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Feature Review **Open Access**

Genetic Tools for Enhancing Tea Plant Resistance to Biotic Stress

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Abstract The tea tree (*Camellia sinensis*) is a crop of significant economic and cultural value worldwide. However, its yield and quality are often affected by various biological stresses, including fungal diseases and pest attacks. Against the backdrop of intensified ecological pressure and restricted pesticide use, enhancing tea trees' resistance to pests and diseases has become a key task for achieving sustainable development of the tea industry. This study systematically explored the genetic tools used to enhance the resistance of tea plants to biological stress, integrating the latest achievements in traditional breeding, molecular biology and modern biotechnology. It reviewed the genetic and physiological basis of tea plant resistance traits, focusing on key resistance genes, their expression patterns and regulatory mechanisms. Based on the comparison of traditional breeding methods with modern molecular strategies (such as molecular marker-assisted selection MAS, RNA interference RNAi, CRISPR/Cas9 gene editing technology), the advantages of precision breeding in the directional enhanced resistance pathway were demonstrated. The functions of defense signaling networks (especially jasmonic acid JA, salicylic acid SA and ethylene ET pathways) as well as transcription factors and epigenetic regulatory factors in resistance expression were also explored. This study provides a comprehensive overview and practical guidance on the genetic techniques required to enhance the biological stress resistance of tea plants, aiming to promote the in-depth integration of tea plant resistance breeding research and industrial application.

Keywords Tea tree (*Camellia sinensis*); Biological stress; Molecular breeding; Gene editing; Regulatory mechanism

1 Introduction

Tea plants are not the kind of crops that are insensitive to pests and diseases. Fungi such as anthrax, basidiomycetes, and Polytrichospora camellia have been entrenched in major tea-growing areas for years, causing a lot of trouble for the yield and quality of tea (Pandey et al., 2021). If diseases are the invisible enemies of tea plants, then the damage caused by some pests is more obvious - armyworm, armyworm, Ornuk's armyworm, and aphid fly. Their gnawing not only damages the leaves but also triggers a series of complex defense responses in tea plants (Chen et al., 2024). Worse still, these stresses can also disrupt the metabolic rhythm within plants, such as affecting the synthesis of catechins and flavonoids, thus reducing the original quality.

Of course, to control these problems, it is not possible to rely solely on insecticides and fungicides for long-term effectiveness. Although chemical control measures take effect quickly, they also bring about many concerns regarding ecology and health. At present, policies are becoming stricter and consumers are becoming more picky. It is obvious that relying solely on pesticides to maintain tea production capacity will not go far. So, more attention began to turn to the tea trees' own resistance. Reducing external input by enhancing its "immunity" against pests and diseases sounds not only environmentally friendly but also more in line with the current demands of green agriculture (Hazarika et al., 2024). To truly enable tea trees to withstand these environmental challenges, the key may not lie in "fighting monsters", but in "practicing skills". By exploring and regulating genes and metabolic pathways related to resistance to make tea plants stronger themselves is the focus of many current studies (Chen et al., 2021; Wang et al., 2024). Although this approach is not as immediate as spraying pesticides, once a genetic resistance foundation is established, the "lasting combat effectiveness" of tea trees will be greatly enhanced, and cultivation can become more stable and long-term.

This study reviews the main biological stresses affecting tea plants and emphasizes the urgent need to enhance the resistance of tea plants through genetic means. This study aims to summarize the current understanding of the genetic mechanism of biological stress resistance in tea plants, evaluate the effectiveness of emerging genetic tools, and point out the research gaps and future directions for the sustainable improvement of tea plants. By integrating insights from molecular biology, genomics, and plant-microbial interactions, this study aims to inform breeding strategies and support the cultivation of adaptable tea tree varieties to achieve a sustainable global tea industry.

