

Review and Progress

Open Access

Prospects for Synthetic Biology and Sustainable Utilization of *Torreya grandis*

Baofu Huang¹, Chuchu Liu², Guangman Xu¹ ✉¹ Traditional Chinese Medicine Research Center, Cuixi Academy of Biotechnology, Zhuji, 311800, Zhejiang, China² Institute of Life Sciences, Jiyang College of Zhejiang A&F University, Zhuji, 311800, Zhejiang, China✉ Corresponding email: guangman.xu@cuixi.orgTree Genetics and Molecular Breeding, 2025, Vol.15, No.5 doi: [10.5376/tgmb.2025.15.0024](https://doi.org/10.5376/tgmb.2025.15.0024)

Received: 11 Sep., 2025

Accepted: 16 Oct., 2025

Published: 26 Oct., 2025

Copyright © 2025 Huang et al., This is an open access article published under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Preferred citation for this article:Huang B.F., Liu C.C., and Xu G.M., 2025, Prospects for synthetic biology and sustainable utilization of *Torreya grandis*, Tree Genetics and Molecular Breeding, 15(5): 202-210 (doi: [10.5376/tgmb.2025.15.0024](https://doi.org/10.5376/tgmb.2025.15.0024))

Abstract This study summarized the molecular regulation and synthetic pathways of *Torreya grandis* in major metabolites such as sterols, amino acids and flavonoids. Through joint analysis of gene cloning, transcriptome and metabolome, it was found that some key genes play important roles in the synthesis and stress resistance of active components, and the regulatory potential of transcription factors in metabolic pathways was explored. The nutrient cycling and utilization of *Torreya grandis* at different forest ages were reviewed. It was expounded that precise nutrition management is crucial for the long-term stability and sustainable development of the forest stand. Combined with the methods of synthetic biology, the prospects and challenges of *Torreya grandis* in high-value utilization and the development of eco-friendly industries were proposed. This research aims to provide theoretical and technical support for the molecular breeding, functional component development and sustainable utilization of *Torreya grandis*.

Keywords *Torreya grandis*; Synthetic biology; Functional ingredients; Molecular regulation; Sustainable utilization

1 Introduction

Torreya grandis is a rare economic tree unique to China and has a long history of cultivation. Its kernel is rich in unsaturated fatty acids, sterols, flavonoids, amino acids and vitamins. These components make *Torreya grandis* not only a highly nutritious nut but also suitable for the production of edible oil and functional foods. Studies have shown that it also has great potential in medicine and has multiple health effects such as antioxidation, anti-inflammation, lipid-lowering and anti-tumor (Yan et al., 2023; Zhang et al., 2023; Gao et al., 2024). Luo et al. (2021) and Quan et al. (2022) found that by-products of *Torreya grandis*, such as seed coat and seed meal, are also rich in polyphenols and proteins, which can be used to develop high-value-added natural products. *Torreya grandis* has significant economic and social value in forestry ecology, food industry and medical health.

However, there are still many problems in the industrial utilization of *Torreya grandis*. Its growth cycle is very long, the fruiting time is late, the yield is limited, and it is difficult to meet the market demand (Hu et al., 2024). It has high requirements for soil nutrients and is often limited by insufficient elements such as nitrogen and phosphorus at different forest age stages, which can affect tree growth and seed quality (Wang et al., 2024; Fan et al., 2025). Meanwhile, the natural distribution range of *Torreya grandis* is limited. The breeding of superior varieties and efficient cultivation techniques are not yet mature. The utilization rate of by-products is also relatively low, which is prone to cause resource waste and environmental pressure (Luo et al., 2021; Quan et al., 2022). All these problems have restricted the efficient utilization and sustainable development of *Torreya grandis*.

This study summarizes the current application status of *Torreya grandis* in the fields of forestry, food and medicine, analyzes the main bottlenecks, and explores the potential of new technologies such as synthetic biology in increasing yield, improving quality and enhancing resource utilization. This study aims to provide a theoretical basis and technical support for the high-value development and sustainable utilization of *Torreya grandis* through research achievements in multi-omics, molecular breeding and metabolic engineering.

2 Biological and Economic Basis of *Torreya grandis*

2.1 Botanical characteristics, distribution, and ecological role

Torreya grandis is a unique evergreen large tree in China, belonging to the Taxaceae family. It is mainly distributed in the central and northern parts of the subtropical region of China (25°~32°N, 109°~121°E), including seven provinces: Zhejiang, Anhui, Jiangsu, Fujian, Jiangxi, Guizhou and Hubei. The average annual temperature suitable for its growth is between 15.2°C and 18.7°C, and the annual precipitation is between 1 000 and 1 900 mm. It prefers sandy loam or light clay soil rich in organic matter and loose in texture, with a pH value suitable for 5.2 to 6.5. The altitude distribution varies depending on the geographical location, generally ranging from 800 meters to 2 000 meters. *Torreya grandis* has a strong ability to adapt to the environment and can grow and bear fruit normally in places with high altitudes, abundant sunlight and low wind force. It plays a significant role in the ecosystem and is beneficial for promoting soil nutrient cycling, maintaining forest stability and protecting biodiversity. During the process of forest age succession, its regulation of elements such as carbon, nitrogen and phosphorus in the soil is also very important (Chen et al., 2023a; Fan et al., 2025).

