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Genomic Studies of *Achyranthes bidentata*: Understanding Its Medicinal Potential and Evolutionary Traits

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Abstract This study aims to explore the genomic foundations of *Achyranthes bidentata*'s medicinal potential and evolutionary traits. By synthesizing current research, we seek to understand the genetic markers, evolutionary adaptations, and pharmacological properties that contribute to its therapeutic efficacy and evolutionary success. Key discoveries include the identification of biosynthetic and transport genes associated with medicinal components such as oleanolic acid and ecdysterone. Adaptive genetic variations driven by environmental factors, particularly temperature and precipitation, have been identified, highlighting the species' ecological adaptability. Comparative chloroplast genome analysis has revealed a highly conserved structure among Achyranthes species, supporting their monophyletic origin and close phylogenetic relationships. Additionally, novel polysaccharides and fructooligosaccharides from *A. bidentata* have demonstrated significant antioxidant and osteoprotective activities, further underscoring its medicinal potential. The genomic insights into *Achyranthes bidentata* provide a deeper understanding of its medicinal properties and evolutionary adaptations. These findings have significant implications for the development of new pharmacological agents and the conservation of this valuable medicinal plant. Future research should focus on elucidating the structure-activity relationships of its bioactive compounds and the long-term effects of its therapeutic use.

Keywords *Achyranthes bidentata*; Genomic studies; Medicinal plants; Evolutionary traits; Pharmacogenomics

1 Introduction

Achyranthes bidentata, a member of the Amaranthaceae family, is a perennial herb widely distributed in China and other parts of Asia. It has been traditionally used in Chinese medicine for centuries, primarily for its therapeutic properties in treating conditions such as osteoporosis, arthritis, and bone hyperplasia (Li et al., 2019). The plant's medicinal potential is largely attributed to its rich composition of bioactive compounds, including saponins, polysaccharides, and various other phytochemicals (Wang et al., 2022). Recent genomic studies have provided deeper insights into the genetic makeup of *A. bidentata*, revealing a highly conserved chloroplast genome structure that is crucial for species identification and phylogenetic analysis (Yuan et al., 2021).

Achyranthes bidentata holds a significant place in traditional Chinese medicine (TCM), where it is commonly used to treat a variety of ailments, including lumbago, arthritis, and bone-related disorders (Lin et al., 2021). The plant's roots, known as Achyranthis Bidentatae Radix, are particularly valued for their anti-inflammatory, anti-osteoporotic, and antioxidant properties. Studies have shown that the polysaccharides extracted from *A. bidentata* can significantly promote osteogenic activity, making it a promising candidate for developing anti-osteoporosis treatments (Zhang et al., 2018). Additionally, the plant's saponins have been systematically characterized, revealing a complex array of compounds that contribute to its medicinal efficacy.

The primary objective of this study is to consolidate and analyze existing genomic studies on *Achyranthes bidentata* to better understand its medicinal potential and evolutionary traits. This study aims to summarize the current knowledge on the genetic and phytochemical composition of *A. bidentata*, and highlight its therapeutic applications, particularly in traditional medicine. Additionally, it discusses the evolutionary relationships and phylogenetic positioning of *A. bidentata* within the Amaranthaceae family, identifies gaps in the current research, and suggests directions for future studies to further explore the medicinal and genetic attributes of this valuable herb. By synthesizing findings from multiple research papers, this study seeks to provide a comprehensive understanding of Achyranthes bidentata, thereby facilitating its effective utilization in both traditional and modern medicinal practices.

2 Botanical and Morphological Characteristics

2.1 Taxonomy and classification

Achyranthes bidentata Blume belongs to the family Amaranthaceae. It is closely related to other species within the genus Achyranthes, such as *Achyranthes aspera* and *Achyranthes longifolia*, as well as species from the genus *Cyathula* (Li et al., 2019). Phylogenetic analyses based on chloroplast genome data have shown that *A. bidentata* is closely related to *Cyathula capitata* and *Alternanthera philoxeroides*, indicating a monophyletic origin for the genus Achyranthes (Park et al., 2019).

2.2 Morphological description

Achyranthes bidentata is a perennial herb that is well-known for its medicinal properties. The plant typically features a robust, erect stem and opposite, simple leaves. The flowers are small, greenish, and arranged in dense spikes. The seeds are small and enclosed in a hard, bidentate (two-toothed) capsule, which is a distinctive feature of the species. The morphological similarities between *A. bidentata* and other species like *A. aspera* often lead to their interchangeable use in traditional medicine, necessitating precise molecular identification methods (Yuan et al., 2021).