2 Genetic Basis of Tea Plant Resistance to Biotic Stress

2.1 Types and functional characteristics of resistance-related genes in tea plants

The disease and pest resistance of tea plants is not achieved through a single mechanism, but rather through the "division of labor and cooperation" of multiple different types of genes. Some genes are responsible for regulating transcription factors such as WRKY, FHY3/FAR1, and JAZ; Some genes themselves are involved in metabolic processes, such as laccase and hydroxycinnamoyltransferase; There are also some genes, such as members of the PYL family, that are important components of plant hormone signaling.

Under different circumstances, these genes do not always function simultaneously. Like CsWRKY48, *CsFHY3/FAR1*, *CsCBF*, etc., they are involved in regulating a series of defense-related genes and also interact with other transcription factors (such as MYC, MYB), corresponding to different stress responses (Liu et al., 2021; Wang et al., 2024). Enzyme genes such as *CsHCTs* and *CsLACs*, which are related to the synthesis of lignin and flavonoids, are usually more active when plants "build walls for self-protection" (Chen et al., 2021).

However, *JAZ* genes are also quite unique. As members of the TIFY family, they are upregulated in the face of insect or fungal attacks, indicating that they are closely related to the defense mechanism of JA signaling. Furthermore, genes that process reactive oxygen species, such as SOD, also play a role in reducing cellular damage during the stress response, and the related miRNA regulatory mechanisms have begun to be revealed. The *PYL* gene in the ABA signaling pathway seems more like a "coordinator", determining whether plants should defend or save water based on environmental conditions.

2.2 Genetic inheritance and sources of variation in resistance traits

The trait of resistance is not always simply "present" or "absent"; its manifestations among groups are highly diverse. One of the reasons for this diversity is the accumulation of genetic variations during natural selection, and another reason may not be so intuitive - the replication and expansion of gene families.

Some genes, such as *BZR1*, *HD-Zip*, and *SAT*, not only exist in cultivated varieties but also have different versions in many wild tea varieties. The differences among these "family members" precisely shape the complexity of traits (An et al., 2023; Li et al., 2023). Genome-wide association studies (GWAS) have helped researchers identify some significant SNP loci related to resistance. For instance, CsNCED1 is a representative one (Deng et al., 2025).

Gene expansion methods such as fragment replication and tandem duplication are actually silently promoting the diversified development of resistance genes, providing many "alternative options" waiting to "take up their positions" in stressful environments (Figure 1) (Liu et al., 2021).

2.3 Regulatory mechanisms of gene expression in response to biotic stress

When it comes to the regulation of gene expression, the response mechanism of tea plants is not static. It is actually a multi-level and multi-channel dynamic process. For example, when attacked by pathogens, some transcription factors will be rapidly activated, such as WRKY, CBF, HD-Zip, etc., which respond very quickly in initiating the expression of defense genes (Hu et al., 2020; Wang et al., 2024; Luo et al., 2025).

However, such reactions are not "fully activated upon activation", as the hormones within the plant are also constantly competing with each other. The mutual restraint or promotion among salicylic acid, jasmonic acid, abscisic acid and gibberellin will adjust the reaction direction according to the type of stress. For example, if ABA is elevated, it may inhibit SA signaling, thereby making plants more likely to "fail" when facing pathogens (Deng et al., 2025).

As for the fineness of regulation, the participation of miRNA may be the most notable aspect. Molecules like csn-miR398a-3p-1 and cs-miR397a can inhibit or activate some key genes at critical moments, such as regulating the expression of SOD or laccase, helping tea plants respond more flexibly to environmental challenges (Zhu et al., 2023).

