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Integrative Breeding Approaches of *Nelumbo nucifera*: Balancing Ornamental Traits and Edible Values

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Abstract This study summarizes the genetic basis and molecular regulatory mechanisms of lotus in ornamental traits such as flower color, flowering period, and plant type, as well as edible qualities such as tubers and seeds. It introduces the process of flower color formation, elaborates the role of key genes such as MUDS-box in the development of floral organs, and the localization of QTL related to tuber yield and the mining of functional genes. It revealed the accumulation patterns of functional components such as flavonoids in different tissues, providing a theoretical basis for simultaneously improving ornamental and edible traits, and explored comprehensive strategies such as the protection of lotus germplasm resources, the utilization of genetic diversity, and molecular marker-assisted breeding. This study aims to provide a molecular basis and technical support for the synergistic improvement of the ornamental and edible quality of lotus and their industrial application.
Keywords *Nelumbo nucifera*; Molecular breeding; Ornamental traits; Edible quality; Multiomics integration

1 Introduction

The lotus (*Nelumbo nucifera*) is a widely used aquatic plant around the world. It can be appreciated, eaten and used in medicine, and also has high economic value. It has a variety of colors and beautiful shapes, and is a common ornamental plant in garden and water feature design. Its rhizome (lotus root) and seeds (lotus seed) are also widely used in Asian diets and traditional medicine (Sun et al., 2025; Yu et al., 2025). In recent years, with the development of genomics and molecular biology, lotus has gradually become an important model plant for research. The related achievements have promoted genetic improvement and functional gene mining, providing theoretical support for the multi-purpose development of lotus (Lin et al., 2019; Li et al., 2021; Sun et al., 2025).

Lotus often have a trade-off between their ornamental traits (such as flower color, shape, and flowering period) and edible qualities (such as the yield, texture, and nutritional components of lotus roots). Some varieties with strong ornamental value perform averagally in terms of consumption, while high-yield and high-quality edible varieties often lack ideal ornamental characteristics (Liu et al., 2016; Huang et al., 2021; Sun et al., 2025). Meanwhile, lotus has great genetic diversity, strong environmental adaptability and complex trait genetic mechanisms, all of which increase the difficulty of comprehensive breeding (Lin et al., 2019; Kumar et al., 2024). Therefore, how to utilize new technologies such as molecular marker-assisted selection and genome editing to enhance ornamental value while taking into account edible quality is the core issue currently faced by breeding (Li et al., 2021; Sun et al., 2025).

This study summarizes the progress of comprehensive lotus breeding in recent years, analyzes the genetic basis, molecular regulatory mechanisms and the relationship between ornamental traits and edible qualities, explores the application prospects of multi-omics and molecular breeding techniques in the improvement of lotus traits, and also proposes breeding strategies that take into account both ornamental and edible values. This study hopes to provide references for the germplasm innovation and industrial development of lotus.

2 Ornamental Traits in Lotus Breeding

2.1 Flower color, morphology, and blooming duration

Flower color and shape have always been the key points in lotus ornamental breeding. The main colors of lotus are white, red and yellow. Artificial hybridization and selection have yielded many mixed-color and multi-color varieties, providing a more diverse ornamental effect. The formation of flower color mainly relies on flavonoid metabolites, such as isorhamnetin and kaempferol. The synthesis of these substances is closely related to the expression of related genes (such as *NnFLS*, *NnOMTs*), and the regulation of different genes causes color differences. The formation mechanism of yellow flowers has been studied most deeply, providing a molecular basis for the directed breeding of yellow varieties (Lin et al., 2019; Zhu et al., 2019). In terms of flower shape, the number of petals and petalization phenomena (such as stamen petalization and heart flap petalization) are related to transcription factors such as MADS-box and bHLH. Studies have found that the molecular markers and regulatory patterns of these genes have been revealed, which is of great significance for breeding new varieties of multi-petal and double-petal types (Deng et al., 2020; Lin et al., 2020; Lin et al., 2021; Gao et al., 2022). In terms of flowering period regulation, some early-flowering varieties have been screened out at present. They can bloom at low temperatures, thereby extending the viewing period and meeting the demands of scenic spots (Jiang et al., 2023).

