

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*

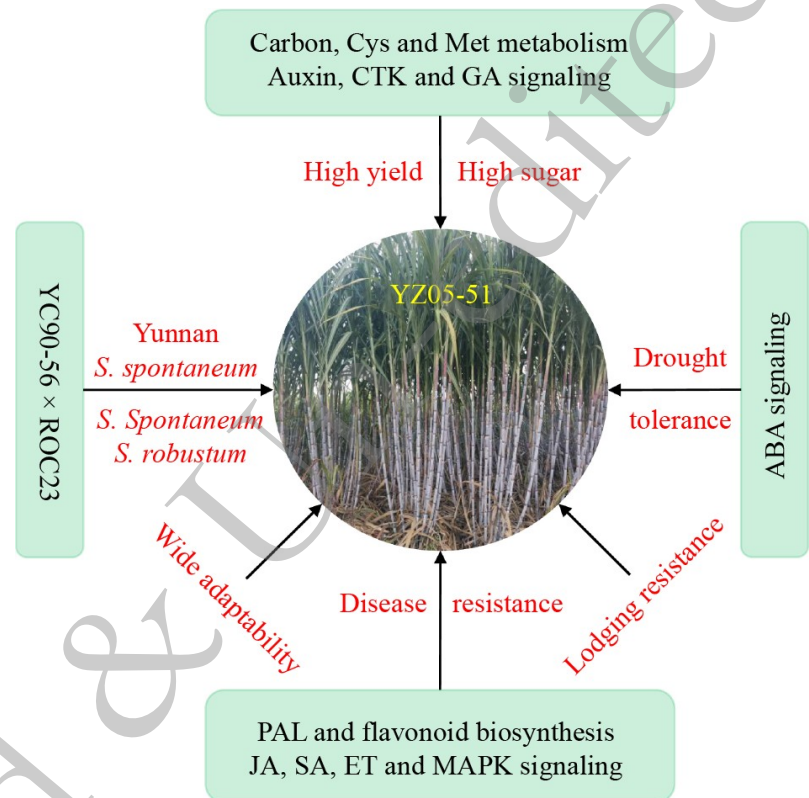
Correspondences

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.

Citation: Wu Q, Li A, Liu J, Zhao Y, Zhao P, et al. 2024. Sugarcane variety YZ05-51 with high yield and strong resistance: breeding and cultivation perspectives. *Tropical Plants* <https://doi.org/10.48130/tp-0024-0019>

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% 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 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 479,200 acres, 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 9.2 tons per acre. To summarize experience and inspire innovation, we detailed here the insights into the breeding logic and genetic characteristics of YZ05-51. Further, the biological mechanisms underlying its agronomic traits were investigated at 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.

Citation: Wu Q, Li A, Liu J, Zhao Y, Zhao P, et al. 2024. Sugarcane variety YZ05-51 with high yield and strong resistance: breeding and cultivation perspectives. *Tropical Plants* <https://doi.org/10.48130/tp-0024-0019>

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% 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 south-western 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 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 desir-

able 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% 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 firstly 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 9.2 tons per acre (about 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, we

breeding and cultivation perspectives of YZ05-51

aim to provide detailed insights into the breeding logic and genetic characteristics of YZ05-51. Furthermore, we explore the biological mechanisms for the formation of desirable agronomic traits. Finally, we address the challenges and future prospects, laying a 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], and hybrid breeding is the most effective one^[4,12,13]. Parental material is crucial for selecting and breeding elite sugarcane varieties. Furthermore, ermplasm 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 a 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 9.2 tons per acre in the Gengma county of Yunnan province, surpassing the previous record for sugarcane yield in non-irrigated areas^[4,10,11]. In China, the intro-

duction 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 a significant progress in sugarcane breeding^[4] (Fig. 1).

