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Utilizing Wild Tea Species for Stress-Resistant Varieties Case Studies

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Abstract The stress resistance of tea plants (*Camellia sinensis*) is crucial for their growth, yield, and quality, as environmental stresses such as drought, low temperatures, high salinity, and pests can severely impact tea production. Wild tea germplasm resources exhibit rich genetic diversity and are regarded as an important genetic reservoir for stress-resistant traits. This study systematically summarizes the genetic basis of stress resistance in tea plants, with a particular focus on key stress-responsive genes, molecular signaling pathways, and their regulatory mechanisms. It also explores the stress resistance traits and genetic diversity of wild tea plants, analyzing their ecological distribution and adaptive characteristics. Regarding stress-resistant tea breeding, this study reviews traditional breeding methods, molecular breeding techniques, and gene editing applications, while also presenting successful cases of breeding stress-resistant varieties using wild tea resources. Despite significant progress in improving stress resistance, challenges remain in the conservation and utilization of wild germplasm resources, as well as in the complex polygenic inheritance of stress resistance traits. This study further examines the prospects of emerging technologies such as genomic selection, transcriptomics, and artificial intelligence in tea breeding. Based on an analysis of current research challenges, future directions for tea breeding are proposed, emphasizing the rational utilization of wild tea germplasm resources to enhance the stress resistance and production stability of cultivated tea plants, enabling them to better adapt to changing environmental conditions.

Keywords Tea plant (*Camellia sinensis*); Stress resistance; Wild germplasm; Genetic diversity; Molecular breeding

1 Introduction

Tea plants (*Camellia sinensis*) are highly sensitive to environmental stresses, including drought, salinity, extreme temperatures, and pests, which significantly impact yield and quality. Drought reduces leaf water potential, salinity disrupts nutrient uptake, and cold stress damages buds and leaves, affecting seasonal productivity. Biotic stress, such as disease outbreaks, also leads to economic losses (Dong et al., 2017). Given the increasing challenges posed by climate change, improving stress resistance in tea plants is essential for maintaining stable production and ensuring the long-term sustainability of the tea industry.

Wild tea species serve as valuable reservoirs of genetic diversity, harboring traits that enhance stress tolerance. Their adaptation to diverse environments has led to the evolution of resistance to drought, cold, and diseases. Integrating wild germplasm into breeding programs introduces beneficial alleles, broadening the genetic base of cultivated tea varieties (Wang et al., 2022; Wang et al., 2024). Zhang et al. (2015) have identified some wild tea trees with strong abiotic and biotic stress tolerance, showing great potential in cultivating highly resistant tea tree varieties. However, the conservation and efficient utilization of wild tea tree germplasm resources remains a key challenge in tea tree breeding (Chen et al., 2024).

This study explores the genetic foundation of stress resistance in tea plants, emphasizing key genes and regulatory mechanisms. It examines the stress resistance traits of wild tea species and their potential contributions to breeding programs. Additionally, it evaluates both traditional and modern breeding approaches, including molecular techniques and gene editing, while highlighting challenges in wild germplasm conservation and genetic enhancement. Finally, the study discusses recent advancements and outlines future directions for the development of stress-resistant tea varieties.

2 Genetic Basis of Stress Resistance Traits in Tea Plants

Tea plants (*Camellia sinensis*) face multiple environmental stresses, including drought, heat, cold, and salinity, which significantly affect their growth and productivity. These stresses trigger complex molecular responses, such as alternative splicing and differential gene expression, to enhance stress adaptation. Key stress-related genes, including the bZIP, SOD, and MYB transcription factor families, play vital roles in drought, cold, and oxidative stress tolerance. Additionally, molecular signaling pathways, such as the ABA and jasmonic acid pathways, regulate stress resistance through intricate networks of transcription factors and regulatory genes. Understanding these genetic and molecular mechanisms provides valuable insights for improving tea plant resilience and developing stress-tolerant cultivars.

2.1 Effects of major environmental stresses on tea plants

Ding et al. (2020) found that tea trees (*Camellia sinensis*) suffer from a variety of environmental stresses, including drought, high temperature, low temperature and salt stress, which significantly affect their growth and productivity. Drought and heat stresses, for instance, trigger alternative splicing in a large number of genes, enhancing the transcriptome's adaptability to these conditions. Cold stress is particularly challenging, affecting the physiological and biochemical processes in tea plants, as seen in the differential responses of cold-resistant and susceptible cultivars. Salinity stress also influences gene expression, with certain genes like the serine acetyltransferase (SAT) family playing a crucial role in enhancing salt tolerance (Ding et al., 2020).

