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Comprehensive Genomic Analysis of *Atractylodes macrocephala*: Unveiling Its Medicinal Functions and Genetic Secrets

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Abstract *Atractylodes macrocephala* is a key herb in traditional medicine with diverse medicinal properties. This study provides an overview of its botanical, phytochemical, pharmacological, and genomic aspects, highlighting its potential in modern medicine and agriculture. The study covers the morphological characteristics, geographic distribution, and cultivation techniques of *A. macrocephala*. It details the phytochemical composition, methods of analysis, and biological activities. Traditional medicinal uses and pharmacological activities such as antioxidant, anti-inflammatory, immunomodulatory, antimicrobial, and antiviral properties are discussed. Genomic analysis includes genome sequencing, functional gene annotation, and comparative genomics. The genetic basis of medicinal properties, including key genes and pathways, phytochemical biosynthesis, and pharmacological activities, is examined. Biotechnological applications like genetic engineering, breeding, conservation, and synthetic biology are also studied. This study consolidates knowledge on *A. macrocephala*, emphasizing its traditional and modern applications. Future research should address knowledge gaps, leverage emerging technologies, and integrate genomic data with traditional knowledge to enhance its medicinal and agricultural use.

Keywords *Atractylodes macrocephala*; Traditional medicine; Phytochemicals; Genomic analysis; Biotechnological applications

1 Introduction

Atractylodes macrocephala Koidz., commonly known as Baizhu in China, is a perennial herb belonging to the Asteraceae family. It is widely distributed across East Asia and is cultivated primarily in China, Japan, and Korea for its medicinal properties (Zhu et al., 2018; Liu et al., 2022). The plant has been extensively studied for its phytochemical composition, revealing a rich array of bioactive compounds including sesquiterpenoids, triterpenoids, polyacetylenes, and polysaccharides (Zhu et al., 2018; Yang et al., 2021). The complete plastome sequence of *A. macrocephala* has been characterized, providing valuable insights into its genetic makeup and evolutionary relationships within the *Atractylodes* genus (Cai et al., 2020; Wang et al., 2020).

Atractylodes macrocephala holds a significant place in traditional Chinese medicine (TCM) and other East Asian medical systems. It has been used for centuries as a tonic agent to treat a variety of ailments including gastrointestinal dysfunction, cancer, osteoporosis, obesity, and fetal irritability (Chen et al., 2018; Zhu et al., 2018). The dried rhizome of *A. macrocephala*, known as Baizhu, is particularly valued for its ability to invigorate the spleen, replenish qi, and remove dampness (Yang et al., 2021). Modern pharmacological studies have confirmed its diverse therapeutic effects, such as anti-tumor, anti-inflammatory, and immunomodulatory activities (Zhu et al., 2018; Gu et al., 2019; Bailly, 2020). The plant's essential oils and specific compounds like atractylenolides have shown promising antioxidant, anti-inflammatory, and anticancer properties (Gu et al., 2019; Bailly, 2020).

This study aims to provide a comprehensive genomic analysis of *Atractylodes macrocephala*, integrating its medicinal functions and genetic secrets. This study summarizes the current knowledge on the phytochemistry and pharmacology of *Atractylodes macrocephala*, explores the genetic diversity and evolutionary relationships within the Asteraceae family, investigates the molecular mechanisms underlying the medicinal properties of *Atractylodes macrocephala*, and identifies potential areas for future research to enhance the therapeutic applications and conservation of this valuable medicinal herb.

2 Botanical Characteristics and Cultivation

2.1 Morphological description

Atractylodes macrocephala, commonly known as Baizhu in China, is a perennial herb belonging to the Asteraceae family. The plant is characterized by its thick, cylindrical rhizomes, which are the primary medicinal part used in traditional medicine. The leaves are alternate, simple, and have a lanceolate to ovate shape with serrated margins. The flowers are small, white to pale yellow, and are arranged in dense capitula. The plant typically blooms from July to September, and the seeds mature from August to Octobe (Figure 1) (Chen et al., 2018; Zhu et al., 2018; Wang et al., 2020).