2.2 Leaf architecture and ornamental foliage characteristics

The shape of lotus leaves also directly affects their ornamental value. The size, straightness and color of leaves are closely related to gene regulation. For instance, the length of the petiole and the size of the leaf area are related to genes associated with the cell wall, such as cellulose and hemicellulose synthesis genes. Large-leaf varieties contain more cellulose and hemicellulose, have thicker cell walls and more upright leaves, making them suitable for large-scale water body landscapes. Small-leaf and dwarf varieties are more suitable for potted plants and small landscapes (Zhao et al., 2023; Hu et al., 2024). In addition, leaf verticality and wax layer thickness can affect stress resistance and viewing time, and are also improvement directions (Zhao et al., 2018).

2.3 Breeding targets for landscape and aesthetic applications

The goal of lotus ornamental breeding needs to take into account flower color, flower shape, flowering period and leaf performance simultaneously. Large plant types are suitable for lakes and wetlands, while small and dwarf varieties are ideal for urban gardens or balcony water features. New varieties such as multicolor, bicolor, double-petal and spotted types are constantly increasing, providing more market choices and enhancing the economic and aesthetic value of lotus (Zhao et al., 2018; Lin et al., 2019; Zhou et al., 2022). Nowadays, new technologies such as molecular marker-assisted selection (MAS) and genomic association study (GWAS) are accelerating the aggregation of superior traits and promoting the creation of new varieties (Gao et al., 2022; Zhao et al., 2023; Hu et al., 2024).

3 Edible Value Traits in Lotus Breeding

3.1 Rhizome yield, texture, and nutritional quality

The yield and quality of lotus roots are related to their market value. The swelling and development of lotus roots are controlled by multiple genes. QTL mapping has identified multiple genetic loci related to yield, providing a basis for molecular marker-assisted breeding. Light and plant hormone signals are important for the development and swelling of lotus roots. Research on related genes is helpful for improving yield and quality (Huang et al., 2021; Qi et al., 2022). The texture and nutritional components of lotus roots (such as starch types) are also regulated by genes. Lotus roots with high amylose content are more suitable for the development of functional foods (Zhu et al., 2022). Nowadays, molecular breeding combined with traditional methods is promoting the simultaneous improvement of lotus root yield and quality (Qi et al., 2022; Sun et al., 2025).

3.2 Seed size, nutritional components, and processing traits

Lotus seeds are highly nutritious ingredients. Components such as size, protein, starch and polyphenols, as well as processing adaptability, are all key focuses in breeding. Lotus seed starch is mostly amylose and is suitable for functional food (Zhu et al., 2022). The differences in seed nutritional components are closely related to the expression of related genes. Combined analysis of transcriptome and metabolome can screen out superior germplasm (Pott et al., 2021; Zhu et al., 2022). Lotus seeds also contain active substances such as polyphenols and flavonoids, which enhance their health value (Lin et al., 2019; Qi et al., 2022). The improvement process of high-quality seeds can be accelerated by using molecular markers and genomic selection (Li et al., 2021; Sun et al., 2025).

3.3 Breeding for stress tolerance to improve edible productivity

Adverse stress conditions (such as salinity, drought and diseases) can seriously affect the yield and quality of lotus. The exploration and verification of genes related to stress resistance have provided a theoretical basis for breeding new varieties with high yield, high quality and strong adaptability (Qi et al., 2022; Sun et al., 2025). Through molecular marker-assisted selection and genome-wide association analysis, stress resistance and edible quality traits can be combined to achieve multi-trait improvement (Li et al., 2021; Sun et al., 2025). Improving stress resistance can also help lotus plants grow on marginal land, thereby increasing food security (Escaray et al., 2014; Qi et al., 2022).