2.2 Stress-related genes and their functions in tea plants

Several gene families have been identified as key players in the stress response of tea plants. The bZIP gene family, particularly the ABF subgroup, is involved in ABA signaling and drought tolerance. The *CsAFS2* gene enhances resistance to cold and insect stress by increasing protective enzyme activity and osmotic regulatory substances (Zhou et al., 2019). The superoxide dismutase (SOD) gene family is crucial for reactive oxygen species (ROS) removal, with specific genes being induced under cold and drought stress. Additionally, the MYB transcription factors are involved in jasmonic acid signal transduction, enhancing cold stress tolerance (Liu et al., 2021) (Figure 1).

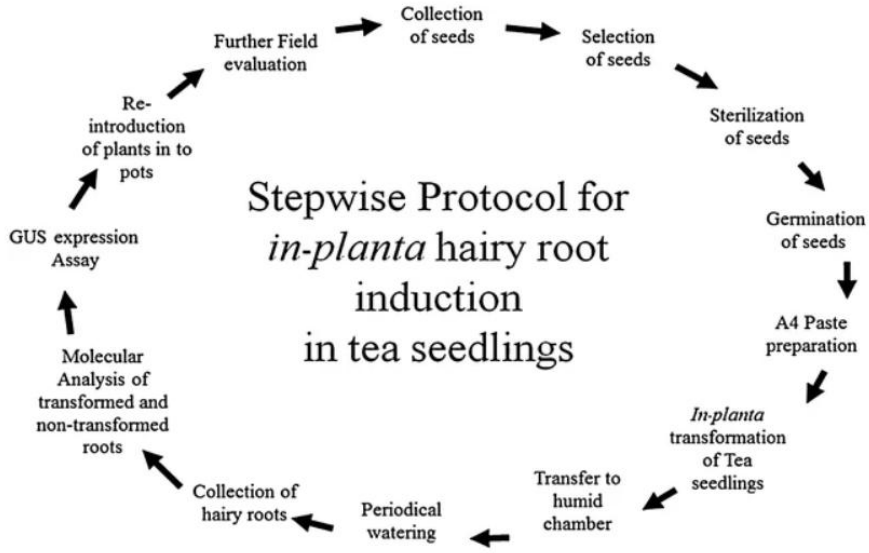

Figure 1 Tea tree seedling cultivation and gene expression (Adopted from Alagarsamy et al., 2018)

2.3 Molecular signaling pathways and regulatory mechanisms of stress resistance

The molecular signaling pathways in tea plants involve complex networks of transcription factors and regulatory genes. The CsMYB transcription factors interact with jasmonic acid pathway components to mediate cold stress responses. The *CsABF* genes are part of the ABA signaling pathway, crucial for drought tolerance (Lu et al., 2021). The YUCCA gene family, involved in IAA biosynthesis, plays a role in stress resistance by regulating

growth and development under stress conditions (Wang et al., 2024). Furthermore, the HD-Zip transcription factors are implicated in various abiotic stress responses, suggesting a broad regulatory role in stress adaptation.

3 Stress Resistance Traits and Genetic Diversity of Wild Tea Plants

Wild tea plants exhibit rich genetic diversity, which provides a crucial foundation for their stress resistance under various environmental conditions. Compared to cultivated varieties, wild tea plants often demonstrate stronger tolerance to drought, cold, salinity, and diseases, primarily due to the accumulation of advantageous stress-resistant genes through long-term natural selection. Studies have shown that stress-responsive gene families, such as bZIP, MYB, and SOD, exhibit higher expression levels in wild tea plants under adverse conditions, enhancing their resilience to drought, low temperatures, and oxidative stress. Additionally, the high genetic variability of wild tea plants allows them to adapt to complex and changing ecological environments, making them valuable genetic resources for tea breeding and the development of stress-resistant cultivars.

3.1 Major wild tea species and their ecological distribution

Wild tea species, primarily *Camellia sinensis*, are distributed across diverse ecological regions, which contribute to their varied stress resistance traits. These species are often found in environments that expose them to a range of abiotic stresses such as drought, cold, and heat, which have driven the evolution of unique adaptive mechanisms. The ecological distribution of these species plays a crucial role in their genetic diversity, providing a rich resource for breeding stress-resistant tea varieties (Han et al., 2022).