Figure 1 Graphic representation of features identified in the plastome of three *Atractylodes* species by using CPGAVAS2 (Adopted from Wang et al., 2020)

Image caption: The map contains four rings. From the center going outward, the first circle shows the forward and reverse repeats connected with red and green arcs, respectively. The next circle shows the tandem repeats marked with short bars. The third circle shows the microsatellite sequences identified using MISA. The fourth circle is drawn using drawgenemap and shows the gene structure on the plastome. The genes were colored based on their functional categories, which are shown at the left corner (Adopted from Wang et al., 2020)

2.2 Geographic distribution

Atractylodes macrocephala is native to East Asia, with its primary distribution in China, Korea, and Japan. In China, it is predominantly found in the provinces of Zhejiang, Anhui, Hunan, and Shaanxi. The plant thrives in temperate climates and is commonly found in mountainous regions and forest edges. The geographic distribution of *A. macrocephala* is influenced by its preference for well-drained, fertile soils and a climate with moderate rainfall (Chen et al., 2018; Zhu et al., 2018; Liu et al., 2022).

2.3 Agricultural practices and cultivation techniques

The cultivation of *Atractylodes macrocephala* has a long history in China, where it is grown for its medicinal rhizomes. The plant is typically propagated through seed or rhizome division. The following are key agricultural practices and cultivation techniques for *A. macrocephala*:

Soil Preparation: The soil should be well-drained, fertile, and rich in organic matter. Prior to planting, the soil is plowed and amended with compost or well-rotted manure to enhance fertility.

Planting: Seeds are sown in the spring, while rhizome divisions are planted in the autumn. The planting depth for seeds is about 1-2 cm, and for rhizome divisions, it is 5-10 cm. The spacing between plants is typically 30-40 cm.

Watering: Regular watering is essential, especially during the initial stages of growth. However, overwatering should be avoided to prevent root rot.

Weeding and Mulching: Weeding is necessary to reduce competition for nutrients and water. Mulching with straw or other organic materials helps retain soil moisture and suppress weeds.

Fertilization: Organic fertilizers, such as compost or manure, are applied during planting and as a top dressing during the growing season. Inorganic fertilizers may also be used to supplement nutrient requirements.

Pest and Disease Management: Common pests include aphids and root-knot nematodes, while diseases such as leaf spot caused by Fusarium commune can affect the plant. Integrated pest management (IPM) strategies, including crop rotation, biological control, and the use of resistant varieties, are employed to manage these issues (Chen et al., 2018; Zhu et al., 2018; Fan et al., 2022).

In summary, the successful cultivation of *Atractylodes macrocephala* involves careful attention to soil preparation, planting techniques, watering, weeding, fertilization, and pest and disease management. These practices ensure the healthy growth of the plant and the production of high-quality medicinal rhizomes.

3 Phytochemical Composition

3.1 Overview of key phytochemicals

Atractylodes macrocephala, a traditional Chinese medicinal herb, is rich in a variety of phytochemicals. Over 79 chemical compounds have been identified, including sesquiterpenoids, triterpenoids, polyacetylenes, coumarins, phenylpropanoids, flavonoids, flavonoid glycosides, steroids, benzoquinones, and polysaccharides (Zhu et al., 2018). Among these, sesquiterpenoids and polysaccharides are particularly notable for their medicinal properties (Zhu et al., 2018; Si et al., 2021; Liu et al., 2022). The sesquiterpenoids, such as atractylone, have been extensively studied for their neuroprotective and anti-inflammatory activities (Gu et al., 2019; Si et al., 2021). Polysaccharides from *A. macrocephala* are composed of glucose, galactose, rhamnose, arabinose, mannose, galacturonic acid, and xylose, and exhibit significant immunomodulatory and antitumor activities (Liu et al., 2022).

3.2 Methods of phytochemical analysis

The phytochemical analysis of *Atractylodes macrocephala* involves several advanced techniques. High-Performance Liquid Chromatography (HPLC) and Gas Chromatography-Mass Spectrometry (GC-MS) are commonly used to identify and quantify the chemical constituents (Gu et al., 2019; Si et al., 2021). Nuclear magnetic resonance (NMR) spectroscopy and high-resolution electrospray ionization mass spectrometry (HRESIMS) are employed to elucidate the structures of isolated compounds (Wang et al., 2018; Si et al., 2021). Additionally, electronic circular dichroism (ECD) and X-ray diffraction analyses are used to determine the stereochemistry of sesquiterpenoids (Si et al., 2021). These methods ensure a comprehensive understanding of the phytochemical profile of *A. macrocephala*.

