Bioscience Evidence 2025, Vol.15, No.4, 200-208
http://bioscipublisher.com/index.php/be

Case Study **Open Access**

Case Study: Successful Genetic Improvements in Tea Cultivation in China

Xichen Wang, Chuchu Liu
Institute of Life Science, Jiyang College of Zhejiang A&F University, Zhuji, 311800, China
Corresponding email: chuchu.liu@jicat.org

Bioscience Evidence, 2025, Vol.15, No.4 doi: 10.5376/be.2025.15.0020
Received:27 Jun., 2025
Accepted: 04 Aug., 2025
Published: 19 Aug., 2025

Preferred citation for this article:
Wang X.C., and Liu C.C., 2025, Case study: successful genetic improvements in tea cultivation in China, Bioscience Evidence, 15(4): 200-208 (doi: 10.5376/be.2025.15.0020)

Abstract As the birthplace of tea trees, China boasts the richest genetic diversity of tea trees in the world. In recent years, significant progress has been made in the genetic improvement of tea plants, covering a variety of strategies ranging from traditional selection and hybrid breeding to molecular marker-assisted selection and pan-genomics. This study reviews the main achievements of genetic improvement of Chinese tea trees, including the selection and breeding of superior varieties, the exploration of genes related to key agronomic and quality traits, and the application of molecular breeding techniques. Large-scale genomic sequencing and association analysis have revealed the genetic basis of important agronomic traits and metabolites in tea plants, providing a theoretical basis and molecular tools for precision breeding. Through the analysis of the above aspects, this study hopes that with the application of cutting-edge technologies such as gene editing and pan-genome, the genetic improvement of tea trees can become more efficient and precise, providing a solid support for the sustainable development of the tea industry in China and even globally.

Keywords Tea tree; Genetic modification; Molecular breeding; Genetic diversity; Pan-genome

1 Introduction

China is the birthplace of tea trees. There are many types of tea trees, rich genetic resources and a long history of cultivation. Tea is not only an important economic crop in China, but also one of the most popular non-alcoholic beverages in the world. Long ago, tea trees were distributed throughout China, forming many local varieties and accumulating rich genetic resources, laying a solid foundation for the development of the tea industry (Liang et al., 2012; Yao et al., 2012; Wang et al., 2020; Xia et al., 2020; Chen et al., 2023; Kong et al., 2025).

However, with the development of modern agriculture and the increase in market demand, traditional tea tree varieties have encountered many problems, such as low yields, declining quality, and weakened resistance to diseases and pests. Long-term artificial selection and cultivation have narrowed the genetic basis of some superior varieties and reduced their ability to adapt to the environment, which has brought pressure to the sustainable development of the tea industry (Chen et al., 2007; Yao et al., 2012; Mukhopadhyay et al., 2015). In addition to external factors such as climate change and land shortage, tea tree production is facing higher demands. Therefore, to improve tea tree varieties and cultivate new varieties with high yield, high quality and strong stress resistance has become an inevitable choice for promoting the high-quality development of China's tea industry (Chen et al., 2007; Mukhopadhyay et al., 2015; Xia et al., 2020; Chen et al., 2023).

This study mainly summarizes successful cases of genetic improvement of Chinese tea trees, including traditional selection and breeding, hybrid breeding, molecular marker-assisted breeding and genomic breeding methods. The article also analyzed the new progress in tea tree genome analysis, gene mining of important traits, molecular breeding, etc. in recent years, and discussed the effects and future directions of these improvement measures in increasing tea yield, quality and stress resistance, hoping to provide theoretical basis and practical reference for tea tree breeding in China and the world.

2 The Genetic Basis and Breeding Goals of Tea Plants

2.1 Genetic structure and diversity of *Camellia sinensis*

The tea tree (*Camellia sinensis*) has a high degree of genetic diversity and a relatively complex population structure. Studies using genome-wide SNP and SSR molecular markers have found that the germplasm of tea trees in China can be classified into several types: wild type, cultivated type, ancient local varieties and modern local varieties. The genetic diversity of ancient local varieties and hybrid wild types is higher than that of pure wild types and modern local varieties (Niu et al., 2019; Zhao et al., 2021; Cheng et al., 2022). There are obvious genetic differences among different groups, among which the differences between pure wild type and modern local species are the most obvious (Niu et al., 2019). However, most of the genetic diversity of tea plants mainly exists within populations, and the differences between populations are relatively small (Zhao et al., 2021; Sharma et al., 2022).

Whole-genome sequencing also found that the two main cultivated varieties of tea plants - the small-leaf variety (*C. sinensis* var. *sinensis*, CSS) and the large-leaf variety (*C. sinensis* var. *assamica*, CSA) - have significant differences in genetic structure. CSS has higher genetic diversity and more rare alleles. CSA has more non-synonymous mutations and shows stronger balanced selection (Figure 1) (An et al., 2020; Wang et al., 2020; Zhang et al., 2021). During the evolution of tea plants, hybridization and gene flow have increased genetic diversity (Wang et al., 2020; Zhang et al., 2021). In addition, the genome of the tea plant has undergone two whole-genome replications, which have amplified some genes related to secondary metabolites and generated new functions (Wei et al., 2018).