3.2 Analysis of stress resistance traits in wild tea plants

Wild tea plants exhibit several stress resistance traits that are crucial for their survival in harsh environments. For instance, in Shen et al. (2019), it was noted that *CsAFS2* genes in tea trees enhance resistance to low temperature and pest stress by increasing protective enzyme activity and upregulating stress-related genes. Cold-resistant traits have been linked to the accumulation of sucrose and the expression of specific genes like *CsCBF1* and *CsDHNs*, which are crucial for cold acclimation (Shen et al., 2019). Additionally, alternative splicing of genes in response to drought and heat stresses increases transcriptome diversity, enhancing the plant's ability to adapt to these conditions. These traits are vital for developing stress-resistant tea cultivars (Ban et al., 2017; Rahimi et al., 2018).

3.3 Molecular studies on the genetic diversity of wild tea plants

Molecular studies have revealed significant genetic diversity among wild tea plants, which is essential for their adaptability to various stresses. The identification of differentially expressed genes (DEGs) and transcription factors involved in stress responses highlights the complex genetic networks that confer stress tolerance. For example, the CsABF gene family plays a significant role in drought tolerance through the ABA signaling pathway, with specific genes like *CsABF2* and *CsABF11* being key regulators. Furthermore, the genetic diversity observed in wild tea species provides a valuable genetic pool for breeding programs aimed at enhancing stress resistance in cultivated tea varieties (Yolcu et al., 2020; Zhang et al., 2023).

4 Application of Wild Tea Resources in Breeding Stress-Resistant Varieties

The integration of wild tea resources into breeding programs through molecular and gene editing technologies offers promising opportunities to develop stress-resistant tea varieties. These approaches address the limitations of traditional breeding and leverage the genetic diversity of wild relatives to enhance the resilience of tea plants against environmental stresses.

4.1 Traditional breeding methods for tea plants and their limitations

Traditional breeding methods for tea plants primarily involve selection and cross-breeding to enhance desirable traits such as yield and quality. However, these methods are often slow and limited by genetic bottlenecks, as they rely heavily on existing genetic diversity within cultivated varieties. The low cross-compatibility and genetic drag from undesirable alleles further constrain the use of wild relatives in traditional breeding, making it challenging to introduce new traits such as stress resistance (Zhao et al., 2022) (Figure 2).

Figure 2 Cultivation of wild tea trees (Adopted from Zhao et al., 2022)
Image caption: Images were taken from the annual plants propagated in the insert (Adopted from Zhao et al., 2022)

4.2 Application of molecular breeding techniques in stress resistance improvement

Molecular breeding techniques, including the use of molecular markers and multi-omics approaches, have significantly advanced the development of stress-resistant tea varieties. These techniques allow for the identification of quantitative trait loci (QTLs) and genes associated with stress tolerance, facilitating targeted breeding efforts. Transcriptomic analyses have identified differentially expressed genes under stress conditions, providing insights into the molecular mechanisms of stress responses in tea plants. These advancements enable the development of tea varieties with enhanced resistance to abiotic stresses such as drought and cold (Kapazoglou et al., 2023).

4.3 Potential of gene editing technology

Gene editing technology holds great potential for enhancing stress resistance and improving desirable traits in tea plants. With precise genome modifications enabled by CRISPR-Cas9 and other advanced gene-editing tools, researchers can target key stress-responsive genes to develop tea varieties with improved drought, cold, and salinity tolerance. For example, editing genes involved in ABA and jasmonic acid signaling pathways, such as CsABF and CsMYB, could enhance adaptive responses to environmental stresses. Additionally, modifications in antioxidant-related genes like SOD may improve oxidative stress tolerance, reducing cellular damage under adverse conditions. Beyond stress resistance, gene editing can also optimize traits such as yield, flavor, and disease resistance by fine-tuning metabolic pathways. As research advances, the integration of gene editing with traditional breeding and genomic selection will accelerate the development of resilient and high-quality tea cultivars, contributing to sustainable tea production in the face of climate change (Mukhopadhyay et al., 2015).

