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The Genetic Basis of Aesthetic and Adaptive Traits in Garden Trees Revealed by GWAS

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Abstract Genome-wide association studies (GWAS), as a powerful genetic tool, can reveal the correlation between genotype and phenotype and have been widely applied in the field of plant genetics, especially in the trait studies of crops and trees. To explore the application of GWAS in the genetic basis research of aesthetic and adaptive traits of ornamental trees, this study comprehensively analyzed the aesthetic traits (such as tree shape, flower color, leaf type, etc.) and adaptive traits (such as drought tolerance, cold resistance, and disease and pest resistance). It was found that GWAS helps identify key genetic factors controlling these traits, providing valuable genetic information to facilitate the improvement and breeding of ornamental tree varieties. However, challenges such as limited sample size, environmental interaction effects, and the genetic control of complex traits remain in practical applications. This study underscores the importance of understanding the genetic diversity and mechanisms of ornamental trees, which is crucial for their sustainable management and utilization, enhancing the aesthetic and practical value of urban greening, and promoting eco-friendly urban development. With continuous progress in genetic research and biotechnology, GWAS is expected to offer more scientific and systematic guidance for the selection, improvement, and conservation of ornamental trees.

Keywords Genome-wide association studies (GWAS); Ornamental trees; Aesthetic traits; Adaptive traits; Genetic basis research

1 Introduction

Genome-wide association studies (GWAS) is a method used to identify associations between genetic variants and specific traits or diseases. It compares genome sequence differences across individuals with the aim of finding genetic variations associated with particular phenotypes or diseases (Uffelmann et al., 2021). The importance of GWAS lies in its ability to provide an efficient way to unravel the genetic mechanisms underlying complex traits, which is critical for understanding biodiversity, disease susceptibility, and adaptive traits. In the field of plant science, GWAS has become a major tool for dissecting plant genetics and phenotypic diversity, particularly in studying the genetic basis of crops and ornamental trees.

Ornamental trees play multiple roles in urban environments, providing shade, improving air quality, enhancing urban landscapes, and promoting the psychological and social well-being of residents. The aesthetic traits of ornamental trees, such as tree form, leaf color, and flowering time, directly influence urban design and the quality of life for residents (Lüttge and Buckeridge, 2020). Meanwhile, adaptive traits, such as tolerance to environmental stresses (including pests, drought, and pollution), are crucial for tree growth, survival, and the sustainable maintenance of urban greening (Callow et al., 2018). Therefore, understanding and improving these traits can help select and breed ornamental tree species suitable for urban environments, achieving optimal ecological and aesthetic benefits.

The application of GWAS in ornamental tree research can reveal the complex genetic basis underlying aesthetic and adaptive traits. By analyzing the associations between genetic variations and specific traits, GWAS helps identify key genes or gene regions responsible for these traits (Chen et al., 2021). This information not only enhances our understanding of the genetic diversity of ornamental trees but also provides scientific guidance for breeding and genetic improvement, enabling targeted improvement of tree aesthetic features and environmental adaptability.

This study aims to explore the genetic basis of aesthetic and adaptive traits in ornamental trees by analyzing their genetic diversity and interactions with environmental factors. This research is expected to provide more scientific guidance for the selection and breeding of ornamental trees. Furthermore, the genetic information revealed by GWAS can support the precise breeding of ornamental trees, making the breeding process more efficient and goal-oriented, thereby accelerating the development and promotion of new varieties. Through these efforts, we can anticipate that future urban greening will not only provide a more vibrant visual experience but also offer stronger ecological services, creating a healthier and more harmonious living environment for urban residents.

2 Overview of GWAS Technology

Genome-wide association studies (GWAS) is a powerful tool in plant genetic research, capable of revealing associations between genetic variations and complex traits without prior assumptions. Through GWAS, researchers can discover new trait-related genes, providing scientific guidance for plant breeding and genetic improvement (Uffelmann et al., 2021). Despite facing challenges such as large sample requirements and complex data interpretation, when combined with other techniques and methods, GWAS is expected to continue playing an important role in the field of plant science, particularly in unraveling the genetic basis of complex traits and driving plant genetic improvement.