2.2 Nutritional and medicinal compounds in seeds and other tissues

The seeds of *Torreya grandis* (*Torreya* seeds) are rich in oil, with the proportion reaching 45.8% to 53.2%. Among them, polyunsaturated fatty acids are the main component, especially sciadonic acid, which has health care functions such as lowering blood lipids and preventing atherosclerosis. In addition to oils, *Torreya* seeds and other tissues also contain amino acids, proteins, sterols (such as β -sitosterol), flavonoids (such as kayaflavone), polyphenols and vitamin E. These components possess activities such as antioxidation, anti-inflammatory, antibacterial and anti-tumor. *Torreya* seeds of different varieties and forest ages vary in the content of amino acids, lipids and active components. The seeds of old trees are more nutritious (Figure 1). *Torreya* seed oil and its by-products have great potential in the development of food, health products and drugs (Cui et al., 2022; Wang et al., 2022b; Chen et al., 2023b; Lou et al., 2023; Gao et al., 2024).

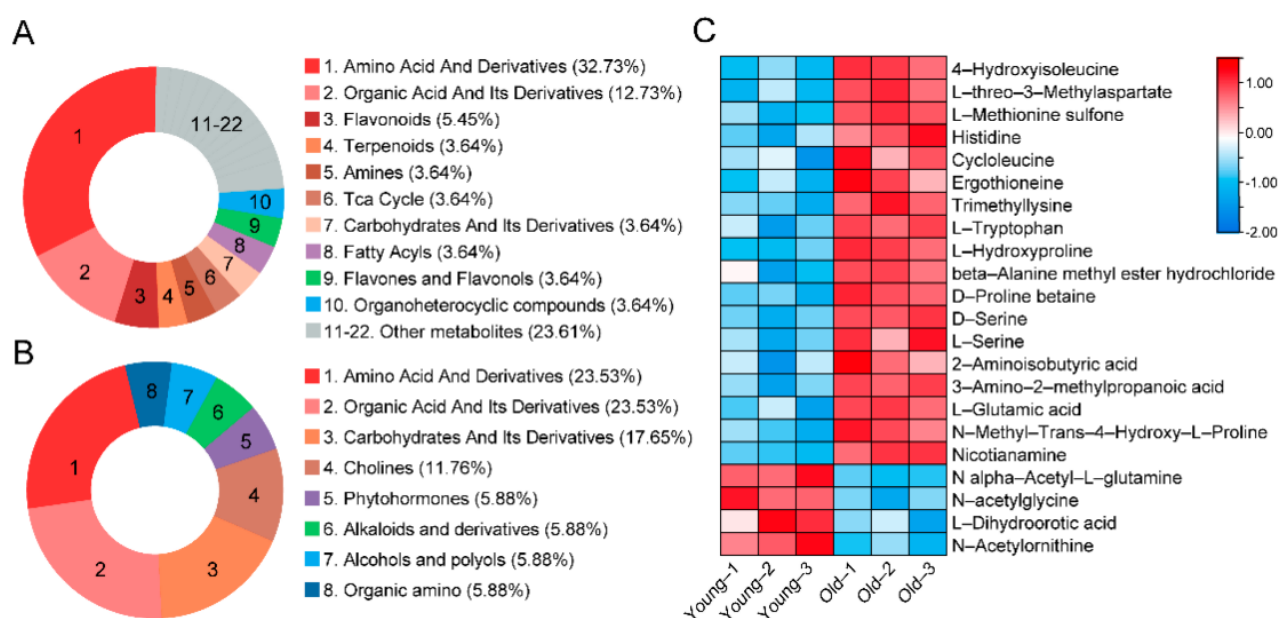


Figure 1 Identification of differentially expressed amino acids between young and old *T. grandis* nuts (Adopted from Chen et al., 2023b)

Image caption: (A) The proportion of up-regulated metabolite categories. (B) The proportion of down-regulated metabolite categories. (C) Heatmap of differential metabolites in amino acid and derivatives between young and old *T. grandis* nuts (Adopted from Chen et al., 2023b)

2.3 Timber, ecological services, and cultural importance

The wood of *Torreya grandis* is hard, dense and resistant to corrosion, making it suitable for high-end furniture, construction and handicrafts. *Torreya grandis* forests play a significant role in soil and water conservation, climate

regulation and biodiversity protection. *Torreya grandis*, as a traditional economic forest tree species, holds an important position in the local economy. *Torreya* seeds and their products can bring stable income to farmers. Its cultivation history dates back over a thousand years and it also carries rich cultural and folk traditions. It is called the “Longevity Tree” and has a unique position in religion, gardens and local culture (Lou et al., 2023; Chen et al., 2023b; Ma et al., 2023).