3.3 Biological activities of phytochemicals

The phytochemicals in *Atractylodes macrocephala* exhibit a wide range of biological activities. Sesquiterpenoids, such as atractylone, have shown significant anti-inflammatory and neuroprotective effects by inhibiting nitric oxide production and interleukin-6 (IL-6) in microglia cells (Gu et al., 2019; Si et al., 2021). Polysaccharides from *A. macrocephala* have demonstrated immunomodulatory, antitumor, gastroprotective, and hepatoprotective activities (Liu et al., 2022). Essential oils from the plant also exhibit antitumor, antiviral, and anti-inflammatory properties, with variations in efficacy depending on the processing methods used (Gu et al., 2019). Furthermore, the plant's extracts have been found to reduce uric acid levels and improve renal injury in hyperuricemia and gouty arthritis models, highlighting its potential in treating inflammatory conditions (Qian et al., 2022).

The diverse phytochemical composition of *Atractylodes macrocephala* underpins its extensive medicinal applications. Advanced analytical techniques have facilitated the identification and structural elucidation of these compounds, while numerous studies have confirmed their significant biological activities, supporting the traditional uses of this valuable herb.

4 Medicinal Uses and Pharmacological Activities

4.1 Traditional medicinal uses

Atractylodes macrocephala, commonly known as Baizhu in China, has been extensively used in traditional Chinese medicine (TCM) for centuries. It is primarily employed as a tonic agent to treat various ailments such as gastrointestinal dysfunction, cancer, osteoporosis, obesity, and fetal irritability (Zhu et al., 2018). The plant's rhizomes are particularly valued for their ability to invigorate the spleen, eliminate dampness, and enhance overall vitality (Gu et al., 2019). Traditional applications also include the treatment of arthritis, splenic asthenia, abnormal fetal movement, Alzheimer’s disease, and obesity (Zhu et al., 2018).

4.2 Antioxidant properties

The essential oils derived from *Atractylodes macrocephala* exhibit significant antioxidant activities. Studies have shown that these oils possess strong ferricyanide reducing power and effective scavenging abilities against 1,1-diphenyl-2-picrylhydrazyl (DPPH) and 3-ethyl-benzothiazoline-6-sulfonic acid (ABTS) radicals (Wu et al., 2020). The major compounds contributing to these antioxidant properties include atractylone, β-eudesmol, thymol, and hinesol (Wu et al., 2020). These findings suggest that *A. macrocephala* can be a potent natural antioxidant source, potentially useful in preventing oxidative stress-related diseases.

4.3 Anti-inflammatory and immunomodulatory effects

Atractylodes macrocephala has demonstrated notable anti-inflammatory and immunomodulatory effects. The plant's extracts and isolated compounds, such as atractylenolide I, have been shown to inhibit the production of nitric oxide (NO) and prostaglandin E2 (PGE2) in lipopolysaccharide (LPS)-activated macrophages (Jeong et al., 2019). Additionally, these compounds suppress the expression of inducible nitric oxide synthase (iNOS) and cyclooxygenase-2 (COX-2) at both protein and mRNA levels (Jeong et al., 2019). The anti-inflammatory activity is further supported by the inhibition of nuclear factor-kappa B (NF-κB) activation and the reduction of pro-inflammatory cytokines such as IL-1β, IL-6, and TNF-α (Jeong et al., 2019; Yang et al., 2020). These properties make *A. macrocephala* a promising candidate for treating inflammatory diseases.

4.4 Antimicrobial and antiviral activities

The essential oils and extracts of *Atractylodes macrocephala* also exhibit antimicrobial and antiviral activities. The oils have shown inhibitory effects against various bacterial strains, including *Escherichia coli*, *Pseudomonas aeruginosa*, *Salmonella enterica*, *Staphylococcus aureus*, and *Bacillus subtilis*, with minimum inhibitory concentrations (MIC) ranging from 0.5 to 2.0 mg/mL (Wu et al., 2020). Additionally, the essential oils have demonstrated antiviral effects, particularly against the H3N2 virus (Gu et al., 2019). These findings highlight the potential of *A. macrocephala* as a natural antimicrobial and antiviral agent.

4.5 Other pharmacological effects

Beyond its antioxidant, anti-inflammatory, and antimicrobial properties, *Atractylodes macrocephala* exhibits a range of other pharmacological activities. The plant has been found to possess anti-tumor properties, with essential oils and atractylone showing efficacy against cancer cell lines such as HepG2, MCG803, and HCT-116 (Gu et al., 2019). Furthermore, *A. macrocephala* has been reported to have anti-hyperuricemic effects, reducing serum uric acid levels and improving renal injury and fibrosis in hyperuricemia models (Qian et al., 2022). The plant also shows potential in treating chronic gastritis by influencing inflammatory responses, amino acid synthesis, and energy metabolism (Yang et al., 2020). These diverse pharmacological effects underscore the therapeutic potential of *A. macrocephala* in various medical conditions (Figure 2).