2.1 Basic principles and methods of GWAS

GWAS is a method used to identify associations between genotypes (genetic variations) and phenotypes (observed traits or disease states). This technique is based on a core premise: specific genetic variations (such as single nucleotide polymorphisms, SNPs) may influence an individual's expression of certain traits. GWAS scans thousands of SNPs across the entire genome to find genetic markers associated with specific traits.

The implementation of GWAS typically involves the following steps: selecting a sufficiently large sample population and sequencing their genomes to obtain genetic variation data; then, measuring the phenotypic characteristics of individuals in the same population and recording relevant trait data; controlling the quality of genotype and phenotype data, filtering high-quality SNPs and reliable phenotypic data, and handling missing data and outliers; determining the genetic structure of the sample population and the relatedness between individuals to avoid false-positive associations in subsequent analyses; finally, using statistical models to analyze the association between genotype and phenotype, identifying genetic markers significantly associated with specific traits, and performing bioinformatics analysis on the significant SNPs to interpret their potential biological functions and validate them through further experimental research. This association analysis can reveal which gene regions may have an important influence on trait expression (Visscher et al., 2017).

2.2 Applications of GWAS in plant genetic research

GWAS has become an important tool for understanding the genetic basis in the field of plant science, particularly in elucidating the genetic mechanisms of traits in crops and trees. It allows researchers to identify genetic markers associated with important agronomic traits, ecological adaptability, and disease resistance across different species.

GWAS has been widely used to identify genetic variations related to crop yield, plant growth rate, root development, flowering time control, and seed quality. Pang et al. (2021) used GWAS analysis in wheat to discover quantitative trait loci (QTLs) associated with disease resistance and cold tolerance, and identified candidate genes through high-resolution genetic analysis, which is significant for wheat genetic breeding. Another GWAS study in rice discovered genes and genetic loci strongly associated with yield under salt stress, providing valuable resources for the breeding of salt-tolerant rice varieties (Liu et al., 2019). In Arabidopsis thaliana, researchers integrated geographic and climatic data with genomic information to identify adaptive genetic variations associated with environmental variables, and through GWAS, found the *AGG3* gene related to cold tolerance (Ferrero-Serrano and Assmann, 2019). By analyzing the associations between genetic variations and plant phenotypes under different environmental conditions, scientists can identify genes involved in plant environmental adaptation and stress tolerance.

In disease management research, GWAS has been used to discover genes associated with plant disease resistance. For example, in a soybean breeding collection from South East and South Kazakhstan, GWAS was used to analyze resistance to multiple fungal diseases, identifying QTLs associated with resistance to multiple pathogens, which is valuable for improving local breeding programs (Zatybekov et al., 2018). GWAS can also be used to study gene-environment interactions, i.e., how genes influence phenotypic expression under specific environmental conditions. Beilsmith et al. (2019) discussed early efforts and future prospects of using GWAS in plant leaf microbiome research. They emphasized that GWAS is an increasingly promising approach for identifying plant genetic variations associated with microbial communities. By considering microbes as a community rather than single host-microbe interactions in GWAS analysis, complex plant-microbiome interactions can be revealed (Figure 1).