2.3 Habitat and geographic distribution

Achyranthes bidentata is native to East Asia, particularly China, Japan, and Korea, where it is commonly found in various habitats ranging from lowland areas to mountainous regions (Yang et al., 2022). The plant thrives in well-drained soils and can often be found in fields, roadsides, and forest edges. Its widespread distribution and adaptability to different environmental conditions contribute to its availability and use in traditional medicine across these regions (Singh et al., 2020).

3 Phytochemical Composition

3.1 Overview of active compounds

Achyranthes bidentata, a prominent medicinal plant, is known for its diverse array of bioactive compounds. These compounds include saponins, flavonoids, and polysaccharides, which contribute to its therapeutic properties. The presence of these phytochemicals underpins the plant's use in traditional medicine systems across various cultures, including Chinese, Japanese, and Korean pharmacopoeias (Singh et al., 2020).

3.2 Methods for phytochemical analysis

The identification and quantification of phytochemicals in *Achyranthes bidentata* are crucial for understanding its medicinal potential. Advanced techniques such as DNA barcoding and chloroplast genome sequencing have been employed to authenticate and analyze the plant species. DNA barcoding, particularly using the internal transcribed spacer 2 (ITS2) region, has proven effective in distinguishing Achyranthes species through genetic divergence and secondary structure modeling1. Additionally, the complete chloroplast genome sequencing provides comprehensive genetic information, facilitating accurate species identification and further phytochemical analysis (Park et al., 2019).

3.3 Pharmacological properties of key compounds

The bioactive compounds in *Achyranthes bidentata* exhibit a range of pharmacological properties. Saponins, for instance, are known for their anti-inflammatory and immunomodulatory effects, making them valuable in treating conditions such as osteodynia and spasms (Yuan et al., 2021). Flavonoids possess antioxidant properties, contributing to the plant's ability to mitigate oxidative stress and related ailments. Polysaccharides, on the other hand, enhance the immune response and exhibit potential anti-cancer activities. These pharmacological properties underscore the medicinal significance of *Achyranthes bidentata* and its potential in developing therapeutic agents (Singh et al., 2020).

4 Medicinal Uses and Applications

4.1 Traditional uses in Chinese medicine

Achyranthes bidentata, commonly known as Huai Niu Xi, has been a staple in traditional Chinese medicine (TCM) for centuries. It is primarily used to treat conditions related to bone health, such as osteoporosis and bone nonunion (Li et al., 2019; Dong et al., 2024). Additionally, it is employed in the treatment of spasms, osteodynia of the lumbar region, and knee pain4. The herb is also mentioned in the pharmacopoeias of Japan and Korea, highlighting its widespread traditional use in East Asian medicine (Singh et al., 2020).

4.2 Modern clinical applications

In modern clinical settings, *Achyranthes bidentata* continues to be valued for its therapeutic properties. Recent pharmacological studies have demonstrated its antioxidant and antidiabetic activities. The methanolic extracts of *A. bidentata* have shown significant free radical scavenging abilities and α-amylase inhibition, indicating potential benefits in managing oxidative stress and diabetes6. Furthermore, molecular techniques such as DNA barcoding and allele-specific PCR have been developed to ensure the accurate identification and quality control of *A. bidentata* in herbal formulations, which is crucial for its clinical application (Park et al., 2019).

4.3 Comparative analysis with other medicinal plants

When compared to other medicinal plants, *Achyranthes bidentata* exhibits unique pharmacological properties (Meng et al., 2018). For instance, it is often used interchangeably with *Achyranthes aspera* due to their similar appearance. However, comparative studies have shown that *A. bidentata* has superior antidiabetic activity and a slightly better antioxidant profile than *A. aspera* (Shukla et al., 2018). Phylogenetic analyses have also placed *A. bidentata* close to other medicinally valuable species like *Cyathula capitata* and *Alternanthera philoxeroides*, suggesting potential similarities in their medicinal properties (Yuan et al., 2021). These comparative insights are essential for understanding the distinct and shared therapeutic potentials of *A. bidentata* and related species.

5 Genomic Studies

5.1 Overview of genomic research on *Achyranthes bidentata*

Achyranthes bidentata, a traditional Chinese medicinal plant, has been the subject of various genomic studies aimed at understanding its medicinal potential and evolutionary traits. The chloroplast genome sequencing of *A. bidentata*, along with *A. longifolia* and *A. aspera*, revealed a highly conserved structure, which includes a pair of inverted repeat (IR) regions, a large single copy (LSC) region, and a small single copy (SSC) region. This study provided a foundation for the identification of germplasm resources and confirmed that Achyranthes is monophyletic, with *A. bidentata* closely related to *A. aspera* and *A. longifolia*1. Additionally, the complete chloroplast genome of *A. bidentata* was assembled, further supporting its close phylogenetic relationship with *Cyathula capitata* (Li et al., 2019).