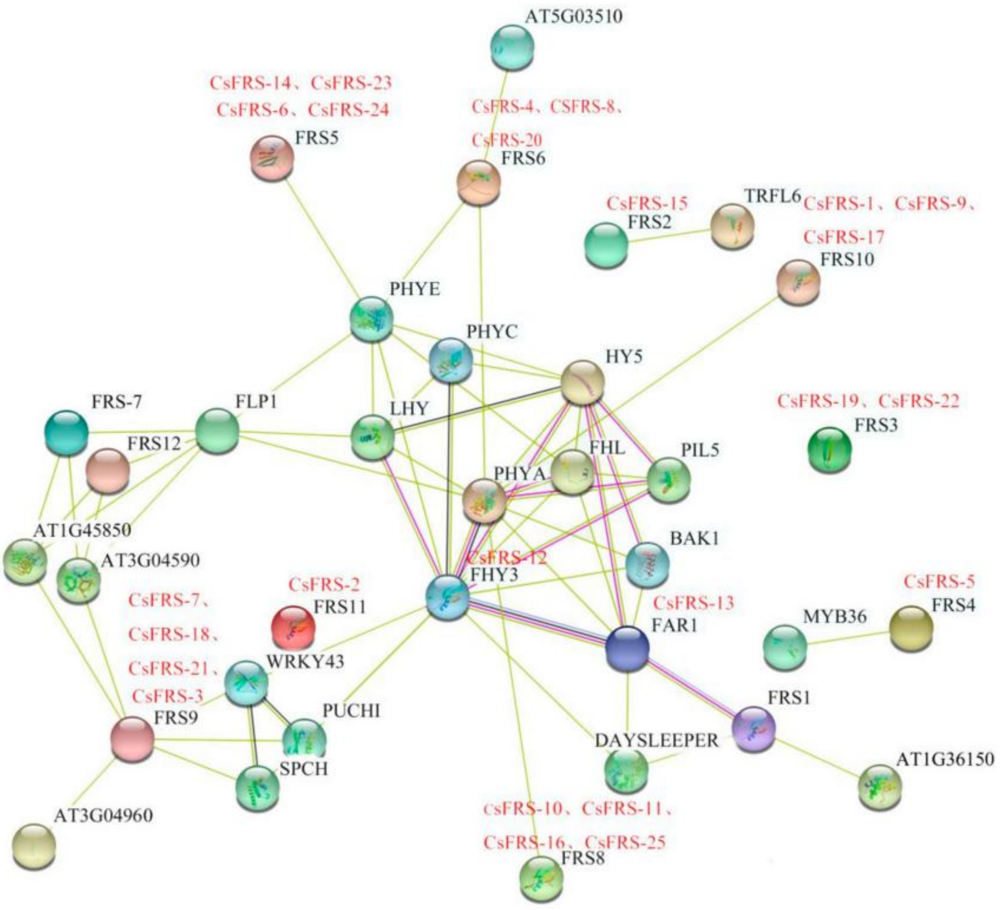

Figure 1 Putative interaction network of CsFHY3/FAR1s in tea plants. The homologous proteins in tea plants and Arabidopsis are shown in red and black, respectively (Adopted from Liu et al., 2021)

3 Comparison of Conventional and Modern Molecular Breeding Approaches

3.1 Limitations of hybrid breeding and resistance resource introduction

In traditional tea tree breeding, hybridization has long been a method adopted, theoretically improving traits by combining the advantages of different parents. But it's easier said than done. Due to some inherent characteristics of tea plants, such as their long life cycle and perennial nature, each round of breeding takes an extremely long time. If the affinity between distant parents is poor, it will be even more troublesome to achieve successful hybridization. The seeds cannot produce, the fruit drop rate is high, and the germination rate is also poor (Mo et al., 2025). In addition, the introduction of wild germplasm was originally intended to enhance resistance, but it may accidentally bring in some "side effects" - such as reduced quality and reduced yield. What is more troublesome is that in the actual breeding process, the two goals of high resistance and high quality are often difficult to achieve simultaneously. Most newly cultivated materials may not gain an advantage in either aspect, being neither disease-resistant nor pleasing to the market.