4 Conventional Breeding Approaches

4.1 Germplasm collection and phenotypic selection

Lotus is an important aquatic plant that has both ornamental and edible value. The collection of germplasm resources and the assessment of phenotypic traits are the basis of conventional breeding. The collection and genetic diversity analysis of lotus germplasm from different regions revealed significant differences in lotus in terms of plant height, leaf shape, flower color, flowering period and tuber yield, which provided a rich genetic basis for subsequent trait improvement and new variety breeding (Lin et al., 2019). Phenotypic selection mainly relies on field investigation and evaluation of target traits (such as flower color, flower shape, tuber size, nutritional components, etc.), and combines multi-environment experiments to screen out superior individual plants or strains (Jiang et al., 2023; Kumar et al., 2024).

4.2 Hybridization and clonal propagation

Hybrid breeding is a commonly used method for lotus. Through artificial pollination, the superior traits of different varieties can be combined to obtain new types that are both aesthetically pleasing and highly productive. For example, hybridization of tuber type and floral type can yield offspring with rich flower colors and high tuber yield (Liu et al., 2016). Lotus has a strong asexual reproductive ability. Therefore, methods such as tuber segmentation and tissue culture are often used for the rapid propagation of superior varieties and can also maintain the stability of traits (Lin et al., 2019; Jiang et al., 2023).

4.3 Successes and limitations in traditional breeding

Traditional breeding has achieved many results, developing many varieties with diverse flower colors, controllable flowering periods and high-yield tubers, meeting the dual demands of ornamental and edible (Lin et al., 2019; Jiang et al., 2023). However, it also has limitations: first, the breeding cycle is too long and the efficiency of trait aggregation is low; second, phenotypic selection is influenced by subjective factors and the environment, making it difficult to precisely improve complex traits. Thirdly, the genetic basis is unclear, making it difficult to achieve precise improvement at the molecular level (Liu et al., 2016; Lin et al., 2019; Kumar et al., 2024). Therefore, it is necessary to combine conventional breeding with modern technologies such as molecular marker-assisted selection to enhance the efficiency and innovation of lotus breeding.

5 Molecular and Genomic Breeding Tools

5.1 Development of molecular markers for ornamental and edible traits

The research on molecular markers of lotus has developed rapidly. Commonly used markers such as SSR, SNP and InDel accelerate trait localization and molecular-assisted selection. Through whole-genome resequencing and transcriptome analysis, researchers have identified millions of SNPs and a large number of SSR/InDel markers. These markers have been widely used in the research and breeding of important traits such as flower color, flower shape, seed starch content and rhizome quality (Lin et al., 2019; Li et al., 2021; Qi et al., 2022). For example, the genetic map constructed with high-density SNP markers has greatly improved the accuracy of agronomic trait localization of lotus (Hu et al., 2015; Liu et al., 2016).

5.2 QTL mapping and GWAS for key traits

QTL mapping and GWAS are the core methods for studying the complex traits of lotus. By combining phenotypic and genotypic data from large populations, researchers have identified QTL and candidate genes related to petal number, flower shape, plant structure and starch content, etc. For instance, GWAS identified gene and transposon variations related to the number of petals and stamen petalization. Some of these genes also have pleiotropy and can affect the traits of multiple floral organs (Gao et al., 2022; Zhao et al., 2023; Hu et al., 2024). In terms of edible quality, QTL mapping and association analysis also identified key genes controlling seed starch synthesis and rhizome expansion, providing theoretical support for molecular design breeding (Li et al., 2020; Sun et al., 2020).

5.3 Genome editing (CRISPR/Cas) and functional genomics for trait improvement

With the continuous improvement of the reference genome, the application prospects of gene editing technologies such as CRISPR/Cas in the lotus research are very promising. At present, the genetic transformation system of lotus is not yet mature, but some progress has been made in the mining of functional genes and the research of transcription factors (Figure 1) (Qi et al., 2022; Song et al., 2022; Sun et al., 2025). In other ornamental plants, CRISPR/Cas has been successfully used to regulate flower color, shape and flowering period. These experiences provide references for achieving precise editing in lotus in the future (Giovannini et al., 2021; Muhammed et al., 2025). Furthermore, the multi-omics combined with functional genomics approach has identified some key genes related to petal morphology, starch synthesis and stress resistance, all of which provide rich target resources for molecular breeding (Sun et al., 2020; Song et al., 2022; He et al., 2025).