4.4 Successful cases of breeding stress-resistant tea varieties using wild tea plants

The rich genetic diversity of wild tea plants provides valuable genetic resources for breeding stress-resistant tea cultivars. Through in-depth investigation and research on wild tea resources, breeding experts have successfully developed multiple high-quality, high-yield, and stress-resistant tea cultivars. As a wild relative of cultivated tea plants, Camellia taliensis is considered a valuable genetic resource due to its strong tolerance to abiotic stress.

Comparative transcriptome analysis has revealed a significant expansion of stress-related genes in *C. taliensis*, which can be utilized to enhance the stress resistance of cultivated tea varieties. In addition, the *CsAFS2* gene identified in tea plants intercropped with chestnut trees has been shown to improve cold and pest resistance, demonstrating the potential of integrating wild tea genes into breeding programs (Li et al., 2023). For example, a research team from Qingdao Agricultural University spent 14 years using single-plant selection methods on the offspring of the Huangshan tea population, successfully developing new cultivars such as Lu Tea 6, Lu Tea 7, and Lu Tea 17. These varieties exhibit strong growth potential, enhanced resistance to cold, drought, and pests, and broad adaptability, making them suitable for cultivation in both northern and southern tea-growing regions. Furthermore, Professor Huang Yahui's team at South China Agricultural University conducted a survey of wild tea resources across Guangdong, Guangxi, Yunnan, and Hainan, identifying numerous unique genetic resources. Utilizing these resources, they spent 12 years selecting a new tea cultivar, Huanong 181, from the Lianzhou tea population in northern Guangdong, which was granted plant variety protection in 2020. This cultivar exhibits strong growth vigor, high resistance and adaptability, excellent quality, and significant market potential (Li et al., 2023).

5 Challenges and Opportunities in Stress-Resistant Tea Breeding

5.1 Conservation and utilization of wild tea germplasm resources

The conservation and utilization of wild tea germplasm resources present both challenges and opportunities for breeding stress-resistant tea varieties. Wild relatives of cultivated tea, such as *Camellia taliensis*, offer valuable genetic resources due to their extensive abiotic tolerance and biotic resistance, which can be harnessed for genetic improvement of cultivated tea trees (Zhang et al., 2022). However, the large and complex genome of these wild species poses a challenge in terms of genetic information availability and resource management. Additionally, the integration of advanced technologies like hyperspectral machine-learning models can facilitate the non-destructive screening of drought-tolerant germplasm, offering a new avenue for evaluating and utilizing these resources effectively (Zheng et al., 2015).

5.2 Challenges in the genetic improvement of stress resistance traits

Genetic improvement of stress resistance traits in tea plants is hindered by several factors. The recalcitrance of tea plants to genetic transformation, due to issues like phenolic oxidation and bactericidal effects of tea polyphenols, complicates the genetic engineering processes (Ramakrishnan et al., 2023). Moreover, the identification and manipulation of key genes involved in stress responses, such as those related to salt and cold stress, require comprehensive transcriptomic and genomic analyses. Despite these challenges, the identification of differentially expressed genes and transcription factors involved in stress responses provides a foundation for future genetic engineering efforts (Alagarsamy et al., 2018).

5.3 Prospects of emerging technologies in tea breeding

Emerging technologies hold significant promise for advancing tea breeding programs. The integration of RNA-Seq and sRNA-Seq technologies has enabled the identification of key molecular players and pathways involved in stress responses, such as those related to cold stress. Additionally, the use of deep learning and image processing techniques for stress detection at the canopy level offers a non-invasive method to monitor and manage plant health, which is crucial for breeding disease-resistant varieties. These technologies, combined with traditional breeding methods, can accelerate the development of stress-resistant tea varieties by providing detailed insights into the genetic and phenotypic traits associated with stress tolerance (Wan et al., 2018).

6 Advances in Stress-Resistant Tea Breeding

6.1 In-depth analysis of stress resistance gene regulatory networks

Recent studies have significantly advanced our understanding of the gene regulatory networks involved in stress resistance in tea plants. For instance, the expression of key genes such as *CsCBF1* and *CsDHNs* has been linked to enhanced cold resistance, highlighting the importance of these genes in the regulatory networks that confer stress tolerance (Wang et al., 2023). Additionally, the *CsAFS2* gene has been identified as playing a crucial role in both

cold and insect resistance, further elucidating the complex gene interactions that underpin stress responses in tea plants. The identification and analysis of these gene networks are crucial for developing new tea varieties with improved stress resistance (Liu et al., 2016).