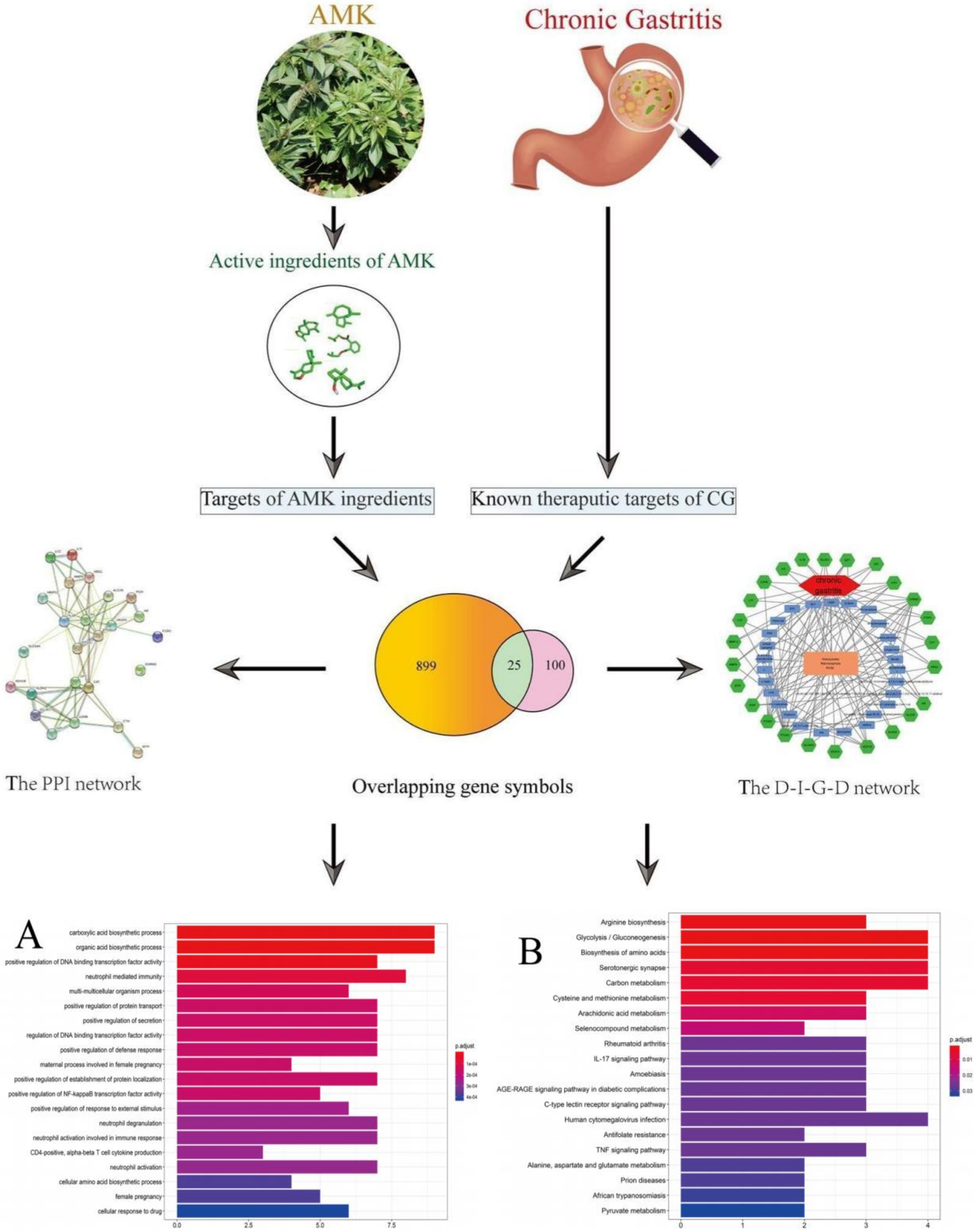

Figure 2 Flowchart of a network pharmacology-based strategy to investigate the pharmacologic mechanisms of *Atractylodes macrocephala* Koidz. for treatment of chronic gastritis (Adopted from Yang et al., 2020)