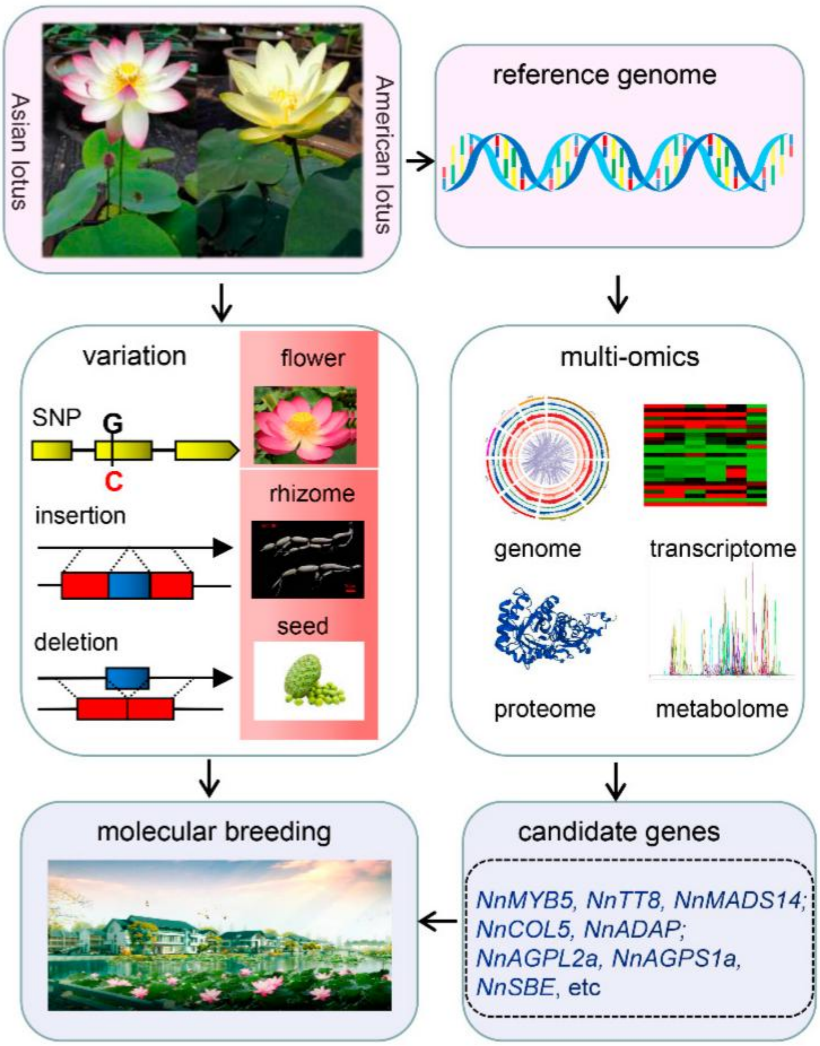

Figure 1 Flowchart of the molecular breeding process of lotus (Adopted from Qi et al., 2022)

6 Integrative Breeding Approaches

6.1 Combining ornamental and edible trait improvement in breeding programs

The ornamental value of lotus mainly lies in its color, shape and flowering period, while its edible value mainly depends on the yield, nutrition and taste of its roots and stems. Modern breeding, through phenotypic screening combined with molecular marker-assisted selection (MAS), can simultaneously improve ornamental and edible traits. For instance, by using QTL mapping and genome selection techniques, researchers have identified key genes that affect flower color (such as genes related to yellow flower color) and rhizome yield, providing tools and theoretical support for the improvement of dual traits (Zhu et al., 2019; Lin et al., 2020; Huang et al., 2021; Li et al., 2021). In addition, the screening of early-flowering varieties and the analysis of nutritional traits have also provided practical experience for breeding that takes into account both ornamental and edible values (Jiang et al., 2023; Yang et al., 2024).