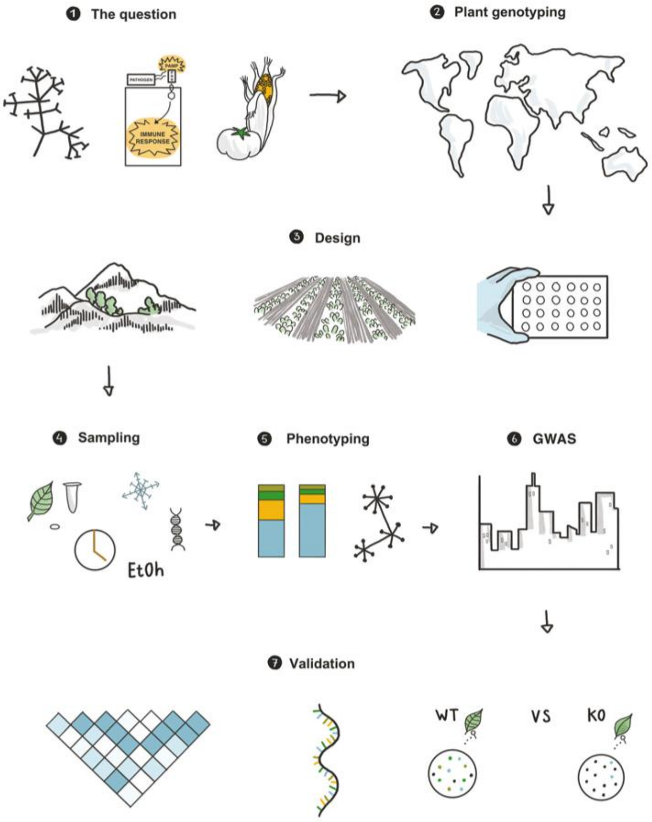

Figure 1 How to use genome-wide association studies (GWAS) with your plant leaf microbiome (Adopted from Beilsmith et al., 2019)

Image caption: 1. THE QUESTION: Understanding the leaf microbiome from an evolutionary, mechanistic plant physiological or agricultural perspective requires different downstream considerations. 2. PLANT GENOTYPING: Selecting the plant panel is an essential step in non-model systems. A plant panel with the appropriate diversity and population structure must be selected. 3. DESIGN: One can sample microbiomes from plant leaves in their natural habitat, in a common garden experiment, or in sterile environments like well plates. 4. SAMPLING: Differences in sampling methods often concern surface cleaning treatments and the time during which leaf samples are stored before DNA is isolated. 5. PHENOTYPING: Microbiota can be quantified with amplicon or metagenomic sequencing, and converted into relevant phenotypic traits for GWAS. 6. GWAS: Several statistical models exist to perform GWAS on the leaf microbiome of plants and estimate the significance of associations with microbiome traits at loci across the genome; 7. VALIDATION: Genes underlying candidate loci can be functionally validated through post-GWAS statistical approaches, such as bioinformatic methods that use transcriptome datasets and reverse genetic gene editing methods (Adopted from Beilsmith et al., 2019)

Through these applications, GWAS has not only deepened our understanding of plant genetic diversity and the genetic mechanisms of complex traits but also provided valuable molecular markers for plant breeding and genetic improvement. These achievements have practical value in improving crop yield, enhancing quality, increasing disease resistance, and promoting environmental adaptability.

2.3 Advantages and limitations of GWAS in revealing the genetic basis of plant traits

GWAS offers significant advantages in revealing the genetic basis of plant traits as it can perform genome-wide analysis without prior information about candidate genes, making it a powerful tool for discovering new trait-related genes and genetic variations (Tam et al., 2019). Additionally, GWAS can leverage the genetic diversity present in natural populations, meaning it can uncover genetic variations that have been beneficial for plant survival and reproduction through long-term evolutionary processes.

However, GWAS also has limitations. For instance, it requires large sample sizes to ensure the effectiveness and reliability of statistical analyses. GWAS may have difficulty distinguishing between genetic markers tightly linked to a trait and the actual causal variations, as many genetic variations are highly associated. Furthermore, the influence of environmental factors on plant traits may also interfere with GWAS results, especially when considering traits with strong environmental dependence. Sometimes, GWAS results may only point to a larger gene region rather than a specific gene or variation, requiring subsequent research through finer genetic mapping or functional validation experiments to identify the causal gene.

Despite these challenges and limitations, the strength of GWAS lies in its ability to systematically evaluate the relationships between genetic variations and traits, providing clues to understand the genetic mechanisms underlying complex traits. To overcome these limitations, researchers often employ multiple strategies, such as increasing sample sizes to improve statistical power, using advanced genomic technologies for fine mapping, or combining GWAS with other genetic and genomic methods (such as linkage analysis, phenomics, and gene expression analysis) to further validate and explore the association signals discovered by GWAS.

3 Data Collection and Analysis Techniques for GWAS in Ornamental Tree Genetic Research

In the genetic research of ornamental trees, data collection and analysis techniques for genome-wide association studies (GWAS) are crucial. These techniques not only help researchers gain a deeper understanding of the genetic basis of trees but also provide scientific guidance for tree selection, breeding, and management. Specifically, they include population structure analysis, association analysis, gene localization and functional prediction, and experimental validation.