Image caption: (A) GO analyses of the 25 gene symbols associated with chronic gastritis. The x-axis represents significant enrichment in the counts of these terms. The y-axis represents the categories of “biological process” in the GO of the target genes ($p < 0.01$). (B) KEGG pathway enrichment analyses. The x-axis represents the counts of the target symbols in each pathway; the y-axis represents the main pathways ($p < 0.01$) (Adopted from Yang et al., 2020)

5 Genomic Analysis

5.1 Overview of genomic studies on *Atractylodes macrocephala*

Atractylodes macrocephala, a prominent medicinal herb in traditional Chinese medicine, has been the subject of various genomic studies aimed at understanding its genetic makeup and medicinal properties. These studies have provided insights into the plant's genetic diversity, phylogenetic relationships, and the molecular basis of its pharmacological activities. For instance, the complete plastome sequence of *A. macrocephala* has been analyzed, revealing a genome length of 153 265 bp with typical quadripartite structures common to Asteraceae species (Cai et al., 2020). Additionally, phylogenetic analyses have been conducted to explore the relationships between *A. macrocephala* and other species within the *Atractylodes* genus, highlighting the complex evolutionary history and potential hybridization events (Wang et al., 2020; Liu et al., 2022).

5.2 Genome sequencing and assembly

The genome sequencing of *Atractylodes macrocephala* has been a significant milestone in understanding its genetic framework. The complete plastome sequence was determined to be 153,265 bp in length, comprising a large single-copy (LSC) region of 84,311 bp, a small single-copy (SSC) region of 18,674 bp, and a pair of inverted repeat (IR) regions of 25,140 bp each (Cai et al., 2020). This sequencing effort has provided a comprehensive view of the genetic structure, including 107 unique genes, which consist of 80 protein-coding genes, 23 tRNA genes, and 4 rRNA genes. The overall GC content of the genome is 37.7%, which is consistent with other members of the Asteraceae family (Cai et al., 2020).

5.3 Annotation of functional genes

Functional annotation of the *Atractylodes macrocephala* genome has identified numerous genes associated with its medicinal properties. For example, high-throughput RNA sequencing has revealed 114 572 unigenes, with 3 570 differentially expressed genes (DEGs) between one-year and three-year growth rhizomes. These DEGs include genes involved in terpenoid synthesis, which are crucial for the plant's pharmacological activities (Fang et al., 2022). Additionally, the identification of autotoxic compounds such as 2,4-Ditertbutyl phenol (2,4-DP) and their impact on the plant's immune system has been explored, providing insights into the molecular mechanisms underlying autotoxicity and systemic acquired resistance (SAR) (Zheng et al., 2018).

5.4 Comparative genomics with related species

Comparative genomic studies have been instrumental in elucidating the evolutionary relationships between *Atractylodes macrocephala* and related species. Phylogenetic analyses using plastome and nuclear gene sequences have shown that *A. macrocephala* shares a high degree of genetic similarity with *A. lancea* and *A. chinensis*, suggesting potential hybridization events (Figure 3) (Wang et al., 2020; Liu et al., 2022). The identification of molecular markers has facilitated the differentiation of these species, despite their morphological similarities (Wang et al., 2020). Furthermore, the cytonuclear discordance observed in the genus *Atractylodes* highlights the complex phylogenetic history and the role of interspecific hybridization in shaping the genetic landscape of these medicinal plants (Liu et al., 2022). In summary, the genomic analysis of *Atractylodes macrocephala* has provided valuable insights into its genetic composition, functional genes, and evolutionary relationships. These findings not only enhance our understanding of the plant's medicinal properties but also pave the way for future research aimed at improving its cultivation and therapeutic applications.

6 Genetic Basis of Medicinal Properties

6.1 Identification of key genes and pathways

Atractylodes macrocephala, a traditional Chinese medicinal herb, has been extensively studied to identify the genetic basis underlying its medicinal properties. Recent genomic analyses have revealed several key genes and pathways that contribute to its pharmacological activities. For instance, the complete plastome sequence of *A. macrocephala* has been characterized, providing insights into its genetic makeup and evolutionary relationships with other species in the *Atractylodes* genus (Cai et al., 2020). Additionally, studies have identified differentially expressed genes (DEGs) in *A. macrocephala* rhizomes from different growth years, highlighting genes involved in terpenoid synthesis, which are crucial for its medicinal properties (Fang et al., 2022). Network pharmacology approaches have also been employed to identify active ingredients and drug targets, revealing key pathways such as the interleukin-17 signaling pathway and the tumor necrosis factor signaling pathway, which are implicated in the treatment of chronic gastritis (Yang et al., 2020).