How about 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. 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

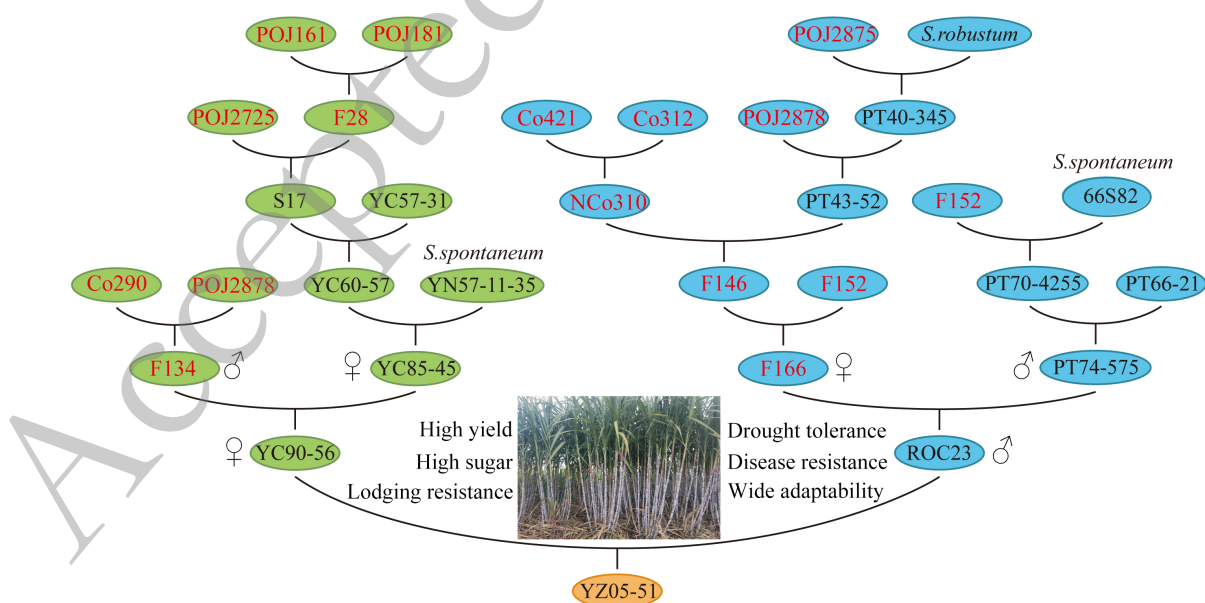


Fig. 1 Pedigree and elite traits of sugarcane variety YZ05-51.