3 Advances in Synthetic Biology Relevant to *T. grandis*

3.1 Key tools: CRISPR/Cas genome editing, metabolic engineering platforms

The commonly used tools for synthetic biology research on *Torreya grandis* include CRISPR/Cas gene editing and metabolic engineering. Gene editing can precisely regulate the expression of key metabolic genes. For instance, researchers have found that the TgSQS (squalene synthase) gene plays a significant role in the synthesis of β -sitosterol and squalene. By introducing it into the model plant, the content of the target product increased significantly, which provided a basis for the metabolic engineering modification of the functional components of *Torreya grandis*. In addition, some transcription factors (such as TgWRKY3) can also regulate metabolic genes, and they are also potential targets in synthetic biology (Zhang et al., 2023).

3.2 Synthetic pathways for oil, flavonoids, and terpenoids

The seeds of *Torreya grandis* contain a lot of high-value substances such as oils (like tocopherol), flavonoids and terpenoids. Full-length transcriptome and multi-omics studies have revealed the synthetic pathways of these substances and key enzyme genes (such as *TgVTE2b*, *TgVTE4*, *TgDFR6*, etc.) (Lou et al., 2019; Tao et al., 2024). In a low-phosphorus environment, the expression of the flavonoid synthesis gene *TgDFR6* increases, thereby promoting the accumulation of flavonoids (Wang et al., 2024). Furthermore, the synthetic pathways of terpenoids such as squalene and β -sitosterol have been resolved, and the heterologous expression of related genes can increase the content of the target products (Figure 2) (Zhang et al., 2023). These achievements provide theoretical support for the reconstruction of the metabolic network of *Torreya grandis* using synthetic biology.

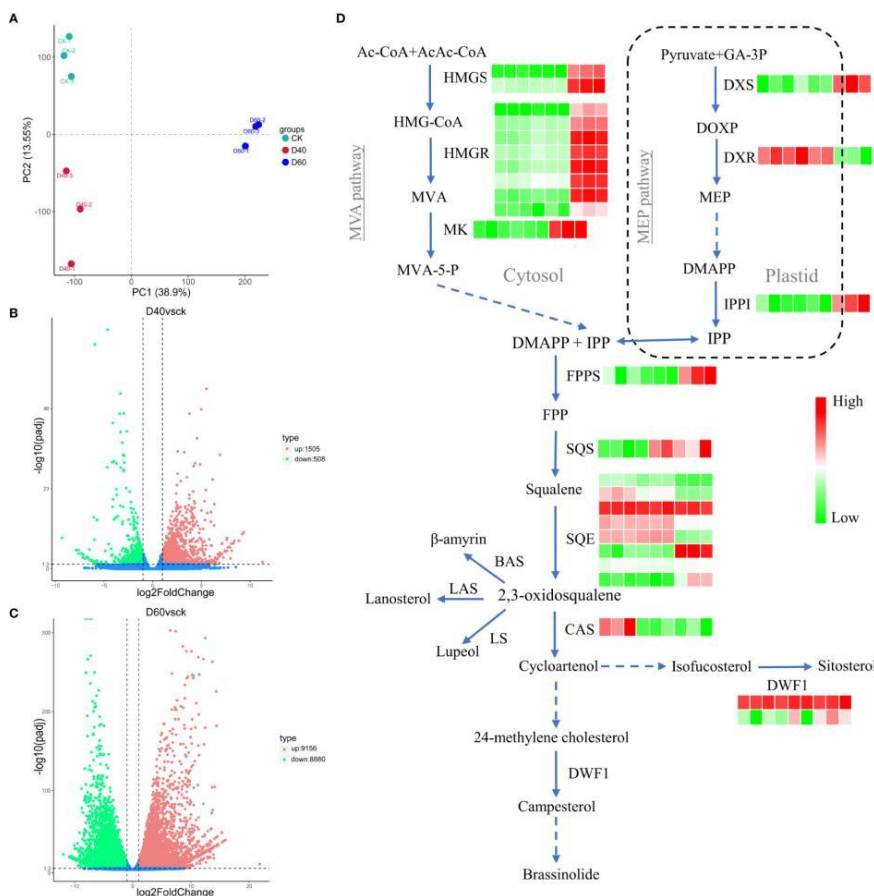


Figure 2 Sterol biosynthesis-related genes in *Torreya grandis* responded to drought stress (Adopted from Zhang et al., 2023)

3.3 Potential of heterologous systems for producing *T. grandis*-derived compounds

In heterologous systems (such as yeast and *Arabidopsis thaliana*), scientists have successfully expressed the key metabolic genes of *Torreya grandis* to efficiently synthesize squalene and β -sitosterol. For instance, after introducing the TgSQS gene into *Arabidopsis thaliana*, not only were the contents of squalene and β -sitosterol increased, but also the drought resistance of the plants was enhanced (Zhang et al., 2023). In addition, the gene functions related to the synthesis of flavonoids and tocopherols in *Torreya grandis* have also been analyzed, providing resources for their expression and large-scale production in microbial or plant cell factories (Lou et al., 2019; Tao et al., 2024; Wang et al., 2024). These research achievements have laid a foundation for the green manufacturing and industrial application of high-value components of *Torreya grandis*.