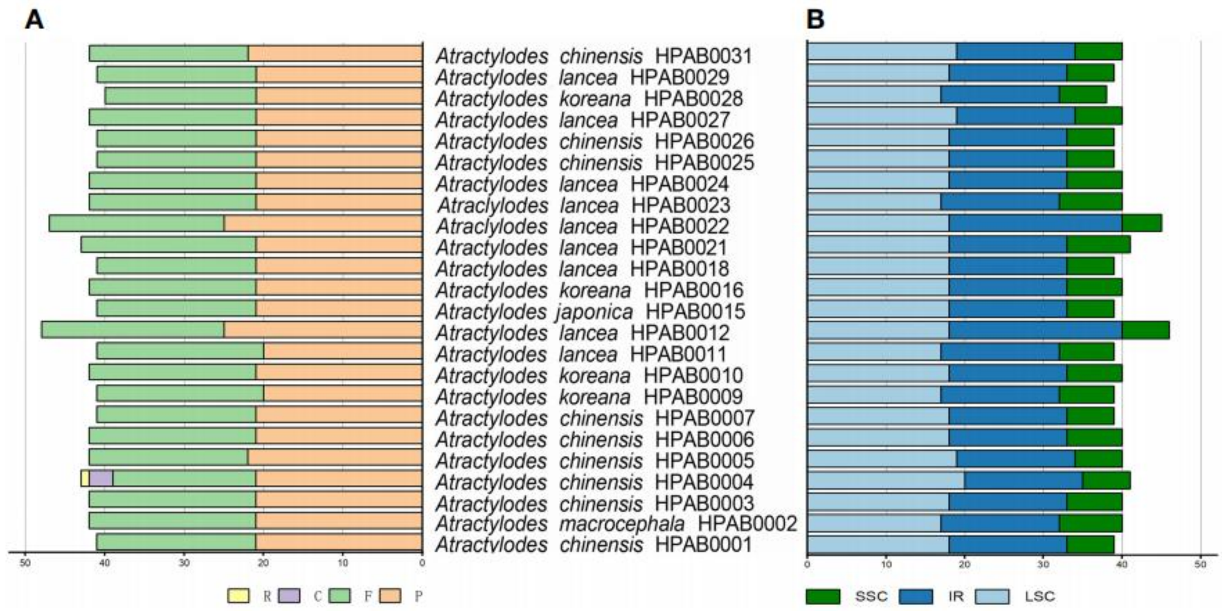

Figure 3 The types and distribution of repeat sequences in 24 *Atractylodes* plastid genomes (Adopted from Liu et al., 2022)

Image caption: (A) The number of each of the four repeat types (F, forward; P, palindrome; R, reverse; C, complement). (B) The distribution of repeat sequences across three regions: LSC, SSC, and IR (Adopted from Liu et al., 2022)

6.2 Genetic regulation of phytochemical biosynthesis

The biosynthesis of phytochemicals in *A. macrocephala* is tightly regulated by its genetic makeup. Studies have shown that the expression of genes involved in terpenoid synthesis is significantly different between one-year and three-year growth rhizomes, with a notable downregulation in the latter (Fang et al., 2022). This suggests that the age of the plant influences the accumulation of bioactive compounds. Furthermore, the complete plastome sequence analysis has identified 107 unique genes, including those coding for proteins, tRNAs, and rRNAs, which play a role in the biosynthesis of various phytochemicals (Cai et al., 2020). The genetic diversity observed in cultivated and wild populations of *A. macrocephala* also indicates that domestication has impacted the genetic regulation of phytochemical biosynthesis, with certain landraces harboring unique gene pools that could be valuable for breeding programs aimed at enhancing medicinal quality (Chen et al., 2018).

6.3 Genomic insights into pharmacological activities

Genomic studies have provided valuable insights into the pharmacological activities of *A. macrocephala*. The identification of sesquiterpenoids and other bioactive compounds from its rhizomes has been linked to its anti-inflammatory, anti-tumor, and neuroprotective effects (Si et al., 2021). For example, sesquiterpenoids isolated from *A. macrocephala* have shown significant inhibition of nitric oxide production in microglia cells, suggesting their potential in treating neuroinflammatory conditions (Si et al., 2021). Additionally, the genetic analysis of *A. macrocephala* has revealed its potential in treating hyperuricemia and gouty arthritis by modulating the AMPK/SIRT1 signaling pathway and inhibiting NF-κB activation (Qian et al., 2022). These findings underscore the importance of genetic studies in understanding the molecular mechanisms underlying the medicinal properties of *A. macrocephala* and in developing new therapeutic applications.