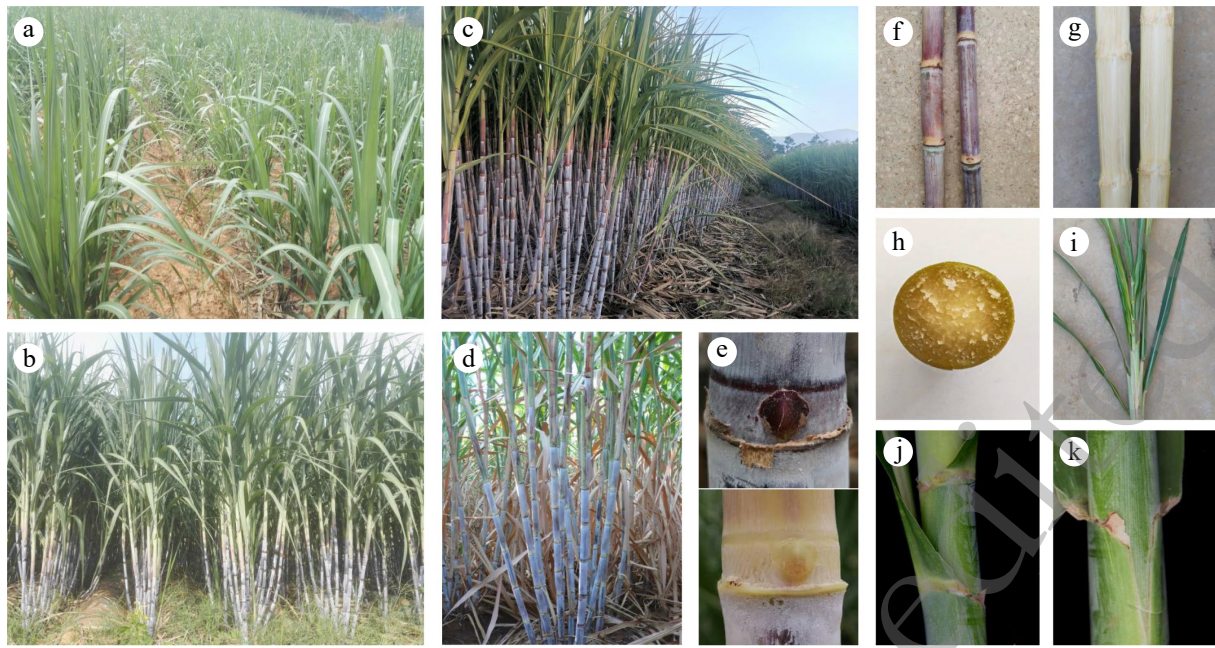


Fig. 2 Genetic characteristics of sugarcane variety YZ05-51. (a) seedling stage, (b) elongation stage, (c) maturity stage, (d) plant type, (e) bud, (f) stem, (g) stem longitudinal section, (h) stem transverse section, (i) leaf, (j) leaf sheath, (k) leaf auricle. The original photos were provided by the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

and controlling thrips^[10]. In national regional trial, the average yield is 6.72 tons per acre, with 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 479,200 acres, accounting for 12.13% of the total cultivated area in Yunnan province (Table 1).

Why YZ05-51 is 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 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 metabolite (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]. Here in our 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.

Why YZ05-51 is drought-tolerance and disease-resistance?

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 (ten thousand acre)	2.07	4.57	8.51	21.96	36.5	41.27	47.92
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