3.1 Population structure analysis

Population structure analysis plays a key role in GWAS by identifying and correcting potential genetic background differences within the sample population. Ignoring population structure may lead to false-positive associations, making a proper understanding and correction of population structure an essential step in GWAS research. Common methods for population structure analysis include principal component analysis (PCA), multidimensional scaling (MDS), and structure equation modeling.

PCA is a widely used method for population structure analysis. Its basic principle is to transform the genetic relatedness between samples into a set of orthogonal principal components, which represent most of the variation in the data and can therefore be used to describe the genetic relatedness between samples (van Waaij et al., 2023). Through PCA, researchers can project samples onto the principal component space and infer population structure and kinship relationships by observing the distribution of samples in this space.

Multidimensional scaling (MDS) is another commonly used method for population structure analysis. It transforms the genetic distances between samples into a set of coordinates in a low-dimensional space, describing the relative positions of samples. Similar to PCA, MDS helps researchers visualize population structure and identify potential kinship relationships by representing samples in two or three-dimensional space.

In addition to PCA and MDS, structure equation modeling is also a commonly used method for population structure analysis. It constructs a genetic similarity matrix between samples and uses maximum likelihood estimation to infer the population structure of the samples. This method can account for complex kinship relationships between samples, improving the accuracy and precision of population structure analysis.

These methods help researchers understand the genetic relatedness and population distribution of samples. By identifying and correcting genetic background differences within the sample population, they reduce the occurrence of false-positive associations, providing a reliable basis for interpreting and understanding GWAS results.

3.2 Association analysis

Association analysis is the core step of GWAS, aiming to detect statistical associations between genotypes and phenotypes. Through association analysis, researchers can determine whether a significant correlation exists between genotypes and phenotypes, thereby identifying genetic markers associated with specific traits. In association analysis, commonly used statistical models include linear mixed models (LMM) and generalized linear mixed models (GLMM), which can account for complex factors such as population structure and kinship relationships, reducing the occurrence of false-positive associations and improving the reliability and accuracy of analysis results (Alamin et al., 2022).

In the association analysis process, appropriate statistical models need to be constructed to integrate genotype and phenotype data. Then, statistical methods are used to evaluate the degree of association between genotypes and phenotypes and determine which genetic markers are significantly associated with specific traits. Finally, by performing statistical significance tests and multiple testing corrections on the association results, the most promising candidate markers can be selected. In addition to considering population structure and kinship relationships, association analysis must also account for other factors that may influence the analysis results, such as environmental factors and phenotypic measurement errors. By comprehensively considering these factors, association analysis can more accurately reveal the relationships between genotypes and phenotypes, providing important data support for genetic research on ornamental trees.

3.3 Gene localization and functional prediction

Once genetic markers significantly associated with a specific trait are discovered, the next crucial step is to localize the genes near these markers and predict their functions. This process is called gene localization and functional prediction, an important step in GWAS research (Mancuso et al., 2017).

Through GWAS analysis, significantly associated genetic markers, i.e., associated SNPs, can be identified for a specific trait. The next task is to determine the genes near these SNPs, which can be achieved by searching for genes in the genome that are adjacent to the SNP positions. Generally, genes located near the associated SNP are considered potentially related to the target trait. After identifying the genes near the associated SNP, the next step is to predict their functions. This process involves using bioinformatics tools and databases to annotate and infer the functions of candidate genes in the associated region. Common functional prediction methods include genome sequence alignment, protein structure prediction, and functional domain analysis. Through these methods, information can be inferred about the biological processes, molecular functions, and cellular functions potentially involved by the candidate genes.

Through gene localization and functional prediction, we can gain a deeper understanding of the genes associated with specific traits and their functions, providing important clues for further functional validation and applied research. This information helps guide the selection and breeding of ornamental trees, as well as the improvement and optimization of tree traits.

3.4 Experimental validation

Ideally, the results of GWAS research need to be validated through experimental methods to confirm the true relationship between the identified genes and specific traits. This validation typically involves experimental proof of gene function and can employ various experimental methods.