3.2 Application of marker-assisted selection (MAS) in screening for resistance

In contrast, molecular marker-assisted selection (MAS) appears to be more efficient and reliable. It does not rely on naked-eye observation. Instead, by detecting DNA fragments associated with target resistance genes, such as markers like SSR and SNP, it can screen out resistant individuals at the seedling stage or even the seed stage (Karunarathna et al., 2020; Li et al., 2023). This bypasses the interference caused by environmental fluctuations, saves time, and makes breeding decisions more grounded (Salgotra and Stewart, 2020). Moreover, a series of practical markers have been developed for some key resistant traits (such as vesicular disease) (Wang et al., 2020). If the transcriptome, metabolome and other data can be combined for analysis, the ability of MAS to analyze complex traits will be further enhanced.

3.3 Breeding strategies for pyramiding multiple resistance genes

Although a single resistance gene can bring short-term effects, in today's era of rapid evolution of pathogenic bacteria, this strategy is often not sustainable enough. Therefore, breeders are increasingly inclined to "package" multiple resistance genes into the same strain, which is commonly referred to as "gene aggregation" or "compound resistance". Traditional breeding has struggled in this regard, but with molecular marker-assisted technology, it becomes more feasible to superimpose QTL or multiple disease-resistant genes. Some studies have also pointed out that this compound strategy can significantly reduce the probability of pathogen escape or resistance failure (De Almeida et al., 2021). In terms of operational methods, marker-assisted backcrossing, cyclic selection, or even gene box design and gene editing techniques can be used for precise operations. However, to be fair, even if the technology is mature and truly effective aggregation is achieved, the right gene combinations still need to be selected to ensure that they can also work synergistically in similar genetic backgrounds.

4 Molecular Tools for Improving Tea Plant Resistance

4.1 Mining resistance genes through transcriptomics and genomics

Often, the resistance of tea plants is not led by a single gene, but by a complete network working together. Research at the transcriptome and genomic levels has long been involved in this matter. Proteins such as the flavonoid pathway and NB-ARC domain are highly active in resisting diseases and low temperatures, and the relevant data are also increasing (Li et al., 2025). In some special scenarios, BAHD acyltransferase and members of the ABA receptor family (PYL) have also been observed to be significantly expressed after pest and disease stress (Qiao et al., 2024), and these genes have now become potential breeding targets. Interestingly, after aggregating and analyzing different transcriptome data, tens of thousands of differentially expressed genes (DEGs) could be screened out, involving the MAPK signaling pathway, various plant hormone pathways (SA, JA, ET), and secondary metabolic pathways (Hazra et al., 2023; Xu et al., 2025). These results not only indicate that the regulation is very complex, but also show that there are actually many clues to follow in resistance breeding.

4.2 Application of RNA interference (RNAi) in pest control

When it comes to precise pest control, RNA interference technology does offer a relatively "clean" approach. Unlike pesticides that strike indiscriminately, RNAi can target specific genes of pests and has an extremely low off-target rate. At present, there are more than one method. Besides transgenic methods to enable tea plants to express double-stranded RNA (dsRNA) by themselves, there are also non-translational methods such as trunk injection and foliar spraying (Cagliari et al., 2019). However, in the final analysis, these Dsrnas can only function if they can exist stably and be effectively absorbed. In this regard, the addition of nanoparticle technology has been of great help and improved the delivery efficiency (Yan et al., 2020; Ahmad et al., 2025). However, it should be said that although RNAi is good, there are still some obstacles before it can be truly promoted. Issues such as its stability in the environment, how to use it on a large scale, and regulatory reviews all remain to be addressed (Chen and De Schutter, 2024).

4.3 Potential of gene editing tools in functional validation and trait improvement

The CRISPR/Cas9 tool has now almost become a "standard configuration" in the field of breeding, but in perennial crops like tea trees, its direct application is still in the trial stage. However, many researchers have already regarded it as a good helper for verifying the functions of candidate resistance genes. For instance, members of the NB-ARC, PYL, and BAHD families can be analyzed for their specific roles in the resistance response through CRISPR knockout or insertion (An et al., 2023). Another advantage of the editing tool is that it can help superimpose multiple resistant traits without having to worry about introducing redundant traits as in traditional hybridization. When gene discovery technology and editing technology truly "join hands", in the future, to cultivate highly resistant varieties in tea trees, it may no longer require so many generations of breeding.