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

breeding and cultivation perspectives of YZ05-51

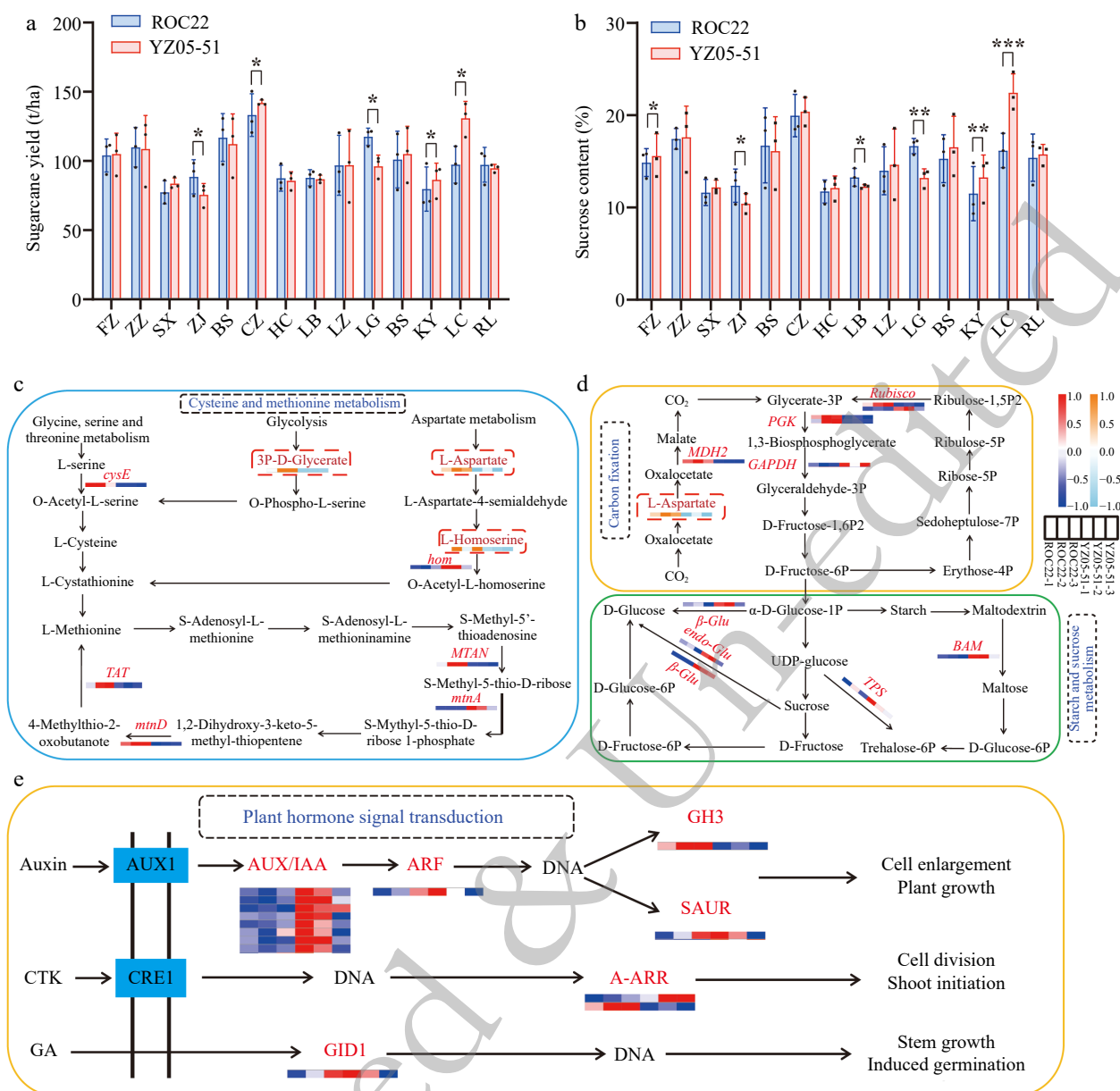


Fig. 3 Biological basis of high yield and high sugar in YZ05-51. (a) and (b) Cane yield and sucrose content of YZ05-51 and ROC22 in eighth national sugarcane regional trial (2011-2012, two plant-cane crops and one ratoon crop). The source of data was referenced to Zhao et al.^[10] and Liu et al.^[11]. t/ha represents 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 nucleosidases; *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.

Since the 1950s, the global temperature has been increasing by approximately 0.13 °C every decade, causing a global water scarcity due to rising temperatures and declining precipitation^[27]. The frequent occurrence of droughts in agri-

cultural 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 our 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, we observed that the expression of several *DREB* (2), *WRKY* (7) and *bZIP* (8) were induced by drought stress (Fig. 4B, 4C). 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 (Vitexin) 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 *XRN4* involved in 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 the resistance, pathogen-associated molecular proteins (PAMPs) bind to receptor-like proteins (RLKs) or disease resistance protein 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, that 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, 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