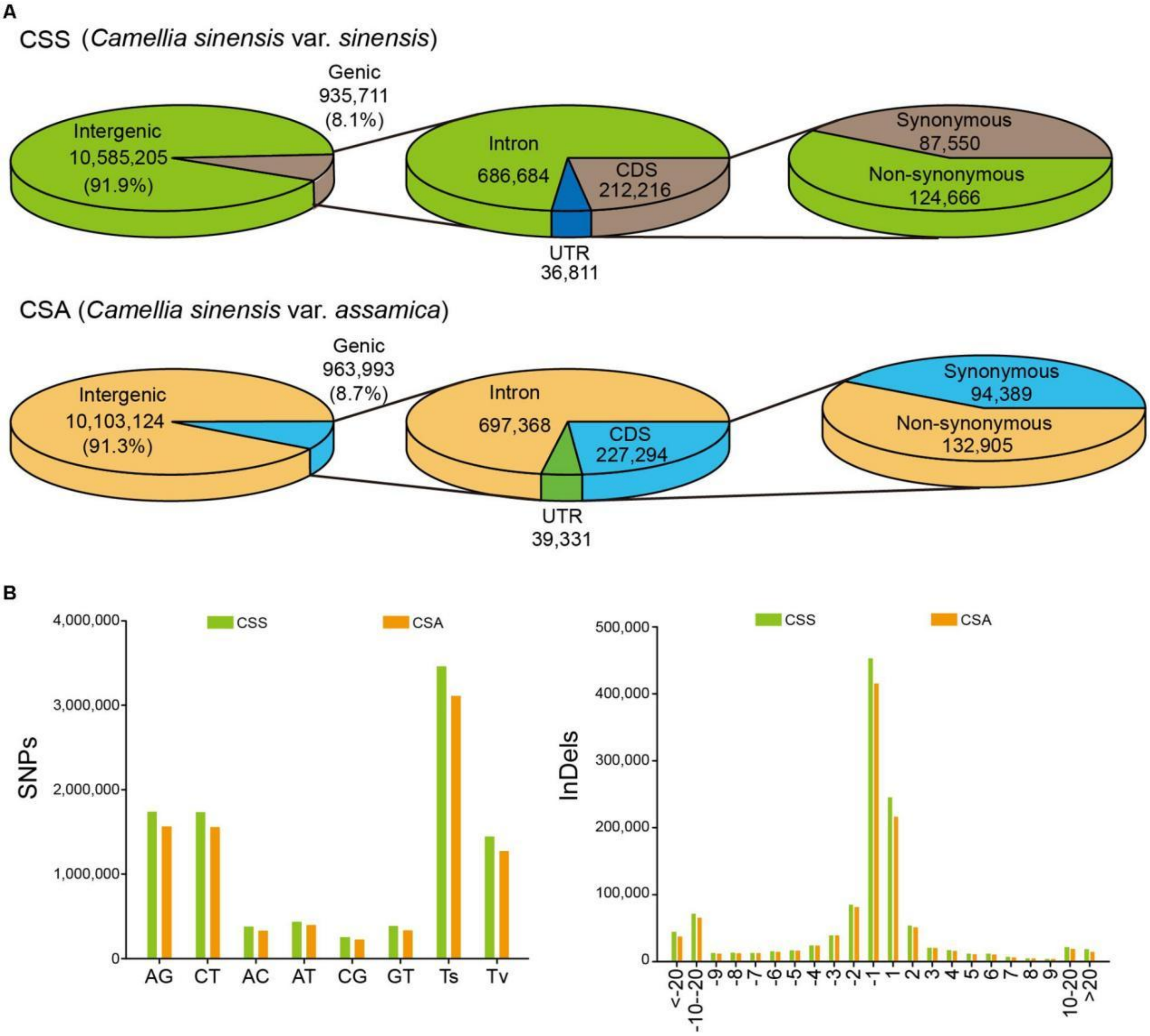

Figure 1 Classification and distribution of identified SNPs/indels among 30 samples (Adopted from An et al., 2020)

Note: (A) Annotation of SNPs identified in CSS and CSA subgroup. (B) The mutation pattern (SNP) and the length distribution (indel) of unique variations for CSS and CSA subgroup, respectively (Adopted from An et al., 2020)

2.2 Tea tree breeding objectives

Breeding of tea trees is mainly for several core goals, including increasing yield, improving quality, enhancing stress resistance (disease resistance, drought resistance, cold resistance, etc.) and adapting to different ecological environments (Wei et al., 2018; Wang et al., 2020; Zhang et al., 2021; Duan et al., 2024). In quality improvement, researchers generally focus on the content and composition of key metabolites such as tea polyphenols, caffeine, and amino acids, because these components directly affect the flavor and health value of the produced tea (Wei et al., 2018; Yu et al., 2020). At present, molecular breeding and marker-assisted selection have become important means of modern tea tree breeding. The principle is to accelerate the breeding of superior varieties by locating candidate genes related to traits such as yield, quality and stress resistance (Wei et al., 2018; Cheng et al., 2022; Duan et al., 2024). Furthermore, protecting and utilizing the germplasm resources of ancient and wild tea trees is also an important strategy for enriching the genetic basis and expanding the diversity of breeding materials (Niu et al., 2019; Zhang et al., 2021; Zhao et al., 2021; Cheng et al., 2022).