5 Resistance-Related Regulatory Networks and Functional Validation

5.1 Role of defense signaling pathways in tea plants

In the defense system of tea plants, the three plant hormones SA, JA and ET almost play an unavoidable role. Their task assignments are also different - SA is responsible for dealing with live trophic pathogens, while JA and ET are more suitable for dealing with necrotrophic pathogens and some pests (Mishra et al., 2024; Zhang et al., 2025). However, things are not always clear-cut. There are often mutual checks and balances among the three. For instance, the antagonistic effect between SA and JA/ET sometimes makes the defense response more complicated. In some studies, in scenarios such as fungal infections, transcriptome data indicated that the ethylene signaling pathway was particularly active (Hazra et al., 2023), but this does not imply that other pathways were inactive. In fact, NO (nitric oxide) is also involved, regulating the expression rhythms of SA and JA/ET. The defense mechanism is not a straight line; it is more like a net that adjusts to the environment, with resistance genes and metabolic pathways all working closely and flexibly within it.

5.2 Functional studies of key transcription factors

There are also many interesting discoveries in the section of transcription factors. Members of the MYB, NAC, WRKY and JAZ families basically all have some role in the immune response. For instance, the relationship between CsMYB72 and CsPR10-9 is not merely a simple promotion or inhibition. CsMYB72 can suppress the expression of CsPR10-9. After silencing it, not only does the activity of antioxidant enzymes increase, but the content of SA also rises, and the resistance is enhanced accordingly (Tao et al., 2025). On the JAZ family side, CsJAZ11 and CsMYC2.2 can form an interactive combination to jointly promote the expression of CsRPM1 of the NS-LRR class. This regulatory mechanism also has a good effect in combating anthrax (Fan et al., 2025). In addition, there is CsNAC29 in the NAC class, which activates CsAFS2 and promotes the synthesis of volatile substances in tea plants, thereby playing a role in combating gray mold (Xu et al., 2025). These examples show that transcription factors are not only transfer stations for signals but also play a key role in coordinating hormone and gene expression.

5.3 Emerging perspectives on epigenetic regulation of resistance

Let's turn to the topic of epigenetic regulation. In the past, people might have paid more attention to genes themselves, but now more and more evidence shows that mechanisms like histone modification also play a considerable role in immune responses. CsPRMT5 in tea plants is a protein arginine methyltransferase that can dimethylate H4R3 under normal conditions, thereby suppressing the expression of some defense genes, such as *CsMAPK3*. However, once tea plants encounter pathogens, the expression of *CsPRMT5* will decline, and the level of *H4R3sme2* will decrease accordingly. That "brake" is released, and the defense system activates (Peng et al., 2025). On the other hand, mirnas are also at play. Whether for sooty ash disease or anthracnose, they all exert fine-tuning functions at the post-transcriptional level by regulating defense genes and transcription factors (Jeyaraj et al., 2025; Wang et al., 2025). Ultimately, these regulatory measures provide tea trees with a faster and more flexible response mechanism. There is no need to rewrite genes; it is sufficient to switch the expression mode.

6 Case Studies: Advances in Tea Plant Resistance Research

6.1 Development of molecular markers for tea geometrid (*Ectropis obliqua*) resistance

The tea foot moth (*Ectropis obliqua*) is often seen in tea gardens. Once an outbreak occurs, both the yield and quality of tea may be affected. To better carry out insect-resistant breeding, some research teams have adopted the enriched motif library technology and developed 11 new microsatellite markers. The polymorphisms of these markers are good. Some loci can detect 2 to 8 alleles, and the heterozygosity is also relatively high. They can be used to construct genetic maps or analyze population structure. Their application value is not only reflected in resistance screening, but also can be used to trace the genetic basis of pest resistance variations. On the other hand, transcriptome studies on the feeding of the armymoth have also revealed many clues - tea plants activate a large number of response genes and mirnas. Factors related to pathways such as jasmonic acid, ethylene signaling, and volatile synthesis have also been mobilized (Gu et al., 2024; Yu et al., 2025). These candidate components may become the breakthrough point for future RNAi prevention and control strategies.