5.2 Genome sequencing techniques

The genomic studies on *Achyranthes bidentata* have employed advanced sequencing techniques to unravel its genetic makeup. Next-generation sequencing (NGS) technology was utilized to sequence the chloroplast genomes of *A. bidentata* and its related species, providing detailed insights into their genomic structures (Xu et al., 2020). The RNA-seq technique was also employed to identify candidate genes responsible for the replanting benefit observed in *A. bidentata*. This technique generated extensive sequencing data, leading to the identification of numerous unigenes and differentially transcribed genes (DTGs) that are crucial for understanding the plant's enhanced growth and development under consecutive monoculture conditions5.

5.3 Functional genomics and gene expression studies

Functional genomics and gene expression studies have been pivotal in elucidating the medicinal potential of *Achyranthes bidentata*. Integrated miRNA-mRNA analysis identified several miRNAs and their target gene modules that are potentially involved in the replanting benefit of *A. bidentata* roots. These miRNA-target modules are believed to enhance root growth, transport activity, and stress tolerance, thereby improving the plant's productivity (Yang et al., 2021) (Figure 1). Furthermore, transcriptome profiling of replanting roots revealed significant changes in the expression patterns of key genes involved in metabolism, antioxidant defense, phytohormone signaling, and pathogen defense systems. These findings provide valuable insights into the molecular mechanisms underlying the replanting benefit and suggest potential applications in enhancing the medicinal properties of *A. bidentata* (Yang et al., 2018). In summary, the genomic studies on *Achyranthes bidentata* have leveraged advanced sequencing techniques and functional genomics approaches to uncover the genetic and molecular basis of its medicinal potential and evolutionary traits. These studies not only enhance our understanding of *A. bidentata*'s genomic structure but also pave the way for future research aimed at optimizing its medicinal applications.

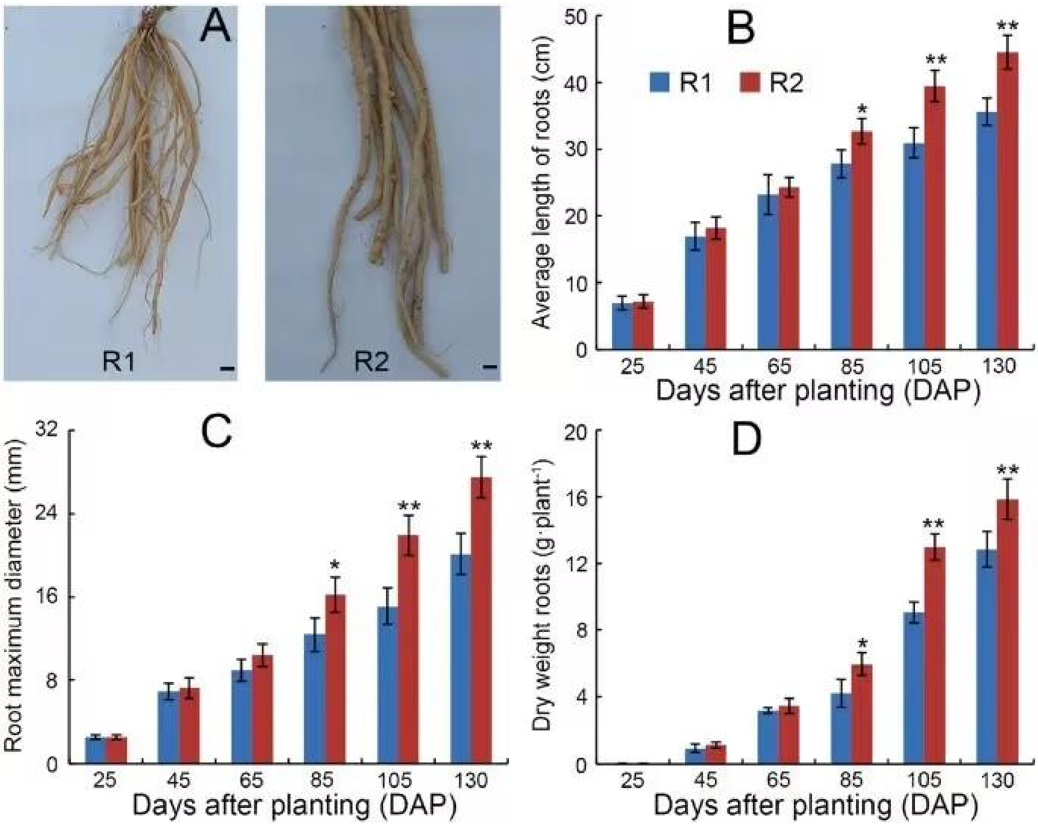

Figure 1 The morphological characteristics from R1 and R2 roots (Adopted from Yang et al., 2021)