3 Main Genetic Improvement Strategies in China

3.1 Conventional breeding methods

China is the birthplace of tea trees, and the genetic diversity of tea trees is the richest in the world. Early tea tree improvement mainly relied on individual selection and hybrid breeding. Breeders will select well-performing plants from naturally mutated populations and then conduct purposeful hybridization to obtain new varieties that are highly adaptable, have high yields and good quality. Up to now, China has cultivated more than two hundred superior varieties, which have played a significant role in promoting the development of the tea industry (Chen et al., 2007). However, the cycle of conventional breeding is long and its efficiency is not high. Moreover, tea plants have the characteristics of self-incompatibility and cross-pollination, making it difficult to concentrate multiple ideal traits together in a short period of time (Kumar et al., 2016).

3.2 Molecular marker-assisted selection (MAS)

With the continuous development of modern molecular biology, in China, molecular marker-assisted selection (MAS) has become an important tool for improving tea plants. Researchers utilized molecular markers such as SNP and SSR to more quickly locate gene loci related to key traits of tea plants, enabling more targeted tea plant breeding (Chen et al., 2023; Liu et al., 2022; Li et al., 2023; Wang et al., 2024). This method can not only shorten the entire breeding cycle but also significantly enhance the overall efficiency. Liu et al. (2022) and Wang et al. (2024) conducted similar research. In their research, they conducted genetic diversity studies on tea tree germplasm resources in Sichuan, Wuyi Mountain and other places through molecular markers, providing reliable basis for the combination of superior parents and the creation of new varieties. Furthermore, combining the association analysis of pan-genome and multi-omics data can also better analyze the genetic mechanisms behind complex traits and screen out more superior genes with breeding value (Chen et al., 2023; Li et al., 2023; Liu, 2024).

3.3 Gene editing and biotechnological means

In addition to molecular marker-assisted selection, gene editing and biotechnology have also begun to be applied in the improvement of tea trees. Researchers usually obtain high-quality tea plant germplasm resources more stably and verify functional genes more conveniently through tissue culture and genetic transformation systems (Mukhopadhyay et al., 2015). CRISPR gene editing tools precisely modify some key functional genes to cultivate new varieties that are more resilient to adverse conditions and of better quality. Methods such as transgenic technology, genome selection (GS), and pan-genome construction are also accelerating the pace of tea tree improvement (Xia et al., 2020; Lubanga et al., 2022; Chen et al., 2023).

4 Case Analysis of Successful Varieties

4.1 Longjing 43: early sprouting, high-yield and high-quality type

Longjing 43 represents a significant breakthrough in the history of tea tree breeding in China. Longjing 43 has a fast germination rate, high yield and stable quality. Genomic sequencing results show that Longjing 43 performs exceptionally well in terms of disease resistance and flavor, playing a significant role in hybrid breeding and gene exchange. The large-scale promotion and cultivation of Longjing 43 has not only significantly improved the output and quality of Chinese green tea, but also provided valuable experience for the molecular marker-assisted breeding of other tea tree varieties in the future (Chen et al., 2007; Wang et al., 2020; Chen et al., 2023).

4.2 Zhongcha 108: disease-resistant and cold-resistant type

The advantages of Zhongcha 108 lie in its strong disease resistance, good cold tolerance and strong adaptability, allowing it to be grown in various environments. Research has found that during the domestication process of Chinese tea trees, the selection of disease-resistant traits is quite obvious, and Zhongcha 108 is a representative of this breeding direction. Molecular markers and genomic association analysis also provided a theoretical basis for its stress resistance traits (Chen et al., 2007; Wang et al., 2020; Li et al., 2023).

4.3 Yunnan Stone Snail Fragrance: high polyphenols, prominent flavor

Yunnan Shiluoxiang tea has a high content of polyphenols and a unique flavor. Tea tree varieties in Yunnan and Southwest China have unique advantages in genes related to flavor substances and polyphenol synthesis, providing a molecular basis for the breeding of high-quality tea (Chen et al., 2023; Wang et al., 2024; Kong et al., 2025). The promotion of Yunnan Shiluoxiang tea has also driven the development of the local characteristic tea industry.

4.4 Regional typical cases

The major tea-growing areas in China will, in light of local ecological conditions and market demands, select and breed representative and superior varieties. For instance, Sichuan tea is renowned for its high content of amino acids and polyphenols. The ancient tea tree resources in Guizhou, Yunnan and other places provide a rich gene pool for maintaining genetic diversity and improving superior traits (Lu et al., 2021; Liu et al., 2022; Zhao et al., 2022; Wang et al., 2024). Gene exchange and diversity conservation among different regions have become an important foundation for the continuous innovation of Chinese tea trees.