One common validation method is to use gene editing techniques, such as CRISPR-Cas9, to perform gene knockout or overexpression experiments on candidate genes. By conducting these experiments in model plants, direct observations can be made on the functional changes of the target genes, confirming their role in the expression of specific traits (Son and Park, 2022). Another validation method is to conduct field trials in the target species. In this case, plant materials, such as mutants or transgenic plants, can be grown to validate the relationship between the associated genes and specific traits. By observing the performance of these plants in natural environments, the associations identified in the GWAS results can be verified, and the degree of contribution of the genes to the traits can be further understood.

Through experimental validation, the reliability and effectiveness of GWAS results can be further established, providing more reliable scientific evidence for genetic research on ornamental trees.

4 Aesthetic and Adaptive Traits of Ornamental Trees

Aesthetic and adaptive traits of ornamental trees are indispensable aspects of garden design and maintenance, jointly determining the overall performance and long-term ecological value of garden plants (Xing et al., 2023). In landscape design practice, the combined effects of these traits must be fully considered to ensure that the selected plants not only enhance the aesthetic appeal but also adapt to local environments, maintaining lasting vitality and functionality. Through in-depth research on the aesthetics and adaptive traits of garden trees, it can better guide the selection and configuration of garden plants and realize the harmonious unity of aesthetic value and ecological function.

4.1 Aesthetic traits of ornamental trees and their role in landscape design

The aesthetic traits of ornamental trees refer to those characteristics that influence ornamental value and aesthetic perception, such as tree form, leaf shape, flower color, fruit appearance, and seasonal changes. These traits are crucial in landscape design because they directly affect the visual appeal and spatial experience of the landscape (Orians, 2022).

Aesthetic traits not only enhance the ornamental value of gardens but also reflect the designer's intentions and cultural connotations, such as using specific tree species and forms to create unique garden environments. Moreover, the aesthetic traits of ornamental trees can harmonize with the surrounding environment, enhancing regional characteristics, and providing seasonal landscape effects, thereby enriching people's visual and emotional experiences.

4.2 Adaptive traits of ornamental trees and their ecological and economic value

Adaptive traits refer to the ability of ornamental trees to adapt to external environmental conditions, survive, and reproduce, including drought tolerance, cold resistance, disease and pest resistance, and pollution tolerance. These traits are essential for tree growth and development in specific environments, especially in complex and harsh urban environments.

Ornamental trees with good adaptive traits can not only grow and develop better but also reduce maintenance costs and enhance the stability and resilience of urban ecosystems. From an ecological perspective, trees with strong adaptability can provide more stable ecological services to cities, such as air purification, soil and water conservation, and biodiversity protection. Economically, selecting tree species with strong adaptability can reduce the maintenance costs of gardens and increase the economic benefits of greening investments.

4.3 Relationship and interaction between aesthetic traits and adaptive traits

There is a complex interaction between the aesthetic traits and adaptive traits of ornamental trees. Ideally, ornamental trees should possess both desirable aesthetic features and adaptive traits. However, in practical applications, these two aspects of traits may sometimes conflict.

Tree species with extremely high ornamental value may have higher environmental requirements and may not grow well in harsh environments, while some highly adaptable tree species may have average aesthetic performance. Therefore, landscape designers need to balance these two considerations when selecting tree species based on specific design goals and environmental conditions. Furthermore, through scientific research and breeding efforts, it is possible to cultivate tree species that possess both aesthetic value and good adaptability, achieving an optimal combination of the two.

Landscape designers and plant scientists need to work closely together to explore the aesthetic characteristics and adaptive abilities of different tree species through scientific research. This includes a comprehensive evaluation of tree morphological features, growth habits, stress tolerance abilities, etc. Additionally, considering the diversity and variability of environmental conditions, the ability of ornamental trees to adapt to future climate change should also be taken into account when selecting and breeding trees. By comprehensively considering the aesthetic traits and adaptive traits of ornamental trees, the aesthetic appeal and practical value of urban greening can be effectively enhanced, promoting the sustainable development of urban green spaces and creating a healthier and more harmonious living environment for urban residents (Tribot et al., 2018).

5 Case Studies of GWAS in Ornamental Tree Genetic Research

5.1 Genetic regulation of flowering duration

GWAS has demonstrated great potential in plant genetic research, particularly in revealing genetic factors influencing complex traits such as flowering time. For instance, in the soybean genome, GWAS has revealed key genetic information associated with flowering duration. Kim et al. (2020) studied the genomic structure of 2 662 soybean cultivars using the 180k Axiom® SoyaSNP array (Figure 2). The research focused on identifying candidate markers associated with flowering time. In this study, they detected 93 single nucleotide polymorphism (SNP) markers significantly associated with flowering time, involving 59 important genes, including E1 and E3, which are major determinants of flowering time.