Image caption: (A) The root photograph at the 130 DAP (bar = 2 cm), (B,C) root morphological index and (D) biomass. The bars represent the standard error (n = 3); "*" and "**" represent different significance $P < 0.05$ and 0.01, respectively. The same below (Adopted from Yang et al., 2021)

Yang et al. (2021) found that R2 roots exhibit significantly greater growth and biomass accumulation compared to R1 roots at various stages of development. The study measured root length, maximum root diameter, and dry weight of roots at intervals of 25, 45, 65, 85, 105, and 130 days after planting (DAP). Results showed that R2 roots consistently outperformed R1 roots in all measured parameters, with notable differences emerging as early as 85 DAP. The differences were statistically significant, particularly at the later stages (105 and 130 DAP), with P-values less than 0.05 and 0.01 indicating strong significance. These findings suggest that the R2 variant has superior root growth characteristics, which could be beneficial for improving plant biomass and overall health.

6 Medicinal Potential

6.1 Genomic insights into bioactive compounds

Achyranthes bidentata, a traditional Chinese medicinal herb, has been extensively studied for its therapeutic properties. This section delves into the genomic insights, pathways involved, and genetic basis of its pharmacological activities. The bioactive compounds of *Achyranthes bidentata*, particularly saponins and polysaccharides, have been identified and characterized through various genomic and metabolomic studies. For instance, *Achyranthes bidentata* saponins (ABS) have been shown to possess significant anti-arthritis properties. Using ultra-performance liquid chromatography quadrupole time-of-flight mass spectrometry (UPLC-QTOF/MS), researchers have identified 26 and 21 metabolites of ABS in rat liver microsomes and plasma, respectively. These metabolites are involved in metabolic pathways such as M+O, M+O-H_2, M+O_2, and M+O_2-H_2, which contribute to the therapeutic effects of ABS against rheumatoid arthritis (RA) (Fu et al., 2021). Additionally, a novel fructan, ABW50-1, isolated from *Achyranthes bidentata*, has demonstrated potential in treating osteoporosis by stimulating bone formation. This compound was characterized using chemical methods and nuclear magnetic resonance, revealing its unique structure and significant osteoprotective effects in a zebrafish model (Yan et al., 2019).

6.2 Pathways involved in medicinal properties

The medicinal properties of *Achyranthes bidentata* are mediated through various biochemical pathways. Network pharmacology analysis has identified key signaling pathways such as MAPK, apoptosis, PI3K-AKT, and p53, which are crucial for the therapeutic effects of ABS on RA. These pathways help in restoring the balance of pro/anti-inflammatory factors and reducing the phosphorylation of ERK in the MAPK pathway (Fu et al., 2021). In the context of osteoporosis, *Achyranthes bidentata* polysaccharides (ABPs) have been shown to regulate lipid metabolism, as evidenced by UPLC/Q-TOF-MS-based metabolomics analysis. Biomarkers such as glutarylcarnitine, lysoPC (18:1), and 9-cis-retinoic acid were significantly increased in osteoporotic rats treated with ABPs, indicating their role in lipid metabolism and bone health (Zhang et al., 2018).

6.3 Genetic basis of pharmacological activities

The genetic basis of the pharmacological activities of *Achyranthes bidentata* has been explored through various genomic studies. The complete chloroplast genome of *Achyranthes bidentata* has been sequenced, revealing a highly conserved structure with 130 genes, including 85 protein-coding genes, 37 tRNAs, and eight rRNAs. Phylogenetic analysis has shown that *Achyranthes bidentata* is closely related to other species within the Amaranthaceae family, providing a genetic foundation for its medicinal properties (Xu et al., 2020). Furthermore, the genetic analysis of *Achyranthes bidentata* has identified key active compounds such as quercetin, baicalein, and berberine, which are strongly related to the treatment of osteoarthritis (OA). These compounds target proteins like TNF, IL-6, and TP53, which are involved in apoptosis, inflammation, and immune regulation, thereby elucidating the genetic basis of its pharmacological activities (Chen et al., 2020) (Figure 2).