5 Assessment of the Impact of Genetic Improvement

5.1 Agronomy and economic benefits

Chinese researchers have spared no effort in the genetic improvement of tea trees, which has significantly enhanced the agronomic traits and economic benefits of Chinese tea trees. Some genes in tea plants are related to key traits such as leaf shape, tea flavor and stress resistance. Researchers can identify these genes through genome-wide association analysis and pan-genome studies to support the cultivation of new high-yield, high-quality and stress-tolerant tea plant varieties (Lu et al., 2021; Chen et al., 2023; Tong et al., 2024; Kong et al., 2025). Tang et al. have already found in their 2023 study that these improvements can increase the amino acid content in tea and enhance its overall quality. This improvement also enhanced the efficiency of nitrogen fertilizer utilization during the planting process, reduced planting costs, and increased the income of tea farmers by 80.2%. Modern methods such as molecular breeding techniques and genomic selection have also significantly accelerated the breeding process of superior varieties and improved the efficiency and gain of genetic improvement (Kumar et al., 2016; Hazra et al., 2018; Xia et al., 2020; Lubanga et al., 2022).

5.2 Social and ecological benefits

The genetic improvement of tea trees combined with ecological planting management has also brought about significant social and ecological benefits. Management methods such as organic farming, ecological control and diversified intercropping not only improve soil nutrients, but also increase microbial diversity and enhance the functions of the ecosystem (Zhang et al., 2021; Liu et al., 2025). In Guizhou and other places, tea gardens can conserve 610 000 cubic meters of water resources each year, store 1.876 5 million tons of carbon, maintain 37 800 tons of soil, and the ecological benefit value reaches 3.173 billion yuan. The improvement of the local ecological environment is obvious (Liu et al., 2020). Meanwhile, the development of the tea industry has also increased farmers' income, driven poverty alleviation, and promoted stability and prosperity in rural areas (Liu et al., 2020; Zheng et al., 2022). Organic and ecological planting models can also reduce the use of chemical fertilizers and pesticides, lower the risk of environmental pollution, make tea safer, and enhance social recognition (Hajiboland, 2017; Liu et al., 2025).

6 Challenges and Limitations Faced

6.1 Genetic bottlenecks and germplasm narrowness

China is the birthplace of tea trees and has a rich genetic diversity. However, in the long-term breeding process, a lot of work relies on traditional selection methods, and the number of superior varieties promoted is limited. This has led to a bottleneck in the utilization of germplasm resources. Conventional breeding mainly relies on individual selection. As a result, the genetic basis has become increasingly narrow, and the diversity and stress resistance of new varieties have been restricted (Chen et al., 2007; Mukhopadhyay et al., 2015; Wang et al., 2020). In addition, there are many difficulties in using wild relatives, such as low hybrid affinity and easy introduction of adverse genes, etc. These problems further reduce genetic diversity (Chen et al., 2007; Mukhopadhyay et al., 2015).

6.2 Obstacles to the application of biotechnology

Biotechnologies such as molecular markers, genomics and transgenes, although providing new methods for tea tree improvement, still have many limitations in application. Tea plants are perennial woody plants with a long life cycle. Therefore, whether it is conventional breeding or molecular breeding, the cycle is very long (Mukhopadhyay et al., 2015; Kumar et al., 2016). In addition, tea plants have strong self-incompatibility, making it difficult to establish inbred lines and to stably transfer superior traits (Mukhopadhyay et al., 2015; Liu et al., 2023). Meanwhile, the low efficiency of somatic cell culture and genetic transformation limits the introduction and expression of superior genes (Mondal et al., 2004; Mukhopadhyay et al., 2015). Furthermore, the incompleteness of bioinformatics and gene function annotation has also affected the accuracy of molecular breeding (Xia et al., 2020; Li et al., 2023).

6.3 Research gaps and data gaps

Although there have been advancements in tea tree genome sequencing and multi-omics studies in recent years, there are still many gaps in aspects such as functional gene mining, genetic mechanisms of complex traits, and environmental adaptability (Maritim et al., 2020; Xia et al., 2020; Li et al., 2023). Complex mechanisms such as polygenic interaction, epigenetic regulation, and interaction between genes and the environment have not been systematically analyzed (Xia et al., 2020; Li et al., 2023). In addition, phenotypic determination is not precise enough, long-term multi-environment trials are insufficient, and the accumulation of phenotypic and genotype association data of large-scale germplasm resources is inadequate. All these have limited the efficiency and scope of genetic improvement (Hazra et al., 2018; Lubanga et al., 2022; Li et al., 2023). Furthermore, systematic studies on the effects of external factors such as climate change and soil ecology on tea tree improvement are still relatively scarce at present (Omer et al., 2025).

7 Future Development Direction

7.1 Integration of artificial intelligence and genomic selection

Under the rapid development of high-throughput sequencing and big data, the combined application of artificial intelligence (AI) and genomic selection (GS) has provided a new direction for the improvement of tea trees. Genomic selection mainly improves breeding efficiency, shortens breeding time, and can more accurately select superior genotypes (Lubanga et al., 2022; Chen et al., 2023; Kong et al., 2025). AI technology mainly processes a large amount of genotype and phenotype data, optimizes trait prediction models, and helps identify candidate genes related to important traits such as yield, quality, and stress resistance (Chen et al., 2023; Kong et al., 2025). In the future, AI-driven genomic selection is expected to improve complex agronomic traits more precisely (Lubanga et al., 2022; Chen et al., 2023; Kong et al., 2025) (Figure 2).