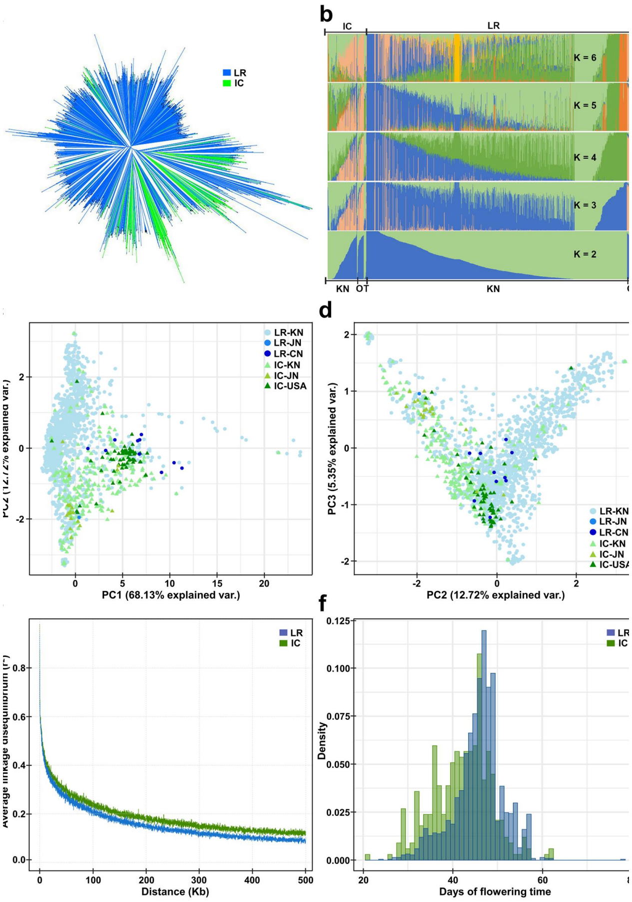

Figure 2 Genomic structure of 2 662 cultivated soybean accessions and their relationship among each other (Adopted from Kim et al., 2020)

Image caption: a. Phylogenetic tree computed using the identical-by-state coefficient. b. Population structure analysis using the number of genetic clusters (K) ranging from K = 2 to K = 6, based on the maximum likelihood-based clustering algorithm. c. Principal component analysis (PCA) plot of PC1 and PC2 derived using the Kimura two-parameter model. d. PCA plot of PC2 and PC3. e. Extent of linkage disequilibrium (LD) decay computed up to 500 kb. f. Distribution of the flowering time of soybean LRs and ICs. Abbreviations, KN, JN, CN, and OT, indicate accessions collected from Korea, Japan, China, and the other regions, respectively (Adopted from Kim et al., 2020)

5.2 Disease resistance studies in trees

In GWAS studies on disease resistance in certain tree species, genetic markers associated with the ability to resist specific pathogens have also been discovered. Younessi-Hamzekhanlu and Gailing (2022) used genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping to dissect disease resistance traits in forest trees (Figure 3). The study highlighted the potential of GWAS in identifying genetic markers associated with disease resistance, which is of great significance for forest tree breeding. By genotyping a large number of individuals, GWAS can precisely localize QTLs to individual genes based on linkage disequilibrium (LD) in unstructured populations. These genes are closely related to the disease resistance of trees, such as the NB-LRR, WRKY, bZIP, and MYB gene families and transcription factors.

Furthermore, by integrating GWAS, QTL mapping, and genomic selection (GS) methods, the study proposed a strategy to accelerate the forest tree disease resistance breeding process. The GS method utilizes information from all genome-wide markers, regardless of their importance for a specific trait, to develop predictive models for individual performance. This finding not only provides a foundation for deepening the understanding of the genetic structure of disease resistance in forest trees but also demonstrates how to leverage genomic data to accelerate breeding programs and improve disease resistance in trees.

