualization: Wu Q, Li A, Liu J, Zhao Y, Zhao P; funding acquisition: Wu Q, Que Y; writing – original draft: Wu Q, Li A; writing – review & editing: Liu J, Zhao Y, Zhao P, Zhang Y, Que Y; data curation: Liu J, Zhao Y, Zhao P; conceptualization, project administration, resources, supervision: Zhang Y, Que Y. All authors reviewed the results and approved the final version of the manuscript.

Data availability statement

The raw RNA-Seq data of this study were deposited in the Genome Sequence Archive at the China National Center for Bioinformation (www.cncb.ac.cn). The original contributions presented in the study are included in the article. Further inquiries can be directed to the corresponding authors.

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Conflict of interest

The authors declare that they have no conflict of interest.

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