4 Sustainable Utilization Pathways

4.1 Enhancing seed oil yield and nutritional composition

Torreya grandis seeds are rich in unsaturated fatty acids, proteins and nutrients, and are an important edible and medicinal resource. Researchers have identified key genes related to lipid and amino acid synthesis, such as *TgOLEO1*, *TgCLO1*, *TgSLO1*, *TgDAHP2*, and *TgASAI*, through molecular breeding, transcriptome and metabolome analysis. These findings provide a theoretical basis for breeding varieties with high oil and high nutrition (Ding et al., 2020; Lou et al., 2022). In terms of cultivation management, reasonably controlling the supply of nutrients such as nitrogen and phosphorus, combined with organic management, can improve the quality and yield of seeds and reduce the environmental pressure caused by excessive fertilization (Han et al., 2021; Fan et al., 2025). Suo et al.'s research in 2025 demonstrated that in the post-harvest stage, treatment with ethylene can further enhance the oil content and nut quality.

4.2 Valorization of by-products (shells, leaves, and timber)

The by-products such as the shells, leaves and wood of *Torreya grandis* also have development value. For instance, shells can be made into biochar to restore soil contaminated by heavy metals, which not only improves soil properties but also promotes crop growth (Li et al., 2025). The protein by-products after seed oil extraction can obtain bioactive peptides with antioxidant activity through enzymatic hydrolysis, which can be used in functional foods and natural additives (Luo et al., 2021). In addition, leaves and wood can also be used as raw materials for under-forest economy, eco-tourism and cultural products, increasing the comprehensive benefits of forestry (Chen and Jin, 2018).

4.3 Integration of *T. grandis* cultivation with agroforestry and ecological conservation

The traditional cultivation system of *Torreya grandis* often ensures high yield, maintains genetic diversity and performs ecological service functions through grafting and mixed planting (GT and NGT tree types) (Zhang et al., 2019). Combined with agroforestry systems, it can also enhance land use efficiency and promote biodiversity and the stability of ecosystems (Chen and Jin, 2018). In addition, by rationally planning the planting area and combining remote sensing and topographic analysis, precise planting and management can be achieved, reducing the damage to the original forest land (Chen and Chen, 2019; Lyu et al., 2025). To maintain the ecological health of the ancient *Torreya grandis* forest, it is also necessary to regulate the soil microbial community and manage soil pH (Wang et al., 2022a).

5 Multi-omics and Systems Biology Integration

5.1 Genomic, transcriptomic, proteomic, and metabolomic resources

In recent years, there have been an increasing number of multi-omics research resources. Full-length transcriptome sequencing has identified key enzyme genes for tocopherol (vitamin E) synthesis, such as *TgVTE2b* and *TgVTE4*. Lou et al. (2019) hold that the expression differences of these genes among different varieties and developmental stages are closely related to the accumulation of tocopherols, providing a basis for molecular-assisted breeding. The combined analysis of the transcriptome and metabolome also revealed the synthetic networks of nutrients such as amino acids and flavonoids, and identified multiple key genes and transcription factors (Lou et al., 2022; Tao et al., 2024). Proteomic and metabolomic data demonstrated the molecular responses of *Torreya grandis* to low phosphorus or nanoplastic stress (Yu et al., 2022; Wang et al., 2024).

5.2 Network-level understanding of biosynthetic regulation

The combination of multi-omics helps us better understand the regulatory mechanisms of secondary metabolites of *Torreya grandis*, such as β -sitosterol, flavonoids and amino acids. The research by Zhang et al. (2023) indicates that SQS (squalene synthase) plays a core role in the synthesis of β -sitosterol, and its expression is directly regulated by the WRKY transcription factor. Regarding flavonoid synthesis, TgERF114 and TgDOF5 can activate the promoter of TgDFR6, thereby promoting flavonoid accumulation under low-phosphorus conditions (Wang et al., 2024). Lou et al. (2022) found that in amino acid synthesis, the expression of TgDAHP2 and TgASA1 is related to the content of multiple amino acids and is positively regulated by multiple transcription factors. These results indicate that the metabolic regulation of *Torreya grandis* is a multi-level network.

5.3 Designing synthetic biology strategies guided by omics data

Multi-omics achievements have provided new possibilities for the design of *Torreya grandis* in synthetic biology. In 2023, Zhang et al. demonstrated through functional verification that some key enzymes and transcription factors can directly affect the synthesis of metabolites. For instance, the heterologous expression of SQS can significantly increase the content of β -sitosterol and enhance drought resistance. Modifying the regulatory elements of genes related to flavonoid and amino acid synthesis is expected to breed new varieties with both high functionality and high adaptability (Lou et al., 2022; Tao et al., 2024; Wang et al., 2024). Proteomics and metabolomics are helpful for screening genotypes with high stress resistance or high nutritional value and providing molecular targets for industrial development (Lou et al., 2019; Yu et al., 2022).

6 Case Study: Application of Synthetic Biology in *Torreya grandis*

6.1 Background: target traits

Torreya grandis is an economic forest tree species unique to China. Its kernel contains a large amount of unsaturated fatty acids, β -sitosterol, vitamin E (tocopherol), amino acids and various types of flavonoids. These components make it highly valuable both in nutrition and medicine. How to increase oil yield and increase the contents of active substances such as β -sitosterol, flavonoids, amino acids and tocopherols is the key goal of synthetic biology in the utilization of *Torreya grandis* (Lou et al., 2019; Lou et al., 2022; Zhang et al., 2023; Tao et al., 2024; Wang et al., 2024).