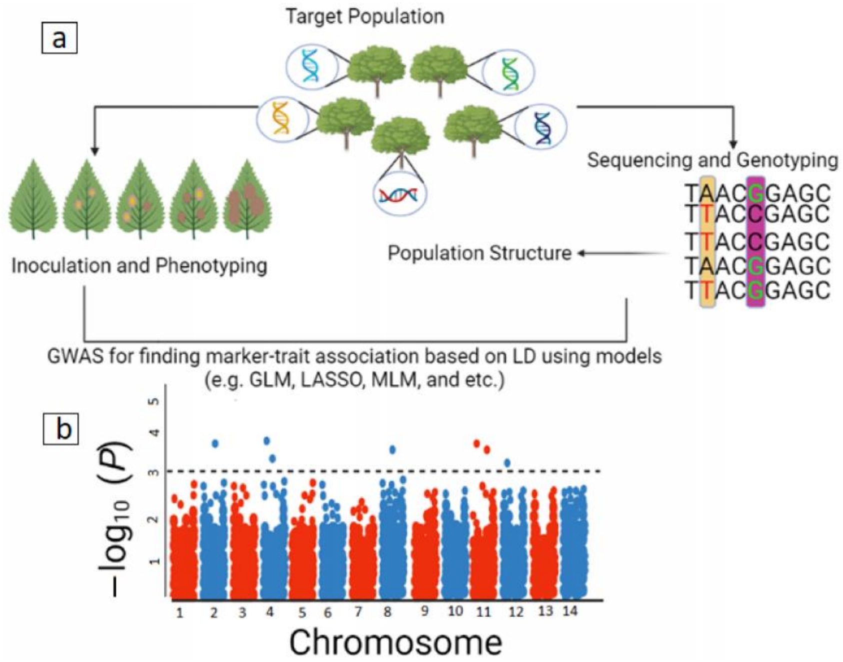

Figure 3 Schematic representation of GWAS (a) and resulting Manhattan plot in forest trees for finding marker-trait associations in disease resistance studies (b) (Adopted from Younessi-Hamzekhanlu and Gailing, 2022)

Image caption: On the x-axis of this plot, the markers are displayed on different chromosomes and on the y-axis, the –log10 p-values related to each marker are displayed. A threshold line is considered for p-values, and the SNP markers located above this line can be considered as potential QTL (Adopted from Younessi-Hamzekhanlu and Gailing, 2022)

5.3 Significance of GWAS research for ornamental tree variety improvement and breeding

The research findings from GWAS provide strong genetic information to support the improvement of ornamental tree varieties. By identifying key genetic markers and genes, breeders can more effectively select or breed ornamental tree varieties with desirable aesthetic and adaptive traits. Utilizing the flower color-related genes discovered through GWAS, new varieties with specific flower colors can be bred through marker-assisted selection (MAS). Similarly, for adaptive traits such as drought tolerance or cold hardiness, GWAS results can guide targeted gene editing or selective breeding to cultivate tree varieties better adapted to local environmental conditions.

Moreover, the results from GWAS also help understand the genetic regulatory networks underlying ornamental tree traits, providing a deeper understanding for the genetic improvement of complex traits. The accumulation and application of this genetic information will greatly promote the innovation and improvement of ornamental tree varieties, meeting the future needs of landscape design and urban greening. By directionally improving the aesthetic and adaptive traits of ornamental trees, more diverse and personalized landscape designs can be achieved while ensuring that trees maintain good growth conditions and ecological functions in the face of increasingly severe environmental challenges.

The application of GWAS technology in ornamental tree variety improvement and breeding not only enhances the aesthetic qualities and adaptability of garden plants but also promotes the development of horticultural science and plant genetics. This progress provides scientific and technological support for the sustainable management and utilization of ornamental trees, helping to balance ecological, aesthetic, and economic benefits, and better meeting the public's pursuit of a quality living environment. With the continuous development and application of GWAS technology, we can expect that garden tree species will show richer diversity and stronger environmental adaptability in the future, making a greater contribution to the creation of livable and sustainable urban green space.