In conclusion, the comprehensive genomic analysis of *Atractylodes macrocephala* has unveiled key genes and pathways involved in its medicinal functions, the genetic regulation of phytochemical biosynthesis, and the genomic insights into its pharmacological activities. These findings provide a solid foundation for future research aimed at enhancing the medicinal quality and therapeutic potential of this valuable herb.

7 Biotechnological Applications

7.1 Genetic engineering for enhanced phytochemical production

Atractylodes macrocephala, a traditional Chinese medicinal herb, has been extensively studied for its diverse pharmacological properties, including anti-inflammatory, anti-tumor, and neuroprotective activities (Yao and Yang, 2014; Zhu et al., 2018; Si et al., 2021). Genetic engineering offers a promising approach to enhance the production of these valuable phytochemicals. For instance, sesquiterpenoids, which are known for their neuroprotective effects, can be produced in higher quantities through the manipulation of specific biosynthetic pathways (Si et al., 2021). Additionally, the identification of key genes involved in the synthesis of terpenoids and polyacetylenes provides targets for genetic modification to boost their production (Fang et al., 2022). The use of high-throughput RNA sequencing has revealed differentially expressed genes that could be manipulated to optimize the yield of these bioactive compounds (Fang et al., 2022).

7.2 Genomic tools for breeding and conservation

The conservation and breeding of *A. macrocephala* can greatly benefit from genomic tools. Studies utilizing chloroplast DNA and microsatellites have shown that cultivated populations of *A. macrocephala* possess higher genetic diversity compared to their wild counterparts, which is crucial for breeding programs aimed at improving medicinal quality (Chen et al., 2018). Furthermore, the complete plastome sequence of *A. macrocephala* has been characterized, providing a comprehensive genetic resource that can be used for phylogenetic studies and the identification of molecular markers for breeding (Cai et al., 2020). Cryopreservation techniques, such as droplet-vitrification, have also been developed to conserve the genetic resources of *A. macrocephala*, ensuring the long-term preservation of its valuable germplasm (Zhang et al., 2015).

7.3 Potential for synthetic biology approaches

Synthetic biology offers innovative strategies to harness the medicinal potential of *A. macrocephala*. By constructing synthetic pathways in microbial hosts, it is possible to produce complex phytochemicals in a controlled environment. The complete plastome and nuclear gene sequences of *A. macrocephala* provide a blueprint for the design of synthetic pathways (Cai et al., 2020; Wang et al., 2020). Additionally, the identification of molecular markers and the understanding of the genetic relationships among *Atractylodes* species can facilitate the development of synthetic biology approaches to produce specific bioactive compounds (Wang et al., 2020; Liu et al., 2022). The integration of genomic data with synthetic biology could lead to the scalable production of high-value phytochemicals, thereby enhancing the medicinal applications of *A. macrocephala*.

In summary, the application of genetic engineering, genomic tools, and synthetic biology holds significant promise for enhancing the phytochemical production, breeding, conservation, and medicinal utilization of *Atractylodes macrocephala*. These biotechnological advancements can lead to the development of more effective and sustainable medicinal products derived from this valuable herb.

8 Future Perspectives and Research Directions

8.1 Gaps in current knowledge

Despite significant advancements in understanding the medicinal properties and genetic makeup of *Atractylodes macrocephala*, several gaps remain. Firstly, while numerous bioactive compounds have been identified, the precise molecular mechanisms and structure-function relationships of these constituents are not fully understood (Zhu et al., 2018). Additionally, the potential synergistic and antagonistic effects among these compounds require further investigation (Zhu et al., 2018). The genetic diversity and population structure of *A. macrocephala* have been studied, but the impact of domestication on its genetic resources and the conservation of unique gene pools need more comprehensive analysis (Chen et al., 2018). Furthermore, the autotoxic effects of certain compounds on the plant's immune system and their broader ecological impacts are not well-documented (Zheng et al., 2018).