6.2 Research methods: pathway reconstruction, metabolic profiling, validation

At present, the research on *Torreya grandis* in synthetic biology mainly covers several aspects. One is the reconstruction of metabolic pathways. Researchers cloned and identified key enzyme genes such as TgSQS, TgDFR6, TgDAHP2, TgASA1, TgVTE2b and TgVTE4, and introduced them into model plants for heterologous expression to reveal the synthetic mechanisms of lipids and secondary metabolites (Zhang et al., 2023; Wang et al., 2024). The other one is the combination of multi-omics. The combined analysis of the transcriptome and metabolome can reveal the accumulation pattern and regulatory mode of metabolites of *Torreya grandis* at different developmental stages or under stress (Lou et al., 2019; Tao et al., 2024). In terms of functional validation, researchers often use model plants such as *Arabidopsis thaliana*. After overexpressing the target gene, they detect the changes in oil and active components and evaluate the stress resistance performance of the plants, thereby confirming the function of the gene (Lou et al., 2022). Research on the regulation of transcription factors is also advancing. Zhang et al. (2023) and Wang et al. (2024) discovered through yeast single-hybrid and dual-luciferase experiments that TgWRKY3, TgERF114 and TgDOF5 can directly regulate some key metabolic genes.

6.3 Outcomes: improved production efficiency, ecological implications, industrial prospects

These synthetic biology methods have brought about obvious effects. For instance, the overexpression of TgSQS can significantly increase the content of β -sitosterol and enhance the drought resistance of plants at the same time. Overexpression of TgDAHP2 and TgASA1 increased amino acid levels (Lou et al., 2022; Tao et al., 2024). Some metabolic engineering strategies can also make *Torreya grandis* more adapted to environments such as drought and low phosphorus (Zhang et al., 2023; Wang et al., 2024). These achievements not only increased the accumulation of functional components in kernels, but also provided molecular resources and theoretical support for the development of functional foods and the sustainable development of the *Torreya grandis* industry (Lou et al., 2019; Tao et al., 2024).

7 Challenges and Research Gaps

7.1 Technical limitations in woody plant transformation and editing

Torreya grandis is a woody gymnosperm with very low gene transformation and editing efficiency. Currently, there is no efficient and stable genetic operation system. This has greatly restricted the application of synthetic biology tools in *Torreya grandis*. Although some gene function studies (such as *TgSQS* and *TgDAHP2*) have been verified in heterologous systems, there are still many technical challenges in achieving precise editing and large-scale functional verification on the *Torreya grandis* itself. In addition, woody plants have a long life cycle and an imperfect regeneration system, making gene function analysis and molecular breeding even more difficult (Suo et al., 2019; Ding et al., 2020; Shen et al., 2024).

7.2 Lack of high-quality genomic databases and functional annotation

In recent years, the transcriptome and multi-omics data of *Torreya grandis* have gradually increased, but a complete and high-quality genomic database is still lacking, and the functional annotations are insufficient. Many important metabolic pathways related to lipids, amino acids and flavonoids have not been fully elucidated yet. This limits the pathway construction of molecular design and synthetic biology (Lou et al., 2022; Yan et al., 2022; Wang et al., 2024). In addition, there is currently a lack of systematic multi-omics integration and functional verification platforms, making it difficult to achieve precise regulation from genes to traits.

7.3 Balancing industrial use with biodiversity conservation

Torreya grandis is a rare tree species with high economic value and also plays an important role in ecology. The research conducted by Fan et al. in 2025 indicates that if large-scale development and utilization are carried out, it may bring risks such as a decline in genetic diversity, soil degradation, and an increase in pests and diseases. Studies on the genetic structure of *Torreya grandis* populations, microbial interactions, and their impacts on ecosystem services under different forest ages and ecological environments are still relatively scarce at present. There is a lack of a scientific management approach that combines industrial development with biodiversity conservation. Environmental stresses such as drought, acidification and pollution also pose challenges to the sustainable utilization of *Torreya grandis*. Therefore, it is necessary to strengthen the research on the ecological adaptability and stress resistance mechanism of *Torreya grandis* (Yu et al., 2022; Zhang et al., 2023; Shen et al., 2024).

8 Future Perspectives

8.1 Integrating synthetic biology with sustainable forestry models

The tools used in synthetic biology include gene editing, synthetic gene circuits and environmental sensors. These methods can precisely regulate plant growth, stress resistance and the synthesis of metabolic products, providing technical support for sustainable forestry. Plant systems engineering and microbiome engineering have shown great potential in biomass materials, carbon sinks and ecological restoration, and are helpful for establishing an efficient, low-carbon and circular forestry production system (McCarty and Ledesma-amaro, 2019; Yang et al., 2022). In the future, the combination of artificial intelligence and synthetic biology will further enhance the intelligence and resource utilization efficiency of forestry management (Iram et al., 2024; Morgan et al., 2024).