6.2 Exploration and utilization of stress-resistant genes from wild tea plants

The exploration of wild tea species has opened new avenues for identifying stress-resistant genes that can be utilized in breeding programs. Wild relatives of tea plants often possess unique genetic traits that confer resilience to various environmental stresses (Zhang et al., 2018). For example, the CsIPT gene family has been studied for its role in abiotic stress resistance, with specific genes like *CsIPT5.2* and *CsIPT6.2* being implicated in cold and drought stress responses. These findings underscore the potential of wild tea species as a genetic reservoir for enhancing stress resistance in cultivated varieties.

6.3 Breeding strategies integrating stress resistance and tea quality improvement

Integrating stress resistance with tea quality improvement is a key focus in current breeding strategies. Advances in genome-based approaches have facilitated the development of climate-resilient tea crops that do not compromise on quality. Techniques such as genomics-assisted breeding and the use of molecular markers have been instrumental in selecting elite genotypes that exhibit both stress tolerance and desirable quality traits. Moreover, biotechnological tools, including genetic transformation and the use of molecular markers, have enabled the precise manipulation of stress resistance traits while maintaining or enhancing tea quality. These strategies are essential for producing high-quality tea that can withstand the challenges posed by climate change and other environmental stresses (Takahashi et al., 2019).

7 Concluding Remarks

Wild tea species, such as *Camellia taliensis*, play a crucial role in the breeding of stress-resistant tea cultivars. Their natural tolerance allows them to withstand various abiotic and biotic stresses. These wild resources contain a wealth of stress-resistant genes, providing essential support for improving the resilience of cultivated tea plants. For example, studies have shown that *C. taliensis* possesses a greater number of LEA genes compared to cultivated tea (*C. sinensis*), which contributes to its enhanced survival ability in extreme environments. Furthermore, incorporating wild relatives into breeding programs can effectively enhance key traits such as cold and drought resistance, thereby improving tea plants' adaptability to climate change and ensuring the sustainable development of the tea industry in the future.

Despite the potential of wild tea species in breeding programs, several challenges remain. One significant gap is the limited genetic information available for many wild species, which hinders their effective utilization in breeding. Moreover, the complexity of tea plant genomes, such as the large and structurally complex genome of *C. taliensis*, poses challenges for genetic studies and breeding efforts. Another challenge is the low cross-compatibility between wild and cultivated species, which can lead to genetic drag and the introduction of undesirable traits. Addressing these challenges requires advanced genomic tools and techniques to facilitate the identification and incorporation of beneficial genes from wild species into cultivated varieties.

Future research should focus on expanding the genetic resources available for tea breeding by conducting comprehensive genomic studies on wild tea species. This includes sequencing and annotating the genomes of wild relatives to identify stress-resistance genes and pathways. Additionally, integrating biotechnological approaches such as transcriptomics, proteomics, and metabolomics can enhance the understanding of stress response mechanisms and aid in the development of stress-resistant cultivars. Emphasizing the use of naturally stress-resistant plants (NSRPs) and minor crops can also diversify tea breeding programs and contribute to sustainable agriculture. By leveraging these strategies, researchers can develop tea varieties that are better equipped to withstand environmental stresses, ensuring yield stability and quality in the face of climate change.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

Reference

Alagarsamy K., Shamala L.F., and Wei S., 2018, Protocol: high-efficiency in-planta Agrobacterium-mediated transgenic hairy root induction of *Camellia sinensis* var. *sinensis*, Plant Methods, 14: 1-8.
https://doi.org/10.1186/s13007-018-0285-8

Ban Q., Wang X., Pan C., Wang Y., Kong L., Jiang H., Xu Y., Wang W., Pan Y., Li Y., and Jiang C., 2017, Comparative analysis of the response and gene regulation in cold resistant and susceptible tea plants, PLoS One, 12(12): e0188514.
https://doi.org/10.1371/journal.pone.0188514

Chen M., Zhu X., Hou M., Luo W., Jiang Y., Yu Y., Wang J., Yuan H., Huang X., and Hua J., 2024, Effects of low-temperature stress on cold resistance biochemical characteristics of Dali and Siqiu tea seedlings, Horticulturae, 10(8): 823.
https://doi.org/10.3390/horticulturae10080823