6.2 Functional characterization and utilization of the anthracnose resistance gene *CsWRKY40*

When it comes to major diseases of tea trees, anthracnose is definitely an issue that cannot be avoided. In recent years, the transcription factor CsWRKY40 has gradually come into the research field. It has been found to directly promote the expression of F-box-LRR genes *CsFBXL13*. This regulatory relationship has been verified by subcellular localization, yeast single-hybrid and luciferase experiments, effectively enhancing the resistance of tea plants to low temperature and pathogen stress (Dou et al., 2025). Of course, CsWRKY40 is not the only candidate gene. Current transcriptome and co-expression network analyses have also identified many potential targets, including NBS-LRR disease-resistant proteins, *PR* genes, etc. These genes are generally upregulated in resistant varieties (Figure 2) (Tao et al., 2025; Xu et al., 2025). These materials have been gradually used for molecular marker selection and functional verification, and may also become an important entry point for improving anthrax resistance in the future.

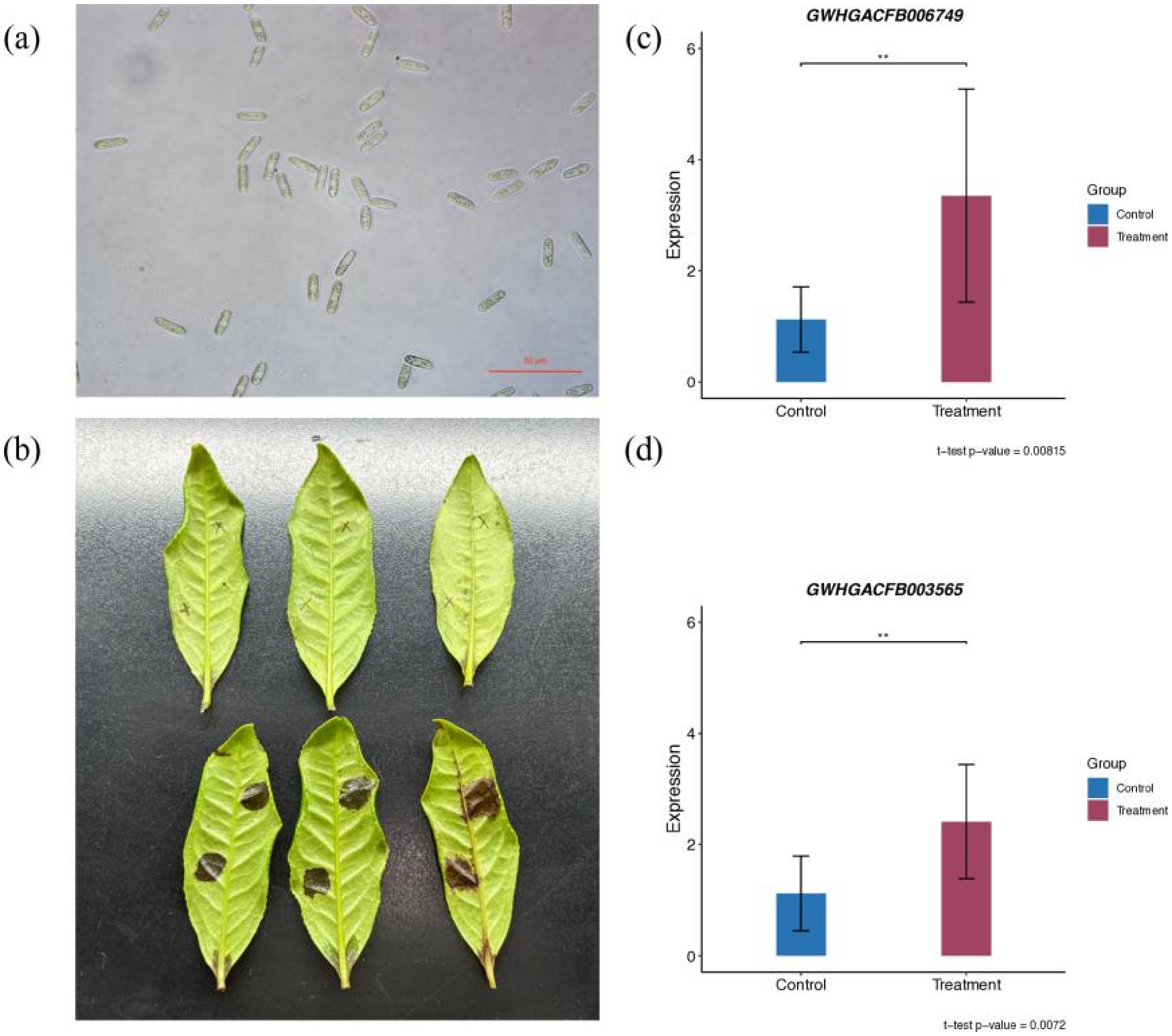

Figure 2 (a) The spore morphology of the pathogenic microorganism for inoculation; (b) lesion morphology in both control and treated groups at 7 days post-inoculation. (c) Relative expression levels of candidate gene *GWHGACFB006749*. (d) Relative expression levels of candidate gene *GWHGACFB00356* (**$p < 0.01$) (Adopted from Xu et al., 2025)

6.3 Exploratory application of CRISPR/Cas9 in editing defense-related genes in tea plants

Although tea plants are not as mature and easy to handle as rice, CRISPR/Cas9 has also begun to be introduced into this system. Although not many reports have been made, some experiments have been attempting to edit some key defense-related genes, such as NLR immune receptors, hormone pathway-related transcription factors, etc. Compared with traditional transgenic methods, CRISPR has the advantage of being precise. It can basically knock out any site or insert any sequence, which opens up the possibility of superimposed multiple resistance traits in the later stage. Next, many studies may focus on the targeted editing of salicylic acid pathways, immune recognition and transcriptional regulatory factors, with the aim of constructing new tea tree varieties that can widely resist various diseases and pests (Li et al., 2025).