8.2 Combining biotechnology with climate-resilient cultivation

Climate change has brought about extreme weather and ecological pressure. Synthetic biology is helpful for breeding *Torreya grandis* varieties that are more drought-tolerant, flood-tolerant and heat-tolerant. Through systematic breeding, microbiome regulation and molecular design, the stress resistance of plants can be enhanced to ensure the stability and productivity of forestry ecosystems (Roell and Zurbruggen, 2019; Kocaoğlu et al., 2023). The combination of these new technologies and traditional measures, such as diversified planting and ecological management, is also helpful for improving overall climate resilience (Chami, 2020; Tan et al., 2022; Kozaeva et al., 2024).

8.3 Policy, industry, and community roles in sustainable utilization

The sustainable utilization of *Torreya grandis* not only relies on science, but also requires the cooperation of policies, industries and communities. At the policy level, incentive mechanisms can be established to support

synthetic biology innovation and green forestry practices and promote industrial upgrading (Archibald et al., 2023; Raman et al., 2024). The industrial sector needs to enhance research and development to implement bio-based products and circular economy models (Zou et al., 2024). The participation of communities and the public is also very important, which can enhance social acceptance and promote knowledge sharing and fair distribution (Karabin et al., 2021; Archibald et al., 2023). In the future, multidisciplinary and cross-departmental cooperation is still needed to enable synthetic biology to play a greater role in ecological protection, economic development and social justice.

Acknowledgments

The authors appreciate the modification suggestions from Professor Wen and Two anonymous peer reviewers on the manuscript of this study.

Conflict of Interest Disclosure

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

References

- Archibald B., Zhong V., and Brophy J., 2023, Policy makers, genetic engineers, and an engaged public can work together to create climate-resilient plants, PLoS Biology, 21(7): e3002208.
<https://doi.org/10.1371/journal.pbio.3002208>
- Chami D., 2020, How can sustainable agriculture increase climate resilience, a systematic review, Sustainability, 12(8): 3119.
<https://doi.org/10.3390/su12083119>
- Chen L., Liu N., Wan Z., Liu F., Cao L., Gao C., Sun N., and Liu C., 2023a, The growth equation and element distribution of *Torreya grandis* in the Huangshan region of China, Forests, 15(1): 68.
<https://doi.org/10.3390/f15010068>
- Chen W., Yan J., Zheng S., Suo J., Lou H., Song L., and Wu J., 2023b, Integrated metabolomics, transcriptome and functional analysis reveal key genes are involved in tree age-induced amino acid accumulation in *Torreya grandis* nuts, International Journal of Molecular Sciences, 24(23): 17025.
<https://doi.org/10.3390/ijms242317025>
- Chen X., and Chen H., 2019, Comparing environmental impacts of Chinese *Torreya* plantations and regular forests using remote sensing, Environment, Development and Sustainability, 23: 133-150.
<https://doi.org/10.1007/s10668-019-00570-7>
- Chen X., and Jin H., 2018, Review of cultivation and development of Chinese torreyia in China, Forests, Trees and Livelihoods, 28: 68-78.
<https://doi.org/10.1080/14728028.2018.1553690>
- Cui J., Li W., Wang C., Huang Y., Lin W., Zhou B., and Yue J., 2022, Antimicrobial abietane-type diterpenoids from *Torreya grandis*, Phytochemistry, 201: 113278.
<https://doi.org/10.1016/j.phytochem.2022.113278>
- Ding M., Lou H., Chen W., Zhou Y., Zhang Z., Xiao M., Wang Z., Yang Y., Yang L., Zhang F., Wu J., and Song L., 2020, Comparative transcriptome analysis of the genes involved in lipid biosynthesis pathway and regulation of oil body formation in *Torreya grandis* kernels, Industrial Crops and Products, 145: 112051.
<https://doi.org/10.1016/j.indcrop.2019.112051>
- Fan A., Jin S., Tan Y., Huan W., Chen W., Wang X., and Han Y., 2025, Nutrient recycling and utilization of *Torreya grandis* 'Merrillii' along an age gradient, Frontiers in Plant Science, 16: 1566140.
<https://doi.org/10.3389/fpls.2025.1566140>
- Gao Y., Wang C., Wu T., Ma Z., Chen W., Chang H., Jing Y., Tao H., Yu W., Jiang H., Farag M., Zhang Z., Wu J., and Song L., 2024, Multiplex approach of metabolite and transcript profiling identify a biosynthetic mechanism for kavaflavone biosynthesis in *Torreya grandis*, Industrial Crops and Products, 214: 118482.
<https://doi.org/10.1016/j.indcrop.2024.118482>
- Han Y., Wang G., Wu T., Chen W., Ji Y., and Jin S., 2021, Fertilization failed to make positive effects on *Torreya grandis* in severe N-deposition subtropics, Sustainability, 13(17): 9736.
<https://doi.org/10.3390/su13179736>
- Hu S., Wang C., Zhang R., Gao Y., Li K., and Shen J., 2024, Optimizing pollen germination and subcellular dynamics in pollen tube of *Torreya grandis*, Plant Science, 348: 112227.
<https://doi.org/10.1016/j.plantsci.2024.112227>
- Iram A., Dong Y., and Ignea C., 2024, Synthetic biology advances towards a bio-based society in the era of artificial intelligence, Current Opinion in Biotechnology, 87: 103143.
<https://doi.org/10.1016/j.copbio.2024.103143>