Ding Y., Wang Y., Qiu C., Qian W., Xie H., and Ding Z., 2020, Alternative splicing in tea plants was extensively triggered by drought, heat and their combined stresses, PeerJ, 8: e8258.
https://doi.org/10.7717/peerj.8258

Dong B., Wu B., Hong W., Li X., Li Z., Xue L., and Huang Y., 2017, Transcriptome analysis of the tea oil camellia (*Camellia oleifera*) reveals candidate drought stress genes, PLoS One, 12(7): e0181835.
https://doi.org/10.1371/journal.pone.0181835

Han Z., Zhang C., Zhang H., Duan Y., Zou Z., Zhou L., Zhu X., and Fang W., 2022, CsMYB transcription factors participate in jasmonic acid signal transduction in response to cold stress in tea plant (*Camellia sinensis*), Plants, 11(21): 2869.
https://doi.org/10.3390/plants11212869

Huang D.D., 2024, CRISPR/Cas9 genome editing in legumes: Opportunities for functional genomics and breeding, Legume Genomics and Genetics, 15(4): 199-209.
https://doi.org/10.5376/lgg.2024.15.0020

Huang W.Z., and Hong Z.M., 2024, Marker-assisted selection in cassava: from theory to practice, Plant Gene and Trait, 15(1): 33-43.
https://doi.org/10.5376/pgt.2024.15.0005

Kapazoglou A., Gerakari M., Lazaridi E., Kleftogianni K., Sarri E., Tani E., and Bebeli P.J., 2023, Crop wild relatives: A valuable source of tolerance to various abiotic stresses, Plants, 12(2): 328.
https://doi.org/10.3390/plants12020328

Li H., Song K., Zhang X., Wang D., Dong S., Liu Y., and Yang L., 2023, Application of multi-perspectives in tea breeding and the main directions, International Journal of Molecular Sciences, 24(16): 12643.
https://doi.org/10.3390/ijms241612643

Liu S., Jin J., Yao M., Li C., Ding Z., and Chen L., 2016, Transcriptomic analysis of tea plant responding to drought stress and recovery, PLoS One, 11(1): e0147306.
https://doi.org/10.1371/journal.pone.0147306

Liu Z., An C., Zhao Y., Xiao Y., Bao L., Gong C., and Gao Y., 2021, Genome-wide identification and characterization of the CsFHY3/FAR1 gene family and expression analysis under biotic and abiotic stresses in tea plants (*Camellia sinensis*), Plants, 10(3): 570.
https://doi.org/10.3390/plants10030570

Lu J., Du J., Tian L., Li M., Zhang X., Zhang S., Wan X., and Chen Q., 2021, Divergent response strategies of CsABF facing abiotic stress in tea plant: perspectives from drought-tolerance studies, Frontiers in Plant Science, 12: 763843.
https://doi.org/10.3389/fpls.2021.763843

Mukhopadhyay M., Mondal T., and Chand P., 2015, Biotechnological advances in tea (*Camellia sinensis* [L.] O. Kuntze): a review, Plant Cell Reports, 35: 255-287.
https://doi.org/10.1007/s00299-015-1884-8

Rahimi M., Kordrostami M., and Mortezavi M., 2018, Evaluation of tea (*Camellia sinensis* L.) biochemical traits in normal and drought stress conditions to identify drought tolerant clones, Physiology and Molecular Biology of Plants, 25: 59-69.
https://doi.org/10.1007/s12298-018-0564-x

Ramakrishnan M., Sudhama V., and Rajanna L., 2023, A review on the genome-based approaches for the development of stress and climate resilient tea crops, Plant Science Today.
https://doi.org/10.14719/pst.1758

Shen W., Li H., Teng R., Wang Y., Wang W., and Zhuang J., 2019, Genomic and transcriptomic analyses of HD-Zip family transcription factors and their responses to abiotic stress in tea plant (*Camellia sinensis*), Genomics, 111(5): 1142-1151.
https://doi.org/10.1016/j.ygeno.2018.07.009

Takahashi Y., Sakai H., Yoshitsu Y., Muto C., Anai T., Pandiyan M., Senthil N., Tomooka N., and Naito K., 2019, Domesticating *Vigna stipulacea*: a potential legume crop with broad resistance to biotic stresses, Frontiers in Plant Science, 10: 1607.
https://doi.org/10.3389/fpls.2019.01607