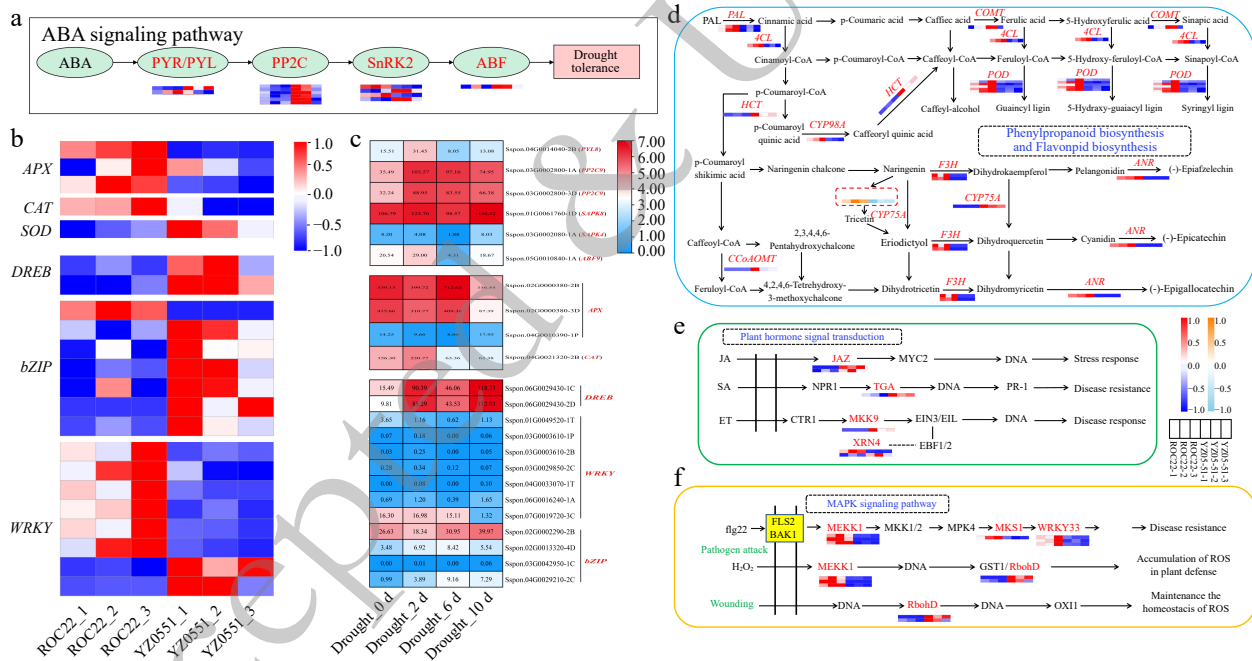


Fig. 4 Biological basis of drought tolerance and disease resistance in YZ05-51. (a) ABA signaling pathway. (b) ROS-related genes and transcription factors (TFs) in YZ05-51 compared to ROC22. (c) Expression patterns of ABA-related, ROS-related, *DREB*, *WRKY*, and *bZIP* genes. (d) Phenylpropanoid and 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; XRN4, 5'-3' exoribonuclease 4; MEKK1, mitogen-activated protein kinase kinase kinase 1; MKS1, MAP kinase substrate 1; WRKY33, WRKY transcription factor 33; RbohD, respiratory burst oxidase D.

breeding and cultivation perspectives of YZ05-51

enterprises are considered to be more actively involved in sugarcane breeding. In order 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 seedling 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, demonstrates 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 9.2 tons per acre in Yunnan province. We can reasonably deduce that, the widespread use of healthy seedlings has contributed to the promotion of YZ05-51, approximately 479,200 acres, 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

QW: Formal Analysis, Methodology, Visualization, Funding acquisition, Writing—original draft; AL: Visualization, Writing—original draft; JL, YZ and PZ: Data curation, Visualization, Writing—review & editing; YZ: Conceptualization, Project administration, Resources, Supervision, Writing—review & editing; YQ: Conceptualization, Funding acquisition, Project administration, Resources, Supervision, Writing—review & editing.

Data availability statement

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

Acknowledgments

This work was funded by the Project of National Key Labora-

tory for Tropical Crop Breeding (NKLTCB20230305, Hainan; NKLTCB-YAAS-2024-S01, Yunnan), China Agriculture Research System of MOF and MARA (CARS-17), Central Public-interest Scientific Institution Basal Research Fund (1630052024003 and 1630052024020), Guangxi Key Laboratory of Sugarcane Genetic Improvement (21-238-16-K-02-03), and Yunnan Key Laboratory of Sugarcane Genetic Improvement (2023KFKT001).

Conflict of interest

The authors declare that they have no conflict of interest.