7 Integration of Genetic Tools and Future Perspectives

7.1 Construction of an integrated breeding model using multiple technologies

In the past, choosing seeds based on experience is no longer the mainstream. Tea tree breeding is moving from a single method to a combination of multiple approaches. Omics technologies such as genomics, transcriptomics, and metabolomics, combined with molecular markers and high-throughput typing, are not merely a pile of tools but are beginning to truly serve the screening of resistance traits and the analysis of genetic mechanisms. Especially when it comes to marker-assisted selection and genomic prediction, these combinations are even more useful (Wang et al., 2025). For example, the TEA5K mSNP chip has begun to be used in tea trees. It is needed for GWAS, QTL localization, and mapping (Yamashita et al., 2020). Of course, this is far from the end. New directions such as single-cell omics and pan-genome research, and even microbial interactions, may also open up another path for future resistance breeding.

7.2 Establishment of tea germplasm databases and resistance breeding platforms

Before good seeds can be grown, there must first be good resources to choose from. The collection of global tea tree germplasm resources has been going on for some time, and the number of resources is not small - more than 15,000 samples. The question is not whether it exists or not, but how to use it. Databases like TPIA are quite helpful. They not only integrate various omics and phenotypic data together, but also come with many practical analysis tools, facilitating researchers to search and compare (Xia et al., 2019). Having a database is not enough; someone needs to build a core germplasm bank and a fingerprint atlas. For example, the marker system based on SSR or SNP can not only explore genetic diversity, but also facilitate the subsequent protection and development of rare resources (Liu et al., 2025). Once these platforms are established, they are not only about data accumulation but also about connecting resources with target traits to enhance the efficiency of selection and breeding.