6.2 Trade-offs and strategies to optimize dual-purpose cultivars

In actual breeding, there is often a conflict between ornamental and edible traits. Some highly ornamental varieties perform poorly in terms of root and stem yield or quality. To solve this problem, breeders adopted methods such as multi-parent hybridization, backcrossing and population improvement, combined with phenotypic and molecular data, to screen out materials that have both excellent flower shapes and high-yield roots and stems (Lin et al., 2019; Huang et al., 2021; Jiang et al., 2023). Meanwhile, regulating the expression of genes related to flowering period and root and stem development can reduce the negative correlation between traits, thereby achieving synergistic improvement (Lin et al., 2020; Hu et al., 2024). In addition, based on large-scale evaluation of germplasm resources and trait association analysis, researchers established trait trade-off and optimization models, providing a reference for the breeding of dual-use varieties (Li et al., 2021; Sun et al., 2025).

6.3 Multi-omics approaches for balancing aesthetics and nutrition

Multi-omics integration provides a new idea for lotus to balance ornamental and edible values. Through the combined analysis of the genome, transcriptome and metabolome, the molecular basis of flower color, nutritional components (such as flavonoids, starch) and their regulatory networks can be revealed (Figure 2) (Zhu et al., 2019; Li et al., 2021; Yu et al., 2025). For instance, transcriptome and metabolome analyses revealed that certain specific transcription factors regulate the synthesis of anthocyanins and nutrients, providing potential targets for molecular design breeding (Zhu et al., 2019; Yu et al., 2025). In addition, the in-depth mining of genomic databases and functional genes has also promoted the development of molecular markers and the application of precision breeding (Li et al., 2021; Sun et al., 2025).

7 Case Study: Breeding Program of *Nelumbo nucifera*

7.1 Breeding objectives and trait prioritization

Lotus is an important aquatic plant, which not only has ornamental value but also edible value. When breeding, it is necessary to strike a balance between ornamental traits such as flower shape, color and plant type and edible qualities such as tuber yield, quality and nutritional components. Recent studies, through genetic diversity analysis, population genomics and trait association research, have clearly identified flower shape, flower color, flower diameter, tuber size, starch content and stress resistance as key traits for improvement. Different types of lotus (flower lotus, seed lotus, lotus root lotus) have significant differences in ornamental and edible traits. Trait weights need to be allocated according to the target during breeding (Li et al., 2020; Kumar et al., 2024; Kumar et al., 2025).

7.2 Methods: hybridization, marker-assisted selection, field evaluation

There are various breeding methods for lotus. Traditional hybridization involves crossing different types of lotus to obtain offspring with complementary traits. Molecular marker-assisted selection (MAS) and genome-wide association study (GWAS) have been widely used for trait localization and screening of superior genes. For instance, based on high-density SNP genetic mapping and QTL mapping, researchers identified genetic loci related to tuber yield and flower shape. These achievements provided tools for early selection and precision breeding (Lin et al., 2020; Huang et al., 2021; Hu et al., 2024). In addition, field assays combined with multi-environment tests were conducted to comprehensively evaluate the flower color, flower shape, yield and quality of the offspring to ensure the stability and adaptability of the new variety in production (Kumar et al., 2024; Kumar et al., 2025).