Dates

Received 20 April 2024; Accepted 29 April 2024; In press 8 May 2024

References

- Rajput MA, Rajput NA, Syed RN, Lodhi AM, Que Y. 2021. Sugarcane smut: current knowledge and the way forward for management. *Journal of Fungi* 7(12):1095
- Lam E, Shine J, Silva JD, Lawton M, Bonos S, Calvino M, et al. 2019. Improving sugarcane for biofuel: engineering for an even better feedstock. *GCB Bioenergy* 1:251–255
- Chen R, Xu L, Lin Y, Deng Z, Zhang M, Luo J, et al. 2011. *Modern sugarcane genetic breeding*. Beijing: China Agriculture Press, pp: 2–12.
- Zhang Y, Wang L, Lu W, Wu C, Liu J, Zhao P, et al. 2022. *Modern sugarcane breeding theory and variety selection-Heterogeneous complex resistant, high yield and high sugar breeding and application*. Beijing: Science Press.
- Qiang L. 2021. Growth and decline of sugarcane cultivar 'ROC22' in Guangxi sugarcane area from 2008 to 2017. *Chinese Journal of Tropical Crops* 42:982–990
- Zhang Y, Zhao P, Hu C, Que Y. 2024. The recent achievements and development trends of sugarcane improvement in China. *China Sugar* 46:87–92
- Luo J, Pan Y-B, Xu L, Grisham MP, Zhang H, Que Y. 2015. Rational regional distribution of sugarcane cultivars in China. *Scientific Reports* 5:15721
- Luo J, Pan Y-B, Que Y, Zhang H, Grisham MP, Xu L. 2015. Biplot evaluation of test environments and identification of mega-environment for sugarcane cultivars in China. *Scientific Reports* 5:15505
- Zhao P, Xia H, Liu J, Wu C, Zhao J, Yang K, et al. 2019. Registration of 'YZ081609' sugarcane. *Journal of Plant Registrations* 13:362–367
- Liu J, Zhao P, Yang K, Xiang H, Wu C, Chen X, et al. 2016. Breeding of new sugarcane variety, Yunzhe05-51. *China Sugar* 38(1):8–10
- Zhao P, Liu J, Yang K, Xiang H, Wu C, Chen X, et al. 2015. Registration of 'YZ05-51' sugarcane. *Journal of Plant Registrations* 9:172–178
- Que Y, Wu Q, Zhang H, Luo J, Zhang Y. 2024. Developing new sugarcane varieties suitable for mechanized production in China: principles, strategies and prospects. *Frontiers in Plant Science* 14:1337144
- Lu G, Liu P, Wu Q, Zhang S, Zhao P, Zhang Y, et al. 2024. Sugarcane breeding: a fantastic past and promising future driven by technology and methods. *Frontiers in Plant Science* 15:1375934
- Zhang Q, Qi Y, Zhang C, Chen Y, Deng H. 2009. Pedigree analysis of genetic relationship among core parents of sugarcane in mainland China. *Guangdong Agricultural Sciences* 10:44–48
- Qi Y, Deng H, Li Q. 2012. Advance in utilization of sugarcane germplasm in China mainland. *Crop Research* 26:443–446
- Liu F, Xing S, Ma H, Du Z, Ma B. 2013. Cytokinin-producing, plant growth-promoting rhizobacteria that confer resistance to drought stress in *Platygladus orientalis* container seedlings. *Applied Microbi-*