7.2 Participatory breeding and local variety protection

The germplasm resources of tea trees in China are very rich. There are a large number of excellent genes in local varieties and ancient tea tree populations, which are important bases for improvement (Yao et al., 2012; Guo et al., 2021; Lu et al., 2021; Zhao et al., 2022). Participatory breeding emphasizes the cooperation among researchers, farmers and communities. By combining local experience with modern molecular breeding techniques, it can not only improve the adaptability and diversity of new varieties, but also protect and rationally utilize local variety resources. Strengthening the investigation of genetic diversity of local varieties, identification of molecular fingerprints and construction of core germplasm banks will lay a solid foundation for tea tree improvement and sustainable development (Yao et al., 2012; Guo et al., 2021; Zhao et al., 2022).

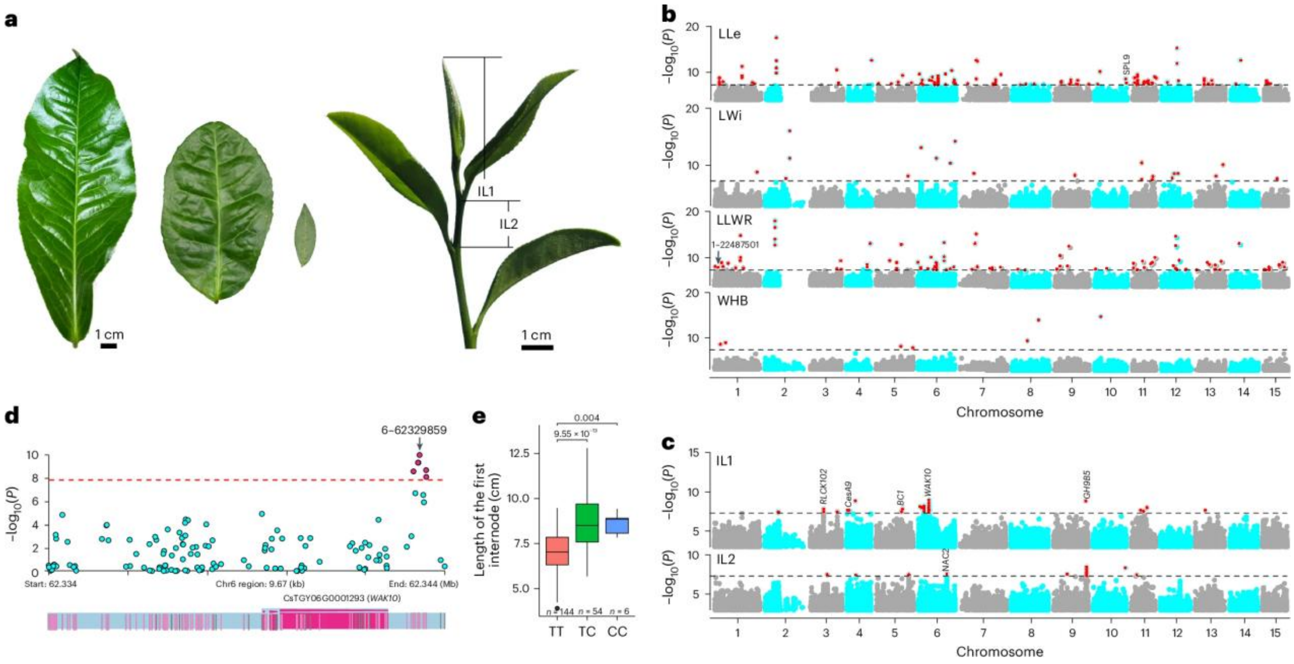

Figure 2 GWAS for agronomic traits in young bud (Adopted from Cheng et al., 2025)

Note: a, Schematic of traits in young shoots. b, Genome-wide sSNPs (the lowest P value from MLM and FarmCPU was used for the Manhattan plot) associated with LLe, LWi, LLWR and WHB). The significance threshold is 1/ total SNPs. c, Genome-wide sSNPs associated with IL1 (including first bud) and IL2. The significance threshold is 1/total SNPs. d, Manhattan plot of sSNPs associating with WAK10 gene (CsTGY06G0001293). Nine sSNPs associated with WAK10 were highlighted by red dots (some red dots were overlapped due to extremely close positions and the same P values). e, Box plots of IL1 trait of different haplotypes of the lead sSNP (chr6: 62 329 859) of WAK10 gene. n represents the sample size in each haplotype. Significance (P value) of differences between haplotypes was determined by two-sided Student's t test. The upper and lower edges of the box plots represent the first and third quartiles, the central line denotes the median and the whiskers extend to 1.5× the interquartile range. b-d, The horizontal dashed line represents the significant threshold ($P<5.08\times10^{-8}$). The statistical analysis was performed with Bonferroni correction (Adopted from Cheng et al., 2025)

7.3 Policy and financial support

The continuous advancement of genetic improvement of tea trees cannot do without the support of policies and funds. The state and local authorities should increase investment in the collection, protection, evaluation and utilization of tea tree germplasm resources, improve laws and regulations, and encourage multiple parties to participate in breeding innovation. Meanwhile, it is necessary to promote the transformation and industrialization of scientific research achievements and establish a stable financial guarantee mechanism. Only in this way can the international competitiveness and sustainable development capacity of China's tea industry be enhanced (Chen et al., 2007; Liang et al., 2012; Guo et al., 2021).