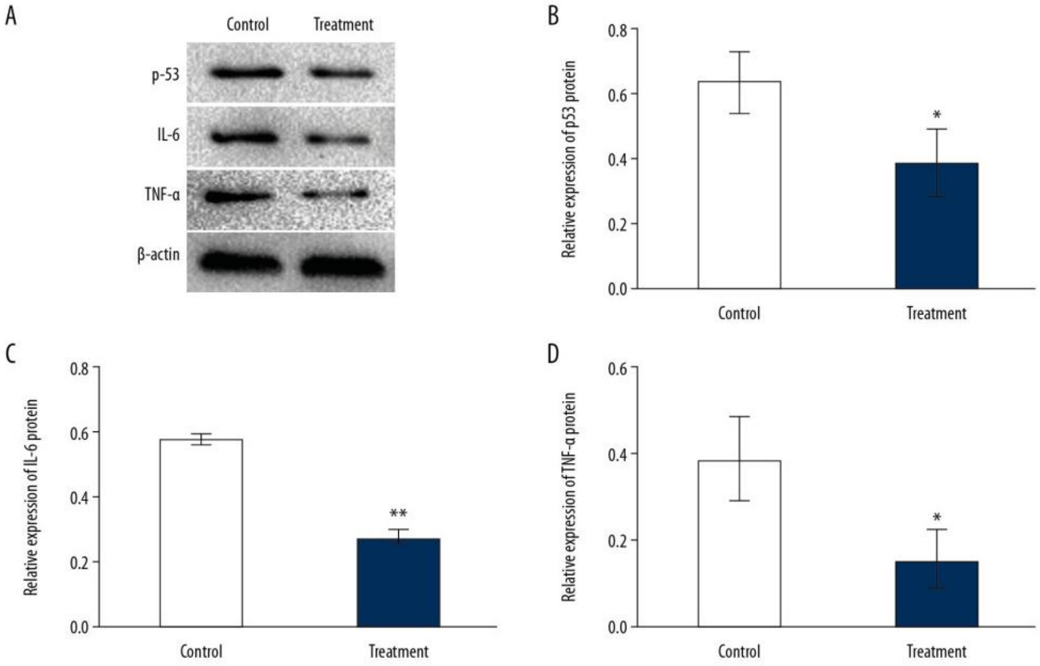

Figure 2 Expression of proteins in chondrocytes exposed to IL-1β and/or *Achyranthes bidentata* extract (A-D) (Adopted from Chen et al., 2020)

Image caption: * $P<0.05$ and ** $P<0.01$ vs. IL-1β-treated chondrocytes (Adopted from Chen et al., 2020)

Chen et al. (2020) found that the treatment significantly reduced the expression of p53, IL-6, and TNF-α proteins in chondrocytes when compared to the control group. The relative expression levels of these proteins were markedly lower in the treatment group, indicating that the treatment effectively mitigated the inflammatory response induced by IL-1β. Specifically, the expression of p53 protein was significantly decreased ($p<0.05$), while the reduction in IL-6 protein expression was even more pronounced ($p<0.01$). Similarly, TNF-α protein levels were also significantly reduced ($p<0.05$) in the treatment group. These findings suggest that the *Achyranthes bidentata* extract may have a potent anti-inflammatory effect on chondrocytes, potentially offering a therapeutic strategy for conditions characterized by inflammation and excessive cytokine production.

7 Evolutionary Traits

7.1 Phylogenetic analysis

Phylogenetic analysis of *Achyranthes bidentata* has provided significant insights into its evolutionary lineage. The complete chloroplast genome of *A. bidentata*, which is 151 543 bp in length, has been sequenced and analyzed. This genome includes a large single-copy (LSC) region, a small single-copy (SSC) region, and a pair of inverted repeat regions (IRs). The phylogenetic analysis of this genome indicates that four samples of *A. bidentata* form a distinct clade with a 100% bootstrap value, suggesting a strong evolutionary relationship within the species (Chen et al., 2020). Additionally, DNA barcoding using the internal transcribed spacer 2 (ITS2) region has been employed to enhance species resolution within the genus Achyranthes. This method has proven effective in differentiating *A. bidentata* from other species, further supporting its unique phylogenetic position (Singh et al., 2020).