- ology and Biotechnology* 97:9155–64
17. Yu Z, Song M, Pei H, Jiang L, Hou Q, Nie C, et al. 2017. The effects of combined agricultural phytohormones on the growth, carbon partitioning and cell morphology of two screened algae. *Biore-source Technology* 239:87–96
 18. Winkel-Shirley B. 2021. Flavonoid biosynthesis. *A colorful model for genetics, biochemistry, cell biology, and biotechnology. Plant Physiology* 126:485–493
 19. Bar-Even A. 2017. Daring metabolic designs for enhanced plant carbon fixation. *Plant Science* 273:71–83
 20. Ducat DC, Silver PA. 2012. Improving carbon fixation pathways. *Current Opinion Chemical Biology* 16:337–44
 21. Patel M, Berry JO. 2008. Rubisco gene expression in C4 plants. *Journal of Experimental Botany* 59(7):1625–34
 22. Vanstraelen M, Benková E. 2012. Hormonal interactions in the regulation of plant development. *Annual Review of Cell and Developmental Biology* 28:463–87
 23. Yu Z, Zhang F, Friml J, Ding Z. 2022. Auxin signaling: Research advances over the past 30 years. *Journal of Integrative Plant Biology* 64(2):371–392
 24. Nakano T, Kimbara J, Fujisawa M, Kitagawa M, Ihashi N, Maeda H, et al. 2012. MACROCALYX and JOINTLESS interact in the transcriptional regulation of tomato fruit abscission zone development. *Plant Physiology* 158(1):439–50
 25. Gao X, Fu X. 2018. Research progress for the gibberellin signaling and action on plant growth and development. *Biotechnology Bulletin* 34(7):1–13
 26. Shani E, Hedden P, Sun TP. 2024. Highlights in gibberellin research: A tale of the dwarf and the slender. *Plant Physiology* 30:kiae044
 27. Volenec ZM, Belovsky GE. 2018. The interaction of temperature and precipitation determines productivity and diversity in a bunchgrass prairie ecosystem. *Oecologia* 188(3):913–920
 28. Chen K, Li GJ, Bressan RA, Song CP, Zhu JK, Zhao Y. 2020. Abscisic acid dynamics, signaling, and functions in plants. *Journal of Integrative Plant Biology* 62(1):25–54
 29. Mittler R, Zandalinas SI, Fichman Y, Van Breusegem F. 2022. Reactive oxygen species signalling in plant stress responses. *Nature Review Molecular Cell Biology* 23(10):663–679
 30. Dubos C, Stracke R, Grotewold E, Weisshaar B, Martin C, Lepiniec L. 2010. MYB transcription factors in *Arabidopsis*. *Trends in Plant Science* 15(10):573–81
 31. Wani SH, Anand S, Singh B, Bohra A, Joshi R. 2021. WRKY transcription factors and plant defense responses: latest discoveries and future prospects. *Plant Cell Reports* 40(7):1071–1085
 32. Feng K, Hou XL, Xing GM, Liu JX, Duan AQ, Xu ZS, et al. 2020. Advances in AP2/ERF super-family transcription factors in plant. *Critical Review in Biotechnology* 40(6):750–776
 33. Nakashima K, Takasaki H, Mizoi J, Shinozaki K, Yamaguchi-Shinozaki K. 2012. NAC transcription factors in plant abiotic stress responses. *Biochimica et Biophysica Acta* 1819(2):97–103
 34. Han H, Wang C, Yang X, Wang L, Ye J, Xu F, et al. 2023. Role of bZIP transcription factors in the regulation of plant secondary metabolism. *Planta* 258(1):13
 35. Wu Q, Chen Y, Zou W, Pan Y-B, Lin P, Xu L, et al. 2023. Genome-wide characterization of sugarcane catalase gene family identifies a ScCAT1 gene associated disease resistance. *International Journal of Biological Macromolecules* 232:123398
 36. Sun T, Meng Y, Cen G, Feng A, Su W, Chen Y, et al. 2022. Genome-wide identification and expression analysis of the coronatine-insensitive 1 (COI1) gene family in response to biotic and abiotic stresses in *Saccharum*. *BMC Genomics* 23(1):38
 37. Yadav V, Wang Z, Wei C, Amo A, Ahmed B, Yang X, et al. 2020. Phenylpropanoid pathway engineering: An emerging approach towards plant defense. *Pathogens* 9:312
 38. Dong NQ, Lin HX. 2021. Contribution of phenylpropanoid metabolism to plant development and plant-environment interactions. *Journal of Integrative Plant Biology* 63:180–209
 39. Zhang P, Du H, Wang J, Pu Y, Yang C, Yan R, et al. 2020. Multiplex CRISPR/Cas9-mediated metabolic engineering increases soya bean isoflavone content and resistance to soya bean mosaic virus. *Plant Biotechnology Journal* 18:1384–1395
 40. Wani SH, Kumar V, Shriram V, Sah SK. 2016. Phytohormones and their metabolic engineering for abiotic stress tolerance in crop plants. *Crop Journal* 4:162–176
 41. Wasternack C, Hause B. 2013. Jasmonates: biosynthesis, perception, signal transduction and action in plant stress response, growth and development. *Annals of Botany* 111:1021–1058
 42. Zhao Z, Zhang R, Wang D, Zhang J, Zang S, Zou W, et al. 2023. Dissecting the features of TGA gene family in *Saccharum* and the functions of ScTGA1 under biotic stresses. *Plant Physiology Biochemistry* 200:107760
 43. Binder BM. 2020. Ethylene signaling in plants. *Journal of Biological Chemistry* 295(22):7710–7725
 44. Wu Q, Su Y, Pan Y-B, Xu F, Zou W, Que B, et al. 2022. Genetic identification of SNP markers and candidate genes associated with sugarcane smut resistance using BSR-Seq. *Frontiers in Plant Science* 13:1035266



Copyright: © 2024 by the author(s). Published by Maximum Academic Press on behalf of Hainan University. This article is an open access article distributed under Creative Commons Attribution License (CC BY 4.0), visit <https://creativecommons.org/licenses/by/4.0/>.