8 Concluding Remarks

China is the birthplace of tea trees, and the genetic diversity of tea trees is the richest in the world. So far, more than 200 superior varieties have been cultivated, which have greatly promoted the development of China's tea industry. In recent years, with the advancement of genomics and molecular breeding techniques, researchers have not only completed the assembly of high-quality tea tree genomes but also revealed the variety lineage and key functional genes of tea trees. New breakthroughs have also been made in the synthesis mechanisms of flavor and functional components such as tea polyphenols and catechins. New methods such as molecular marker-assisted selection and genomic selection have significantly enhanced breeding efficiency and genetic gain, accelerating the breeding process of superior varieties.

A comprehensive analysis of the economy, environment and energy value indicates that after adopting new and superior varieties and improving the efficiency of fertilizer utilization, China's tea industry can significantly reduce greenhouse gas emissions, lower its environmental impact and make production more sustainable. Promoting sustainable agricultural technologies (SATs) can not only increase tea production but also protect the ecological environment. However, farmers' acceptance of these new technologies still needs to be enhanced, so continuous efforts should be made in policy guidance and technology promotion.

Combining modern molecular breeding and genomic selection techniques with China's rich tea tree germplasm resources and traditional planting experience is the key to promoting the high-quality development of the tea industry. For instance, the intercropping system of tea trees and chestnut and other tree species not only enhances the quality of tea but also strengthens the stress resistance and ecological adaptability of tea trees. This precisely reflects the integration of traditional wisdom and modern technology. Genomic research also provides a theoretical basis for the diversification of tea flavors and the improvement of functional components, which is conducive to meeting the diverse demands of global consumers.

Acknowledgments

We sincerely appreciate the valuable opinions and suggestions provided by the three anonymous reviewers, whose meticulous review greatly helped me improve the quality of this manuscript.

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.

References

An Y., Mi X., Zhao S., Guo R., Xia X., Liu S., and Wei C., 2020, Revealing distinctions in genetic diversity and adaptive evolution between two varieties of *Camellia sinensis* by whole-genome resequencing, Frontiers in Plant Science, 11: 603819.
https://doi.org/10.3389/fpls.2020.603819

Chen L., Zhou Z., and Yang Y., 2007, Genetic improvement and breeding of tea plant (*Camellia sinensis*) in China: from individual selection to hybridization and molecular breeding, Euphytica, 154: 239-248.
https://doi.org/10.1007/s10681-006-9292-3

Chen S., Wang P., Kong W., Chai K., Zhang S., Yu J., Wang Y., Jiang M., Lei W., Chen X., Wang W., Gao Y., Qu S., Wang F., Wang Y., Zhang Q., Gu M., Fang K., , C., Sun W., Ye N., Wu H., and Zhang X., 2023, Gene mining and genomics-assisted breeding empowered by the pangenome of tea plant *Camellia sinensis*, Nature Plants, 9: 1986-1999.
https://doi.org/10.1038/s41477-023-01565-z

Cheng L., Dong X., Liu Q., Wang R., Li Y., Huang X., and Zhao Y., 2022, SLAF-Seq technology-based genome-wide association and population structure analyses of ancient *Camellia sinensis* (L.) kuntze in Sandu County, China, Forests, 13(11): 1885.
https://doi.org/10.3390/f13111885

Duan S., Yan L., Shen Z., Li X., Chen B., Li D., Qin H., Meegahakumbura M., Wambulwa M., Gao L., Chen W., Dong Y., and Sheng J., 2024, Genomic analyses of agronomic traits in tea plants and related Camellia species, Frontiers in Plant Science, 15: 1449006.
https://doi.org/10.3389/fpls.2024.1449006

Guo R., Xia X., Chen J., An Y., Mi X., Li R., Zhang C., Chen M., Wei C., and Liu S., 2021, Genetic relationship analysis and molecular fingerprint identification of the tea germplasms from Guangxi Province, China, Breeding Science, 71: 584-593.
https://doi.org/10.1270/jsbbs.21007

Hajiboland R., 2017, Environmental and nutritional requirements for tea cultivation, Folia Horticulturae, 29: 199-220.
https://doi.org/10.1515/fhort-2017-0019

Hazra A., Dasgupta N., Sengupta C., and Das S., 2018, Next generation crop improvement program: progress and prospect in tea (*Camellia sinensis* (L.) O. Kuntze), Annals of Agrarian Science, 16(2): 128-135.
https://doi.org/10.1016/J.AASCI.2018.02.002