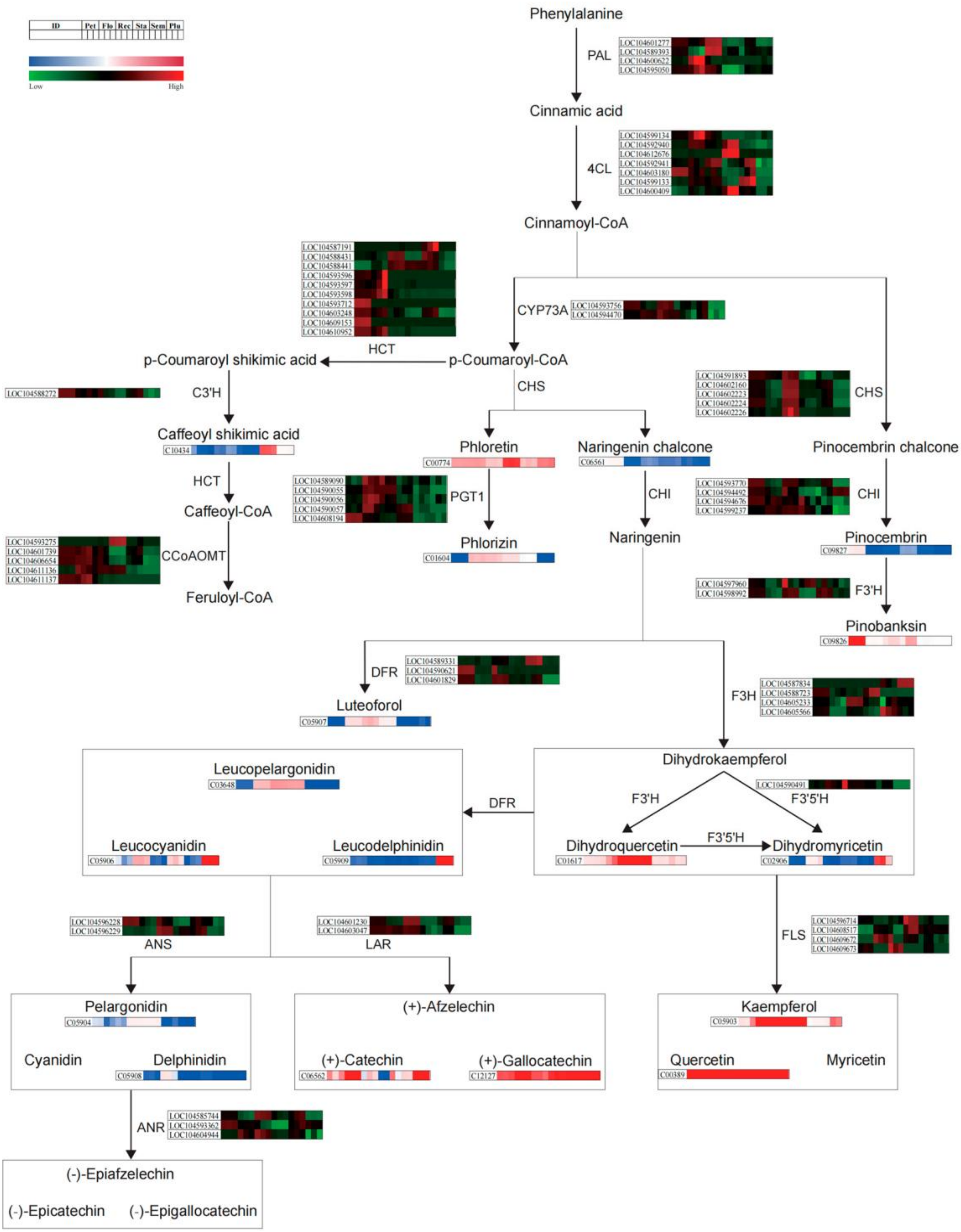

Figure 2 Heatmap of key genes and metabolites expression in flavonoid biosynthesis pathway of 6 lotus tissues (Adopted from Yu et al., 2025)

7.3 Outcomes: cultivars with enhanced ornamental appeal and edible quality

Through these integrated methods, breeders have developed a number of new lotus varieties that are both ornamental and edible. Some new varieties performed better in ornamental traits such as flower diameter, flower color and number of petals. Meanwhile, the yield, starch content and nutritional quality of tubers were also improved (Li et al., 2020; Huang et al., 2021; Kumar et al., 2024; Kumar et al., 2025). The application of molecular breeding methods has accelerated the aggregation of superior genes and enhanced the efficiency of breeding. Some studies have also attempted to use methods such as gene transformation to further expand the possibility of improving the traits of lotus (Verma et al., 2025).