Wan S., Wang W., Zhou T., Zhang Y., Chen J., Xiao B., Yang Y., and Yu Y., 2018, Transcriptomic analysis reveals the molecular mechanisms of *Camellia sinensis* in response to salt stress, Plant Growth Regulation, 84: 481-492.
https://doi.org/10.1007/s10725-017-0354-4

Wang J., Dao M., Yang Z., Bai Y., Qin Y., and Wu T., 2024, CsAFS2 gene from the tea plant intercropped with Chinese chestnut plays an important role in insect resistance and cold resistance, Forests, 15(2): 380.
https://doi.org/10.3390/f15020380

Wang L., Liu D., Jiao X., Wu Q., and Wang W., 2024, The Serine Acetyltransferase (SAT) gene family in tea plant (*Camellia sinensis*): identification, classification and expression analysis under salt stress, International Journal of Molecular Sciences, 25(18): 9794.
https://doi.org/10.3390/ijms25189794

Wang X., Zeng X., Luo L., Chen X., Yan H., Xie Z., and Zhou Y., 2022, Plant growth-promoting activity of *Herbaspirillum aquaticum* ZXN111 on the Zijuan tea plant (*Camellia sinensis* var. *assamica*), Journal of Agricultural and Food Chemistry, 70(12): 3757-3764.
https://doi.org/10.1021/acs.jafc.1c08178

Wang Y., Samarina L., Mallano A.I., Tong W., and Xia E., 2023, Recent progress and perspectives on physiological and molecular mechanisms underlying cold tolerance of tea plants, Frontiers in Plant Science, 14: 1145609.
https://doi.org/10.3389/fpls.2023.1145609

Yolcu S., Alavilli H., and Lee B.H., 2020, Natural genetic resources from diverse plants to improve abiotic stress tolerance in plants, International Journal of Molecular Sciences, 21(22): 8567.
https://doi.org/10.3390/ijms21228567

Zhang H., Li Y., and Zhu J., 2018, Developing naturally stress-resistant crops for a sustainable agriculture, Nature Plants, 4: 989-996.
https://doi.org/10.1038/s41477-018-0309-4

Zhang H.B., Xia E.H., Huang H., Jiang J.J., Liu B.Y., and Gao L.Z., 2015, De novo transcriptome assembly of the wild relative of tea tree (*Camellia taliensis*) and comparative analysis with tea transcriptome identified putative genes associated with tea quality and stress response, BMC Genomics, 16: 1-14.
https://doi.org/10.1186/s12864-015-1494-4

Zhang L., Jin S., Bai P., Ge S., Yan P., Li Z., Zhang L., Han W., Zeng J., and Li X., 2023, Genome-wide analysis and expression profiling of YUCCA gene family in developmental and environmental stress conditions in tea plant (*Camellia sinensis*), Forests, 14(11): 2185.
https://doi.org/10.3390/f14112185

Zhang Y., Zhang J., Yan C., Fang M., Wang L., Huang Y., and Wang F., 2022, Metabolome and microbiome signatures in the leaves of wild tea plant resources resistant to *Pestalotiopsis theae*, Frontiers in Microbiology, 13: 907962.
https://doi.org/10.3389/fmicb.2022.907962

Zhao X., Zhang J., Tang A., Yu Y., Yan L., Chen D., and Yuan L., 2022, The stress detection and segmentation strategy in tea plant at canopy level, Frontiers in Plant Science, 13: 949054.
https://doi.org/10.3389/fpls.2022.949054

Zheng C., Zhao L., Wang Y., Shen J., Zhang Y., Jia S., Li Y., and Ding Z., 2015, Integrated RNA-Seq and sRNA-Seq analysis identifies chilling and freezing responsive key molecular players and pathways in tea plant (*Camellia sinensis*), PloS One, 10(4): e0125031.
https://doi.org/10.1371/journal.pone.0125031

Zhou C., Zhu C., Fu H., Li X., Chen L., Lin Y., Lai Z., and Guo Y., 2019, Genome-wide investigation of superoxide dismutase (SOD) gene family and their regulatory miRNAs reveal the involvement in abiotic stress and hormone response in tea plant (*Camellia sinensis*), PloS One, 14(10): e0223609.
https://doi.org/10.1371/journal.pone.0223609

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