Kong W., Kong X., Xia Z., Li X., Wang F., Shan R., Chen Z., You X., Zhao Y., Hu Y., Zheng S., Zhong S., Zhang S., Zhang Y., Fang K., Wang Y., Liu H., Zhang Y., Li X., Wu H., Chen G., Zhang X., and Chen C., 2025, Genomic analysis of 1,325 Camellia accessions sheds light on agronomic and metabolic traits for tea plant improvement, Nature Genetics, 57: 997-1007.
https://doi.org/10.1038/s41588-025-02135-z

Kumar R., Kuldip, Ahuja P., and Sharma R., eds., 2016, Status and opportunities of molecular breeding approaches for genetic improvement of tea, Sustainable Development and Biodiversity, Springer, Cham, pp.101-125.
https://doi.org/10.1007/978-3-319-27090-6_5

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

Liang C., Ming-Zhe Y., Xin-Chao W., Ya-Jun Y., and Zongmao C., 2012, Tea genetic resources in China, Journal of Tea Science, 8: 55-64.

Liu C., Yu W., Cai C., Huang S., Wu H., Wang Z., Wang P., Zheng Y., Wang P., and Ye N., 2022, Genetic diversity of tea plant (*Camellia sinensis* (L.) Kuntze) germplasm resources in wuyi mountain of China Based on single nucleotide polymorphism (SNP) markers, Horticulturae, 8(10): 932.
https://doi.org/10.3390/horticulturae8100932

Liu S., Guo R., Zhao J., Xia E., Tao Y., Zhou Q., Chen Z., Xie H., Zhu J., and Wei C., 2023, Cytological and transcriptional insights of late-acting self-incompatibility in tea plants (*Camellia sinensis*), Beverage Plant Research, 3: 19.
https://doi.org/10.48130/bpr-2023-0019

Liu S., Yao X., Zhao D., and Lu L., 2020, Evaluation of the ecological benefits of tea gardens in Meitan County, China, using the InVEST model. Environment, Development and Sustainability, 23: 7140-7155.
https://doi.org/10.1007/s10668-020-00908-6

Liu Z., Wang Q., , Y., and Zhao M., 2025, Influence on soil ecology, tea yield, and quality of tea plant organic cultivation: a mini-review, Frontiers in Agronomy, 7: 1557723.
https://doi.org/10.3389/fagro.2025.1557723

Liu, F., 2024, The influence of plant genomics on plant evolution. MedScien, 1(5): 1-5.
https://doi.org/10.61173/8mne6e71

Lu L., Chen H., Wang X., Zhao Y., Yao X., Xiong B., Deng Y., and Zhao D., 2021, Genome-level diversification of eight ancient tea populations in the Guizhou and Yunnan regions identifies candidate genes for core agronomic traits, Horticulture Research, 8: 190.
https://doi.org/10.1038/s41438-021-00617-9

Lubanga N., Massawe F., Mayes S., Gorjanc G., and Bančič J., 2022, Genomic selection strategies to increase genetic gain in tea breeding programs, The Plant Genome, 16(1): e20282.
https://doi.org/10.1002/tpg2.20282

Maritim T., Seth R., Parmar R., and Sharma R., 2020, Multiple-genotypes transcriptional analysis revealed candidates genes and nucleotide variants for improvement of quality characteristics in tea (*Camellia sinensis* (L.) O. Kuntze), Genomics, 113(1): 305-316.
https://doi.org/10.1016/j.ygeno.2020.12.020

Mondal T., Bhattacharya A., Laxmikumaran M., and Ahuja P., 2004, Recent advances of tea (*Camellia sinensis*) biotechnology, Plant Cell, Tissue and Organ Culture, 76: 195-254.
https://doi.org/10.1023/B:TICU.0000009254.87882.71

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

Niu S., Song Q., Koiwa H., Qiao D., Zhao D., Chen Z., Liu X., and Wen X., 2019, Genetic diversity, linkage disequilibrium, and population structure analysis of the tea plant (*Camellia sinensis*) from an origin center, Guizhou plateau, using genome-wide SNPs developed by genotyping-by-sequencing, BMC Plant Biology, 19: 328.
https://doi.org/10.1186/s12870-019-1917-5

Omer A., Zhang C., Liu J., and Shan Z., 2025, Comprehensive review of mapping climate change impacts on tea cultivation: bibliometric and content analysis of trends, influences, adaptation strategies, and future directions, Frontiers in Plant Science, 15: 1542793.
https://doi.org/10.3389/fpls.2024.1542793

Sharma S., Kumar A., Rajpal V., Singh A., Babbar S., and Raina S., 2022, Evaluation of genetic diversity and population structure in elite south Indian tea [*Camellia sinensis* (L.) Kuntze] using RAPD and ISSR markers, Genetic Resources and Crop Evolution, 70: 381-398.
https://doi.org/10.1007/s10722-022-01433-3