8 Challenges and Research Gaps

8.1 Long breeding cycles and trait complexity

Lotus is a perennial aquatic plant with a rather complex genetic background and a wide variety of traits. Its ornamental traits (such as flower color, flower shape, and plant type) and edible qualities (such as root and stem yield and nutritional components) are usually regulated by multiple genes. There are also genetic correlations and environmental interactions among different traits, which prolongs the traditional breeding cycle and makes it difficult to concentrate superior traits in one variety. In addition, the genetic mechanisms of some traits (such as flower color and plant type) have not been fully understood, which also increases the difficulty of molecular breeding and precise improvement (Zhu et al., 2019; Lin et al., 2020; Qi et al., 2022; Hu et al., 2024).

8.2 Limited genomic resources compared to other crops

Although the genome sequencing and database construction of lotus have made progress in recent years, compared with major food crops, its genomic resources are still not rich enough. High-quality genome assembly, functional gene annotation and molecular marker development are all relatively limited. This to some extent restricts the application of modern breeding methods such as GWAS, QTL mapping and MAS. Meanwhile, the existing genomic databases and germplasm resource banks have insufficient coverage and diversity, which poses obstacles to the analysis of complex traits and the mining of excellent genes (Gui et al., 2018; Li et al., 2021; Qi et al., 2022).

8.3 Consumer-driven demand versus ecological adaptability

The market demand for lotus is becoming increasingly diverse. It is not only required that the flower colors and shapes be rich, but also that the roots and stems be high-yielding and have high nutritional value. However, if one overly pursues a certain trait, such as only focusing on yield or flower color, it may lead to problems like a decline in genetic diversity, weakened stress resistance, and even affect the ecological adaptability of plants. Moreover, some excellent traits do not behave stably in different environments. How to meet consumer demands while ensuring the ecological adaptability and sustainable utilization of varieties is a key issue that needs to be addressed in current lotus breeding (Huang et al., 2018; Lin et al., 2019; Mekbib et al., 2020; Gowthami et al., 2021; Kumar et al., 2024).

9 Future Perspectives

9.1 Application of synthetic biology and metabolic engineering

With the progress of research on the genome and molecular biology of lotus, synthetic biology and metabolic engineering have brought new opportunities for the improvement of lotus. By regulating key metabolic pathways (such as flavonoids and anthocyanins), the flower color, nutritional components and medicinal active substances can be specifically changed, thereby taking into account both ornamental and edible values. For instance, studies on transcription factor families have revealed their roles in regulating flavonoid synthesis, which provides a theoretical basis for enhancing the accumulation of functional components in specific tissues and lays the foundation for molecular breeding and resource utilization (Zhu et al., 2019; Sun et al., 2025; Yu et al., 2025). In addition, based on high-density genetic mapping and QTL mapping, combined with technologies such as gene editing, it is expected to accelerate the breeding of new varieties of lotus (Liu et al., 2016; Huang et al., 2021).

9.2 Integration of lotus breeding into sustainable agriculture and urban landscaping

Lotus not only have ornamental value but also edible and ecological value, thus having unique advantages in sustainable agriculture and urban landscape construction. Breeding early-flowering, stress-resistant and nutrient-rich varieties can not only enhance economic benefits, but also promote wetland protection and urban ecosystem diversity (Lin et al., 2019; Jiang et al., 2023). The superhydrophobicity of lotus leaves and the long lifespan of seeds also make it potentially useful in rainwater management, ecological restoration and landscaping (Gowthami et al., 2021). In the future, lotus breeding needs to better integrate ecological agriculture and sustainable urban development, and promote multi-functional utilization.

9.3 Prospects for global collaboration and germplasm innovation

Genetic diversity and germplasm innovation are the foundation of comprehensive lotus breeding. Nowadays, basic research and applied development are becoming increasingly active worldwide, and multi-level data platforms such as genomics, phenotypes and metabolomics have been established (Li et al., 2021; Sun et al., 2025). Strengthening international resource sharing, joint breeding and data intercommunication is conducive to breaking through the limitations of innovation in a single region and promoting the global application of new lotus varieties (Lin et al., 2019; Li et al., 2021; Sun et al., 2025). Meanwhile, in the face of problems such as habitat loss and overexploitation, it is also necessary to promote protective breeding and diversity maintenance to ensure the long-term development of the lotus industry (Gowthami et al., 2021).

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Conflict of Interest Disclosure

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

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