7.2 Evolution of medicinal traits

The medicinal properties of *Achyranthes bidentata* have evolved to include significant anti-inflammatory and immunomodulatory effects. Traditional Chinese medicine has long utilized *A. bidentata* for its kidney-protective properties, which are enhanced through salt processing. Recent studies have shown that both raw and salt-processed *A. bidentata* can attenuate lipopolysaccharide (LPS)-induced acute kidney injury in mice by inhibiting reactive oxygen species (ROS) and apoptosis via an estrogen-like pathway. This suggests that the medicinal traits of *A. bidentata* have evolved to include complex biochemical pathways that confer protective effects against inflammation and oxidative stress (Wang et al., 2020) (Figure 3).

Wang et al. (2020) found that the treatments with HQ, NX, and YNX significantly reduced the inflammatory response induced by LPS in mice. The mean fluorescence intensity (MFI) measurements revealed a substantial decrease in inflammation markers in the HQ, NX, and YNX treated groups compared to the model group. Specifically, the HQ treatment showed a significant reduction in inflammation ($p<0.001$), demonstrating its strong anti-inflammatory effect.

Similarly, NX treatment also resulted in a notable decrease in inflammation ($p<0.001$), suggesting the effectiveness of raw Achyranthes aqueous extract. Furthermore, the YNX treatment, which involved salt-processed Achyranthes aqueous extract, significantly attenuated the inflammatory response ($p<0.001$), indicating that both forms of the extract have potent anti-inflammatory properties. These findings highlight the potential therapeutic use of Achyranthes extracts in managing inflammation.

7.3 Genomic adaptations to environmental stress

Achyranthes bidentata has developed several genomic adaptations that enable it to withstand environmental stress. The complete chloroplast genome sequencing has revealed the presence of 131 genes, including 86 protein-coding genes, which are likely involved in various stress response mechanisms (Yuan et al., 2021).

Furthermore, the secondary structure modeling of the ITS2 region has identified specific single-nucleotide polymorphisms (SNPs) that could be crucial for the plant's adaptation to different environmental conditions. These SNPs may play a role in the plan’s ability to thrive in diverse habitats, thereby contributing to its medicinal efficacy (Singh et al., 2020).

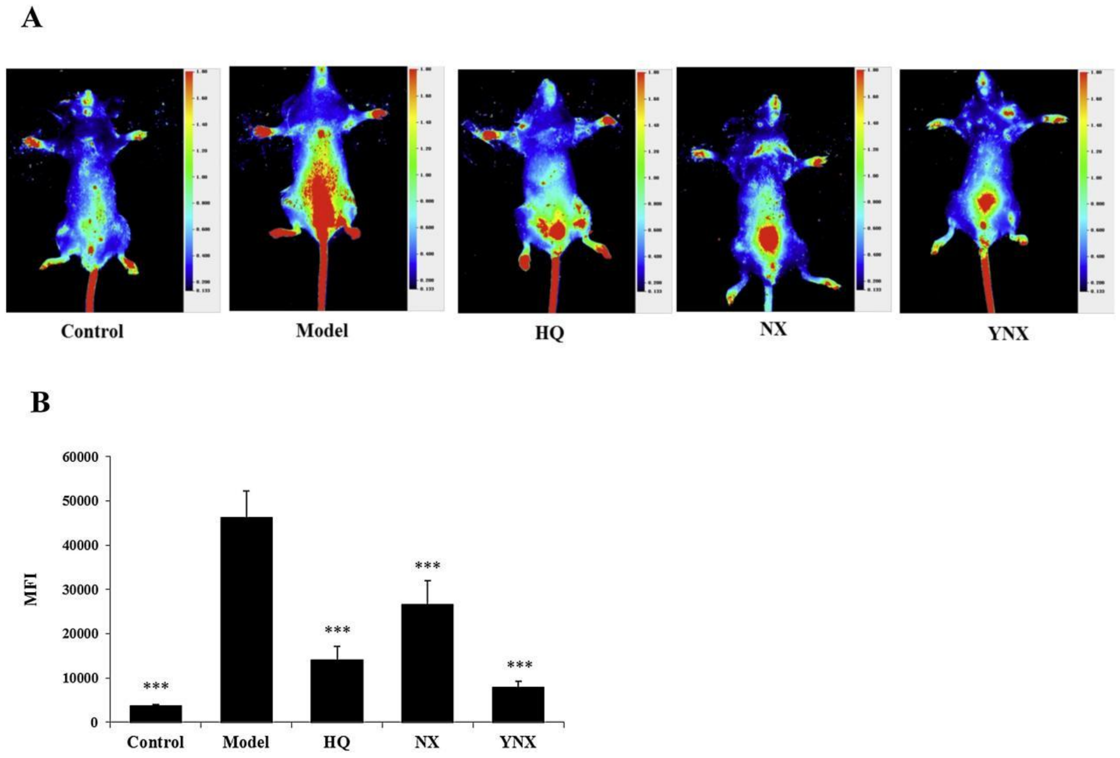

Figure 3 HQ, NX, and YNX reduce LPS-induced inflammatory response (Adopted from Wang et al., 2020)