7.3 Strategic responses to emerging biotic stresses under climate change

The environment waits for no one. Climate warming, less rainfall and more unpredictable pests and diseases are bringing more and more challenges to tea tree production. Traditional experience is clearly difficult to deal with such new variables. At this point, if one relies solely on the efforts of a single discipline, it is likely that they won't go far. Nowadays, many studies have begun to attempt to integrate molecular mechanisms, physiological responses, and even ecological perspectives. For example, omics techniques are used to screen key genes, and climate simulation tools are combined to predict future suitable regions (Omer et al., 2025). In addition, agronomy should not be relaxed either. For instance, agroforestry models, conservation tillage, and rational crop rotation can all play a role in responding to climate stress (Baruah and Handique, 2021). The path from the laboratory to the tea garden, in the final analysis, still depends on people from different fields working together to connect the "points" into "lines", and then turn them into real resistant varieties that can be promoted.

8 Conclusion

In recent years, research on tea tree resistance breeding has indeed made some crucial progress, and many of these advancements have been inseparable from the support of genetic tools. From molecular markers to multi-omics and then to functional genomics, the means are becoming increasingly diverse and the perspectives are getting more and more detailed. Techniques such as genome-wide association analysis (GWAS) and SNP typing have helped us identify many core genes related to resistance, especially in the salicylic acid (SA) signaling pathway, where progress has been relatively rapid. Meanwhile, MAS (Molecular marker-assisted Selection) has also begun to be effectively applied in the breeding process of pest and disease-resistant varieties, no longer remaining just on paper. The research results of some transcription factors, such as CsAFS1, CsAFS2 and WRKY, have gradually become clear. Their functions in responding to stress are becoming increasingly clear, providing practical references for future breeding design. More importantly, the integration among different omics (such as genomics, transcriptomics, and metabolomics) has enabled us to have a more systematic understanding of the way tea trees resist adversity.

But things don't always go so smoothly. After all, tea trees are perennial crops. The breeding cycle can be delayed for several years. Verifying a trait relies on experience and waiting slowly. This is very difficult to advance in the pace of industrialization. Let's talk about resources - the mutant library is incomplete and the transformation system is unstable. Compared with those "laboratory darlings" model crops, the foundation of tea trees in functional genomics is still far behind. There is another practical issue: the genes you can find are one thing, but whether they can be put to use is another. The network mechanism behind resistance regulation is complex and the epigenetic factors are also unclear. Relying solely on omics data cannot be quickly transformed into feasible breeding solutions. Even if the technology is up to par, genetically modified organisms and gene editing still have to face the two thresholds of policy regulation and public acceptance. It is almost impossible for them to be implemented quickly.

By the way, these problems are not unsolvable either. To shorten the distance between the laboratory and the field, it is not about making breakthroughs at a single point, but about integrating multiple technical routes. For instance, building an integrated breeding platform - combining omics analysis, genotyping and phenotypic screening - can significantly enhance the efficiency of identifying and deploying resistance genes. Furthermore, the germplasm resource bank also needs to make up for its shortcomings, especially in some local tea trees and wild species, which may contain key resistance alleles. The transformation technology can no longer be delayed. We must have the courage to invest and promote the practical application of new tools such as CRISPR/Cas9 in tea plants. Furthermore, breeding experts, molecular researchers and the industrial end must sit at the same table to discuss and form a synergy, so as to truly transform the achievements at the molecular level into practical resistant varieties. As for the resistance from regulation and the public, it is likely that it still needs to be alleviated through scientific communication and transparent mechanisms. If necessary, a non-GMO approach can also be chosen to take a detour. To truly unlock the potential of these genetic tools, it is not only about technological progress but also about breakthroughs in mechanisms and continuous cooperation. Otherwise, even the most advanced means may get "stuck" at the last mile of application.

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Conflict of Interest Disclosure

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

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