8.2 Emerging technologies and approaches

Emerging technologies such as next-generation sequencing (NGS) and network pharmacology offer promising avenues for advancing our understanding of *A. macrocephala*. The complete plastome and chloroplast genome sequencing have already provided valuable insights into the genetic structure and phylogenetic relationships of this species (Cai et al., 2020; Li and Yang, 2020; Wang et al., 2020). These genomic tools can be further utilized to identify specific molecular markers for distinguishing between closely related species and understanding their evolutionary relationships (Wang et al., 2020). Network pharmacology can elucidate the complex interactions between bioactive compounds and their targets, offering a systematic approach to uncovering the mechanisms of action in treating diseases like chronic gastritis (Yang et al., 2020). Additionally, advanced metabolomic techniques such as 1H NMR spectroscopy can aid in the precise identification and classification of *Atractylodes* species, enhancing the quality control of medicinal products (Shirahata et al., 2021).

8.3 Integration of genomic data with traditional knowledge

Integrating genomic data with traditional knowledge of *A. macrocephala* can lead to a more holistic understanding of its medicinal properties. Traditional uses of *A. macrocephala* in treating various ailments are well-documented, but combining this ethnopharmacological knowledge with modern genomic and pharmacological data can validate and potentially expand its therapeutic applications (Zhu et al., 2018). For instance, understanding the genetic basis of bioactive compound production can help in the selective breeding of high-yielding and disease-resistant varieties (Chen et al., 2018). Moreover, integrating genomic insights with traditional processing methods can optimize the extraction and efficacy of essential oils and other bioactive compounds (Gu et al., 2019). This interdisciplinary approach can bridge the gap between traditional practices and modern scientific research, paving the way for innovative therapeutic strategies and sustainable cultivation practices.

By addressing these gaps and leveraging emerging technologies, future research can unlock the full potential of *Atractylodes macrocephala*, ensuring its continued relevance and efficacy in modern medicine.

9 Concluding Remarks

Atractylodes macrocephala, a traditional medicinal plant widely used in East Asia, has been the subject of extensive genomic and pharmacological research. The complete plastome sequence of *A. macrocephala* has been characterized, revealing a genome of 153 265 bp with 107 unique genes, including 80 protein-coding genes, 23 tRNA genes, and 4 rRNA genes. This genomic information provides a foundation for understanding the genetic basis of its medicinal properties. Phylogenetic analyses have confirmed the monophyletic nature of *Atractylodes* and its close relationship with other species in the Cardueae tribe. Phytochemical studies have identified over 79 chemical compounds in *A. macrocephala*, including sesquiterpenoids, triterpenoids, polyacetylenes, and polysaccharides, which contribute to its diverse pharmacological activities. These compounds exhibit anti-tumor, anti-inflammatory, anti-aging, anti-oxidative, and neuroprotective effects, among others. Network pharmacology has further elucidated the molecular mechanisms underlying these effects, highlighting key pathways such as the interleukin-17 signaling pathway and the tumor necrosis factor signaling pathway.

The comprehensive genomic and pharmacological insights into *A. macrocephala* have significant implications for both medicine and agriculture. In medicine, the identification of bioactive compounds and their mechanisms of action supports the traditional use of *A. macrocephala* in treating various ailments, including gastrointestinal dysfunction, cancer, and inflammatory diseases. The anti-hyperuricemic and anti-inflammatory properties of *A. macrocephala*, demonstrated in animal models, suggest its potential as a therapeutic agent for conditions such as gout and rheumatoid arthritis. In agriculture, the genomic data can be leveraged to improve the cultivation and quality control of *A. macrocephala*. Understanding the genetic basis of its medicinal properties can inform breeding programs aimed at enhancing the production of bioactive compounds. Additionally, the identification of molecular markers can aid in the accurate identification and differentiation of *A. macrocephala* from related species, ensuring the authenticity and efficacy of medicinal products.

The research on *Atractylodes macrocephala* has unveiled its genetic secrets and medicinal functions, providing a robust foundation for future studies. However, several areas warrant further investigation. The molecular mechanisms and structure-function relationships of the identified bioactive compounds need to be elucidated in greater detail. Additionally, the potential synergistic and antagonistic effects of these compounds should be explored to optimize their therapeutic efficacy. Future research should also focus on the long-term toxicity and clinical efficacy of *A. macrocephala*, ensuring its safe and effective use in modern medicine. The integration of genomic, phytochemical, and pharmacological data will be crucial in developing standardized and high-quality medicinal products. Overall, the continued exploration of *A. macrocephala* holds promise for advancing both traditional and modern medicinal practices, as well as enhancing agricultural practices for this valuable herb.

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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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