Image capton: A. Representative images showed the fluorescent signal of 2-DG probe in mice at 24 h. B. Representative optical density data showed that the treatment of HQ, NX, and YNX significantly attenuated the inflammatory response in model mice at 24 h. Data are mean±SD, n=3 mice per group. *$P<0.05$ vs model group. **$P<0.01$ vs model group. ***$P<0.001$ vs model group. Model: LPS (5 mg/kg); HQ: positive control drug (2 g/kg, LPS 5 mg/kg); NX: Raw Achyranthes aqueous extract (referred to as NX in this study 4 g/kg, LPS 5 mg/kg); YNX: Salt-processed Achyranthes aqueous extract (referred to as YNX in this study 4 g/kg, LPS 5 mg/kg) (Adopted from Wang et al., 2020)

8 Comparative Genomics

8.1 Comparative analysis with related species

Comparative genomics of *Achyranthes bidentata* with related species such as *Achyranthes longifolia* and *Achyranthes aspera* has revealed significant insights into their genetic makeup (Shukla et al., 2018). The chloroplast genomes of these species are highly conserved, with similar lengths and structural features, including large single-copy (LSC) regions, small single-copy (SSC) regions, and inverted repeat (IR) regions. Specifically, the chloroplast genome lengths are 151 520 bp for *A. longifolia*, 151 284 bp for *A. bidentata*, and 151 486 bp for *A. aspera*. Phylogenetic analysis indicates that *A. bidentata* is closely related to *A. aspera* and *A. longifolia*, with *A. bidentata* and *A. longifolia* clustering together, suggesting a common origin (Xu et al., 2020).

8.2 Insights from comparative genomics

The comparative genomic studies have provided valuable insights into the evolutionary traits and medicinal potential of *A. bidentata*. The high degree of conservation in the chloroplast genomes among the Achyranthes species supports their monophyletic nature. Additionally, the close phylogenetic relationship between *A. bidentata* and other species in the genus, as well as with *Alternanthera philoxeroides*, highlights the evolutionary pathways and genetic divergence within the Amaranthaceae family (Singh et al., 2020). These findings are crucial for understanding the genetic basis of the medicinal properties of *A. bidentata*, such as its anti-osteoporosis effects, which have been attributed to specific polysaccharides and other bioactive compounds (Lin et al., 2021).

8.3 Implications for breeding and conservation

The comparative genomic data have significant implications for the breeding and conservation of *A. bidentata*. The identification of conserved genetic regions and phylogenetic relationships can aid in the development of molecular markers for species identification and quality control in herbal medicine. This is particularly important given the widespread use of *A. bidentata* in traditional Chinese medicine and its potential for treating conditions like osteoporosis (Yan et al., 2019). Furthermore, understanding the genetic diversity and evolutionary history of *A. bidentata* can inform conservation strategies to preserve its genetic resources and ensure sustainable use. The insights gained from comparative genomics can also facilitate the breeding of improved varieties with enhanced medicinal properties and resilience to environmental stresses (Xu et al., 2020). In summary, the comparative genomics of *A. bidentata* with related species provides a comprehensive understanding of its genetic structure, evolutionary traits, and medicinal potential. These insights are invaluable for breeding, conservation, and the development of high-quality medicinal products.

9 Challenges and Future Directions

9.1 Current gaps in genomic research

Despite significant advancements in the genomic study of *Achyranthes bidentata*, several gaps remain. One major gap is the limited understanding of the complete genomic architecture and its functional implications. While the chloroplast genome has been sequenced and characterized, providing insights into the phylogenetic relationships and structural features of the genome (Xu et al., 2020), there is still a need for comprehensive nuclear genome sequencing. Additionally, the role of non-coding RNAs, such as miRNAs, in regulating gene expression and contributing to the medicinal properties of *A. bidentata* is not fully understood. Furthermore, the genetic basis of the replanting benefit observed in *A. bidentata* remains to be elucidated, which could provide valuable information for improving crop yield and quality (Yang et al., 2021).