6 Challenges and Future Prospects

6.1 Challenges faced by GWAS in ornamental tree genetic research

Although Genome-wide association studies (GWAS) have achieved significant results in ornamental tree genetic research, there are multiple challenges in practical applications. For example, obtaining reliable GWAS results relies on a large number of samples with diverse genetic backgrounds, but in ornamental trees, sample acquisition may be limited by factors such as seasonal changes, long growth cycles, and limited germplasm resources. As in the case of the Norway spruce breeding program, there is a large amount of phenotypic data available, but how to handle the high heterogeneity of this data remains a major challenge (Chen et al., 2021). The phenotypic expression of ornamental trees is influenced not only by genetic factors but also closely related to environmental conditions. Precisely separating and evaluating the specific effects of genetic and environmental factors on traits is a complex issue in GWAS research. Furthermore, many traits in ornamental trees, such as aesthetic traits and adaptive traits, are typically controlled by multiple genes and influenced by environmental factors, increasing the complexity of studying their genetic regulation mechanisms.

Protecting the rare or locally endemic genetic resources in ornamental trees while making reasonable use of these resources for variety improvement and breeding is also an important challenge. These challenges need to be addressed through a combination of scientific methods and interdisciplinary collaboration to fully realize the potential of GWAS in ornamental tree genetic research.

6.2 Future prospects

Facing the challenges in ornamental tree genetic research, future prospects are mainly focused on several key areas. On the one hand, improving the resolution of Genome-wide association studies (GWAS) is an important direction for development. This can be achieved by integrating more genetic and phenotypic data and adopting more advanced statistical methods to more accurately localize genes or genetic regions controlling traits. Secondly, multi-omics integrative analysis will become a research focus. By combining transcriptomics, proteomics, epigenetics, and other data, researchers can gain a deeper understanding of the genetic regulatory mechanisms underlying traits and unravel the interactions between gene expression, protein function, and epigenetic modifications.

Furthermore, the application of precision breeding technologies, particularly the use of gene editing techniques such as CRISPR/Cas9, will enable precise modification of target genes in ornamental trees, facilitating trait improvement and increasing the efficiency and accuracy of breeding. Strengthening the conservation of ornamental tree genetic resources is also a key direction for future research. Establishing genetic resource databases and realizing the digitization and informatization of resource management can not only protect these valuable genetic resources but also support genetic research and sustainable utilization of ornamental trees (Wegrzyn et al., 2019). These measures will jointly drive the progress of ornamental tree genetics, providing scientific and technological foundations for the future improvement and conservation of garden plants.

7 Conclusion

Through the application of Genome-wide association studies (GWAS), we can gain a deeper understanding of the genetic basis underlying the aesthetic and adaptive traits of ornamental trees, which is of great significance for the breeding and landscape design of garden plants. GWAS research has revealed many key genetic factors associated with the aesthetic traits and adaptive traits of ornamental trees, providing scientific guidance for the improvement and breeding of ornamental tree varieties.

In terms of aesthetic traits, GWAS has helped identify genes controlling tree characteristics such as flower color, leaf shape, and tree form, enriching our understanding of the genetic regulatory mechanisms underlying these aesthetic traits. These findings not only provide scientific guidance for the selection and application of tree species in landscape design but also contribute to breeding new varieties with specific ornamental features through marker-assisted selection. Regarding adaptive traits, such as drought tolerance, cold hardiness, and disease and pest resistance, GWAS has started to unravel the genetic basis of environmental adaptability in ornamental trees. This is of practical significance for enhancing the sustainability of urban greening and reducing maintenance costs.

Although there are challenges in applying GWAS to study ornamental trees, such as limited sample size, genetic diversity, and environmental interactions, by continuously optimizing research methods and techniques, and integrating multi-omics data analysis, we can more accurately dissect the genetic mechanisms underlying complex traits. Future research should focus more on the conservation and rational utilization of genetic resources, harnessing the potential of modern biotechnology in ornamental tree breeding, and achieving more precise and efficient variety improvement.

Overall, the development and application of GWAS technology has opened new avenues for genetic research on ornamental trees, providing scientific foundations and technological support for the breeding of garden plants and the construction of garden environments. With the continuous advancement of genetic research and biotechnology, we can look forward to better control and utilization of ornamental tree traits, promoting the sustainable development of urban gardens and creating more beautiful, healthy, and eco-friendly living environments for humans.

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.

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