- Karabin J., Mansfield I., and Frow E., 2021, Exploring presentations of sustainability by US synthetic biology companies, PLoS One, 16(9): e0257327.
<https://doi.org/10.1371/journal.pone.0257327>
- Kocaoğlu E., Radhakrishnan D., and Nakayama N., 2023, Synthetic developmental biology: molecular tools to re-design plant shoots and roots, Journal of Experimental Botany, 74(13): 3864-3876.
<https://doi.org/10.1093/jxb/erad169>
- Kozaeva E., Eida A., Gunady E., Dangl J., Conway J., and Brophy J., 2024, Roots of synthetic ecology: microbes that foster plant resilience in the changing climate, Current Opinion in Biotechnology, 88: 103172.
<https://doi.org/10.1016/j.copbio.2024.103172>
- Li F., Xie L., Shu X., Wen X., Zhang H., Xing H., Huang L., Xu C., Sun Y., and Lv J., 2025, Application of *Torreya grandis* peel biochar in cadmium contaminated soil remediation and pakchoi growth enhancement, International Journal of Phytoremediation, 27(9): 1178-1187.
<https://doi.org/10.1080/15226514.2025.2485304>
- Lou H., Ding M., Wu J., Zhang F., Chen W., Yang Y., Suo J., Yu W., Xu C., and Song L., 2019, Full-length transcriptome analysis of the genes involved in tocopherol biosynthesis in *Torreya grandis*, Journal of Agricultural and Food Chemistry, 67(7): 1877-1888.
<https://doi.org/10.1021/acs.jafc.8b06138>
- Lou H., Song L., Li X., Zi H., Chen W., Gao Y., Zheng S., Fei Z., Sun X., and Wu J., 2023, The *Torreya grandis* genome illuminates the origin and evolution of gymnosperm-specific sciadonic acid biosynthesis, Nature Communications, 14: 1315.
<https://doi.org/10.1038/s41467-023-37038-2>
- Lou H., Yang Y., Zheng S., Ma Z., Chen W., Yu C., Song L., and Wu J., 2022, Identification of key genes contributing to amino acid biosynthesis in *Torreya grandis* using transcriptome and metabolome analysis, Food Chemistry, 379: 132078.
<https://doi.org/10.1016/j.foodchem.2022.132078>
- Luo X., Wu S., Xue J., Hu H., He Z., Liu X., and Wu F., 2021, The bioactive peptide screening from *Torreya grandis* meal protein hydrolysates, Food Bioscience, 44: 101419.
<https://doi.org/10.1016/j.fbio.2021.101419>
- Lyu Y., Wang Y., and Shen X., 2025, The extraction of *Torreya grandis* growing areas using a spatial-spectral fused attention network and multitemporal sentinel-2 images: a case study of the Kuaiji Mountain region, Agriculture, 15(8): 829.
<https://doi.org/10.3390/agriculture15080829>
- Ma X., Huang D., Huang C., Tong Y., Yuan F., Ma X., Liu H., and Fu S., 2023, The application of nitrogen, phosphorus, and potassium regulate the growth and morphological development of *Torreya grandis* (Taxaceae) saplings, Horticulturae, 9(11): 1203.
<https://doi.org/10.3390/horticulturae9111203>
- McCarty N., and Ledesma-Amaro R., 2019, Synthetic biology tools to engineer microbial communities for biotechnology, Trends in Biotechnology, 37(2): 181-197.
<https://doi.org/10.1016/j.tibtech.2018.11.002>
- Morgan M., Diab J., Gilliam M., and Mortimer J., 2024, Green horizons: how plant synthetic biology can enable space exploration and drive on Earth sustainability, Current Opinion in Biotechnology, 86: 103069.
<https://doi.org/10.1016/j.copbio.2024.103069>
- Quan W., Xu Y., Xie Y., Peng F., and Lin Y., 2022, In vitro antioxidant properties and phenolic profile of acid aqueous ethanol extracts from *Torreya grandis* seed coat, Molecules, 27(17): 5560.
<https://doi.org/10.3390/molecules27175560>
- Raman R., Manalil S., Dénes D., and Nedungadi P., 2024, The role of forestry sciences in combating climate change and advancing sustainable development goals, Frontiers in Forests and Global Change, 7: 1409667.
<https://doi.org/10.3389/ffgc.2024.1409667>
- Roell M., and Zurbruggen M., 2019, The impact of synthetic biology for future agriculture and nutrition, Current Opinion in Biotechnology, 61: 102-109.
<https://doi.org/10.1016/j.copbio.2019.10.004>
- Shen H., Hou Y., Wang X., Li Y., Wu J., and Lou H., 2024, Genome-wide identification, expression analysis under abiotic stress and co-expression analysis of *MATE* gene family in *Torreya grandis*, International Journal of Molecular Sciences, 25(7): 3859.
<https://doi.org/10.3390/ijms25073859>
- Suo J., Tong K., Wu J., Ding M., Chen W., Yang Y., Lou H., Hu Y., Yu W., and Song L., 2019, Comparative transcriptome analysis reveals key genes in the regulation of squalene and β -sitosterol biosynthesis in *Torreya grandis*, Industrial Crops and Products, 131: 182-193.
<https://doi.org/10.1016/j.indcrop.2019.01.035>
- Suo J., Zhou Z., Farag M., Zhang Z., Wu J., Hu Y., and Song L., 2025, Ethylene mitigates nut decay and improves nut quality of *Torreya grandis* during postharvest by changing microbial community composition, Postharvest Biology and Technology, 219: 113250.
<https://doi.org/10.1016/j.postharvbio.2024.113250>
- Tan C., Kalhor M., Faqir Y., Ma J., Osei M., and Khaliq G., 2022, Climate-resilient microbial biotechnology: a perspective on sustainable agriculture, Sustainability, 14(9): 5574.
<https://doi.org/10.3390/su14095574>
- Tao H., Zhu M., Chen M., Liu K., Zhang Z., Song L., and Gao F., 2024, Diversity of flavonoids in five *Torreya grandis* cultivars: integrating metabolome and transcriptome to elucidate potential applications for health and metabolic engineering, Food Research International, 198: 115374.
<https://doi.org/10.1016/j.foodres.2024.115374>