9.2 Technological and methodological challenges

The study of *A. bidentata* faces several technological and methodological challenges. One significant challenge is the complexity of the plant's secondary metabolites, such as saponins and polysaccharides, which require advanced analytical techniques for their characterization and comparison8. High-resolution mass spectrometry and two-dimensional liquid chromatography have been employed to identify and compare these compounds, but the development of more efficient and accurate methods is necessary. Another challenge is the integration of multi-omics data, including genomics, transcriptomics, proteomics, and metabolomics, to provide a holistic understanding of the plant's biology and medicinal potential (Lin et al., 2021). Additionally, the lack of standardized protocols for the extraction and purification of bioactive compounds from *A. bidentata* poses a challenge for reproducibility and consistency in research findings (Zhang et al., 2018).

9.3 Future research priorities

To address the current gaps and challenges, several future research priorities can be identified. First, comprehensive nuclear genome sequencing and annotation of *A. bidentata* should be prioritized to provide a complete picture of its genetic makeup and functional elements. Second, the role of non-coding RNAs, particularly miRNAs, in regulating the plant's medicinal properties and stress responses should be further investigated through integrated miRNA-mRNA analysis (Li et al., 2019). Third, the development of advanced analytical techniques for the characterization of secondary metabolites, such as saponins and polysaccharides, should be pursued to enhance our understanding of their structure-activity relationships and therapeutic potential8. Fourth, multi-omics approaches should be employed to integrate genomic, transcriptomic, proteomic, and metabolomic data, providing a comprehensive understanding of the plant's biology and its medicinal properties9. Finally, standardized protocols for the extraction and purification of bioactive compounds should be established to ensure reproducibility and consistency in research findings, facilitating the development of new therapeutic agents from *A. bidentata* (Wang et al., 2022). By addressing these research priorities, we can enhance our understanding of the genomic and biochemical basis of *A. bidentata*'s medicinal potential and evolutionary traits, paving the way for the development of novel therapeutic agents and improved crop varieties.

10 Concluding Remarks

The genomic studies of *Achyranthes bidentata* have provided significant insights into its medicinal potential and evolutionary traits. The complete chloroplast genome of *A. bidentata* has been sequenced and characterized, revealing a highly conserved structure with a length of approximately 151 451 bp, including a large single-copy

(LSC) region, a small single-copy (SSC) region, and a pair of inverted repeat (IR) regions. Phylogenetic analyses have consistently shown that *A. bidentata* is closely related to species such as *Cyathula capitata* and *Alternanthera philoxeroides*, indicating its evolutionary relationships within the Amaranthaceae family. DNA barcoding and secondary structure modeling have enhanced the resolution of Achyranthes species identification, with the ITS2 barcode proving to be the most effective marker. Proteomics studies have identified potential biomarkers and therapeutic targets for osteoporosis, highlighting the role of mitochondria in the treatment of glucocorticoid-induced osteoporosis6. Additionally, systematic pharmacology and in vitro studies have identified active compounds such as quercetin, baicalein, and berberine, which target key proteins involved in osteoarthritis, including TNF, IL-6, and TP537.

The findings from these genomic studies have several important implications for both medicine and evolutionary biology. In the medical field, the detailed characterization of the chloroplast genome and the identification of active compounds provide a foundation for developing targeted therapies for conditions such as osteoporosis and osteoarthritis. The identification of potential biomarkers and therapeutic targets, such as MT-CYB and NDUFA9 for osteoporosis, and TNF, IL-6, and TP53 for osteoarthritis, opens new avenues for drug development and personalized medicine. From an evolutionary biology perspective, the phylogenetic analyses offer insights into the evolutionary relationships within the Amaranthaceae family. The close genetic relationship between *A. bidentata* and other species such as *Cyathula capitata* and *Alternanthera philoxeroides* suggests a shared evolutionary history and provides a basis for further studies on the diversification and adaptation of these species.

In conclusion, the genomic studies of *Achyranthes bidentata* have significantly advanced our understanding of its medicinal potential and evolutionary traits. The comprehensive genomic data, coupled with proteomics and pharmacological analyses, underscore the importance of *A. bidentata* in traditional medicine and its potential for modern therapeutic applications. Future research should focus on exploring the functional roles of the identified genes and compounds, as well as their interactions, to fully harness the medicinal properties of *A. bidentata*. Additionally, further phylogenetic studies are needed to elucidate the evolutionary pathways and genetic diversity within the Achyranthes genus and related species. By integrating genomic, proteomic, and pharmacological data, we can better understand the complex biological mechanisms underlying the medicinal effects of *A. bidentata* and leverage this knowledge to develop effective treatments for various diseases.

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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