Tang S., Fu H., Pan W., Zhou J., Xu M., Han K., Chen K., , Q., and Wu L., 2023, Improving tea (*Camellia sinensis*) quality, economic income, and environmental benefits by optimizing agronomic nitrogen efficiency: a synergistic strategy, European Journal of Agronomy, 142: 126673.
https://doi.org/10.1016/j.eja.2022.126673

Tong W., Wang Y., Li F., Zhai F., Su J., Wu D., Yi L., Gao Q., Wu Q., and Xia E., 2024, Genomic variation of 363 diverse tea accessions unveils the genetic diversity, domestication, and structural variations associated with tea adaptation, Journal of Integrative Plant Biology, 66(10): 2175-2190.
https://doi.org/10.1111/jipb.13737

Wei C., Yang H., Wang S., Zhao J., Liu C., Gao L., Xia E., Lu Y., Tai Y., She G., Sun J., Cao H., Tong W., Gao Q., Li Y., Deng W., Jiang X., Wang W., Chen Q., Zhang S., Li H., Wu J., Wang P., Li P., Shi C., Zheng F., Jian J., Huang B., Shan D., Shi M., Fang C., Yue Y., Li F., Li D., Wei S., Han B., Jiang C., Yin Y., Xia T., Zhang Z., Bennetzen J., Zhao S., and Wan X., 2018, Draft genome sequence of *Camellia sinensis* var. sinensis provides insights into the evolution of the tea genome and tea quality, Proceedings of the National Academy of Sciences of the United States of America, 115: E4151-E4158.
https://doi.org/10.1073/pnas.1719622115

Wang X., Feng H., Chang Y., Ma C., Wang L., Hao X., Li A., Cheng H., Wang L., Cui P., Jin J., Wang X., Wei K., Ai C., Zhao S., Wu Z., Li Y., Liu B., Wang G., Chen L., Ruan J., and Yang Y., 2020, Population sequencing enhances understanding of tea plant evolution, Nature Communications, 11: 4447.
https://doi.org/10.1038/s41467-020-18228-8

Wang X., Sun M., Xiong Y., Liu X., Li C., Wang Y., and Tang X., 2024, Restriction site-associated DNA sequencing (RAD-seq) of tea plant (*Camellia sinensis*) in Sichuan province, China, provides insights into free amino acid and polyphenol contents of tea, PLOS ONE, 19(12): e0314144. https://doi.org/10.1371/journal.pone.0314144

Xia E., Tong W., Wu Q., Wei S., Zhao J., Zhang Z., Wei C., and Wan X., 2020, Tea plant genomics: achievements, challenges and perspectives, Horticulture Research, 7: 7. https://doi.org/10.1038/s41438-019-0225-4

Yao M., Ma C., Qiao T., Jin J., and Chen L., 2012, Diversity distribution and population structure of tea germplasms in China revealed by EST-SSR markers, Tree Genetics & Genomes, 8: 205-220. https://doi.org/10.1007/s11295-011-0433-z

Yu X., Xiao J., Chen S., Yu Y., Ma J., Lin Y., Li R., Lin J., Fu Z., Zhou Q., Chao Q., Chen L., Yang Z., and Liu R., 2020, Metabolite signatures of diverse *Camellia sinensis* tea populations, Nature Communications, 11: 5586. https://doi.org/10.1038/s41467-020-19441-1

Zhang G., Chu X., Zhu H., Zou D., Li L., and Du L., 2021, The response of soil nutrients and microbial community structures in long-term tea plantations and diverse agroforestry intercropping systems, Sustainability, 13(14): 7799. https://doi.org/10.3390/SU13147799

Zhang X., Chen S., Shi L., Gong D., Zhang S., Zhao Q., Zhan D., Vasseur L., Wang Y., Yu J., Liao Z., Xu X., Qi R., Wang W., Ma Y., Wang P., Ye N., Ma D., Shi Y., Wang H., Ma X., Kong X., Lin J., Wei L., Ma Y., Li R., Hu G., He H., Zhang L., Ming R., Wang G., Tang H., and You M., 2021, Haplotype-resolved genome assembly provides insights into evolutionary history of the tea plant *Camellia sinensis*, Nature Genetics, 53: 1250-1259. https://doi.org/10.1038/s41588-021-00895-y

Zhao Y., Wang R., Liu Q., Dong X., and Zhao D., 2021, Genetic diversity of ancient *Camellia sinensis* (L.) O.Kuntze in Sandu County of Guizhou Province in China, Diversity, 13(6): 276. https://doi.org/10.3390/d13060276

Zhao Z., Song Q., Bai D., Niu S., He Y., Qiao D., Chen Z., Li C., Luo J., and Li F., 2022, Population structure analysis to explore genetic diversity and geographical distribution characteristics of cultivated-type tea plant in Guizhou Plateau, BMC Plant Biology, 22: 55. https://doi.org/10.1186/s12870-022-03438-7

Zheng R., Ma Y., Liu L., Jiang B., Ke R., Guo S., He D., and Zhan J., 2022, Synergistic improvement of production, economic return and sustainability in the tea industry through ecological pest management, Horticulturae, 8(12): 1155. https://doi.org/10.3390/horticulturae8121155