- Wang B., Li Z., Zhou Z., Huang J., Yu H., Peng T., Song Y., and Na X., 2022a, Factors driving the assembly of prokaryotic communities in bulk soil and rhizosphere of *Torreya grandis* along a 900-year age gradient, *The Science of the Total Environment*, 837: 155573.
<https://doi.org/10.1016/j.scitotenv.2022.155573>
- Wang H., Li Y., Wang R., Ji H., Lu C., and Su X., 2022b, Chinese *Torreya grandis* cv. *Merrillii* seed oil affects obesity through accumulation of sciadonic acid and altering the composition of gut microbiota, *Food Science and Human Wellness*, 11(1): 58-67.
<https://doi.org/10.1016/j.fshw.2021.07.007>
- Wang Q., Wang Y., Xie Q., Wang L., Dai W., Yu C., and Wu J., 2024, Integrated transcriptomics and metabolomics unravel the molecular mechanisms governing flavonoid synthesis in *Torreya grandis* under low phosphorus stress, *Industrial Crops and Products*, 210: 118080.
<https://doi.org/10.1016/j.indcrop.2024.118080>
- Yan J., Chen W., Zeng H., Cheng H., Suo J., Yu C., Yang B., Lou H., Song L., and Wu J., 2022, Unraveling the malate biosynthesis during development of *Torreya grandis* nuts, *Current Research in Food Science*, 5: 2309-2315.
<https://doi.org/10.1016/j.crf.2022.11.017>
- Yan J., Zeng H., Chen W., Luo J., Kong C., Lou H., and Wu J., 2023, New insights into the carotenoid biosynthesis in *Torreya grandis* kernels, *Horticultural Plant Journal*, 9(6): 1108-1118.
<https://doi.org/10.1016/j.hpj.2023.02.010>
- Yang Y., Chaffin T., Ahkami A., Blumwald E., and Stewart C., 2022, Plant synthetic biology innovations for biofuels and bioproducts, *Trends in Biotechnology*, 40(12): 1454-1468.
<https://doi.org/10.1016/j.tibtech.2022.09.007>
- Yu C., Zeng H., Wang Q., Chen W., Chen W., Yu W., Lou H., and Wu J., 2022, Multi-omics analysis reveals the molecular responses of *Torreya grandis* shoots to nanoplastic pollutant, *Journal of Hazardous Materials*, 436: 129181.
<https://doi.org/10.1016/j.jhazmat.2022.129181>
- Zhang F., Kong C., Ma Z., Chen W., Li Y., Lou H., and Wu J., 2023, Molecular characterization and transcriptional regulation analysis of the *Torreya grandis* squalene synthase gene involved in sitosterol biosynthesis and drought response, *Frontiers in Plant Science*, 14: 1136643.
<https://doi.org/10.3389/fpls.2023.1136643>
- Zhang J., Hu L., Guo L., Ren W., Zhao L., Wang N., Zhang E., Tang J., and Chen X., 2019, The maintenance of stable yield and high genetic diversity in the agricultural heritage torreya tree system, *BMC Ecology*, 19: 41.
<https://doi.org/10.1186/s12898-019-0256-6>
- Zou G., Li T., Mijakovic I., and Wei Y., 2024, Synthetic biology enables mushrooms to meet emerging sustainable challenges, *Frontiers in Microbiology*, 15: 1337398.
<https://doi.org/10.3389/fmicb.2024.1337398>

**Disclaimer/Publisher's Note**

The statements, opinions, and data contained in all publications are solely those of the individual authors and contributors and do not represent the views of the publishing house and/or its editors. The publisher and/or its editors disclaim all responsibility for any harm or damage to persons or property that may result from the application of ideas, methods, instructions, or products discussed in the content. Publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.