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# The Study on Molecular Marker-Based Variety Selection and Breeding Applications of Wuyao in Qinchuan County

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**Abstract** This study investigates the application of molecular marker technology in the breeding of Qingchuan Wu, aiming to increase the content of bioactive compounds and the overall medicinal quality of Qingchuan Wu, enhance its genetic diversity and resistance, and address issues such as insufficient genetic variation and environmental stress in Qingchuan Wu. Research has found that molecular markers are an effective means to identify the desired traits of Qingchuan Wu, which can provide support for the breeding of plants with high medicinal value and disease resistance. The application of Marker-assisted selection (MAS) in the breeding program has significantly enhanced the breeding efficiency, accelerated the breeding process of superior varieties, and ensured the sustainable cultivation of Qingchuan Wu. This study provides a useful reference for the application of molecular breeding technology in the field of traditional Chinese medicine and lays a foundation for the development of new germplasm with improved medicinal properties.

**Keywords** Qingchuan Wu; Molecular markers; Marker-assisted selection; Bioactive compounds; Medicinal breeding

## 1 Introduction

Qingchuan Wu has high economic and medicinal value and plays an important role in traditional Chinese medicine. These herbs have attracted much attention because they contain bioactive compounds, which is closely related to their clinical effects. Increasing the content of these bioactive compounds is crucial for improving the quality and efficacy of traditional Chinese medicine. Therefore, cultivating high-quality varieties of Qingchuan Wu is an important task at present (Song and Li, 2020).

Molecular marker technology has become an important method for cultivating plants, providing a brand-new idea for the cultivation of medicinal plants. This technology detects the genes of plants, identifies those good genetic characteristics, and then selects them. In this way, new plant varieties with better aspects can be cultivated. When cultivating traditional Chinese medicinal materials, by using this gene-assisted cultivation method, new varieties containing more effective components can be cultivated more quickly, opening up a new direction for the research on cultivating good medicinal materials (Qian et al., 2020; Song and Li, 2020). The mapping of genetic linkage maps, the search for QTLS and genetic diversity, as well as the analysis of the differences in genes among different plants, are all commonly used methods in this research field. These efforts are particularly crucial for ensuring the stable quality of Chinese medicinal materials (Qian et al., 2020).

This study will look into how molecular marker technology can be used in breeding Qingchuan Wu medicinal materials. The goal is to boost the amount and overall quality of bioactive compounds in these herbs, so they can meet high medical standards. This research isn't just about raising the economic value of Qingchuan Wu. It also aims to help with the sustainable use and protection of traditional Chinese medicinal materials.

## 2 Background and Significance

### 2.1 Overview of Qingchuan Wu’s botanical and medicinal characteristics

Qingchuan Wu is a famous plant in Qinchuan County. It’s widely known because of its special growth features and medical benefits. The plant has many substances that are good for people and has been used to treat lots of illnesses for a long time. Research shows these substances can reduce inflammation and fight oxidation. Also, it can grow well in the local climate and soil, making it really significant in traditional medicine and local farming (El-Hack et al., 2018; Zhao et al., 2018).

Besides being used for medicine, Qingchuan Wu's role in environmental protection has drawn attention. It can survive in various conditions and is vital to the local ecosystem. Planting this Qingchuan Wu helps keep different species alive and provides local farmers with steady earnings. When grown in agriculture, Qingchuan Wu passes on old planting methods and safeguards natural resources at the same time (Cai et al., 2019).

### 2.2 Current challenges in Qingchuan Wu cultivation and breeding

Although Qingchuan Wu has many benefits, there are still quite a few difficulties in its cultivation and breeding of new varieties. One of the major problems is that the variety differences among them are small, which leads to the plants being prone to diseases and pests. The small differences in varieties also make it difficult to cultivate new varieties using the old methods. Therefore, it is urgently necessary to find new methods to enrich the varieties of Qingchuan Wu and make it more resistant to pests and diseases (El-Hack et al., 2018).

Another challenge is the trouble that environmental changes have brought to the cultivation of Qingchuan Wu. The climate is constantly changing and the soil is getting worse and worse, which has seriously affected the growth of Qingchuan Wu, causing a significant decline in yield. In order to ensure that the Qingchuan Wu can always have a harvest, it is necessary to develop more environmentally friendly planting and cultivation methods. Only by solving these problems can the medicinal and ecological values of Qingchuan Wu be preserved (Zhao et al., 2015; Cai et al., 2019).

### 2.3 The potential of molecular markers for improving genetic diversity and quality

Molecular marker technology has brought new hope for solving the problems in the cultivation of Qingchuan Wu. Markers such as single nucleotide polymorphisms (SNPs) can help people select good variety characteristics at the genetic level. By using molecular marker technology, breeders can cultivate more diverse varieties of Qingchuan Wu, improve the quality, make the plants grow stronger and better adapt to harsh environments (El-Hack et al., 2018).

When cultivating new varieties, the use of molecular marker technology can greatly accelerate the speed of breeding high-quality varieties of Qingchuan Wu. Compared with the old methods, this technology can accurately select the cultivation objects and save time and resources (Xu et al., 2012). Integrating molecular marker technology into the breeding plan can not only improve the cultivation efficiency, but also ensure the stable and high yield of Qingchuan Wu chinensis cultivation (Cai et al., 2019).

## 3 Molecular Markers in Plant Breeding

### 3.1 Definition and types of molecular markers

Molecular markers are specific fragments in DNA that can be used to identify specific locations in the genome. They are markers of gene mapping and it is very important to track the inheritance of traits in plant breeding. Among various types of molecular markers, simple sequence repeats (SSRs), single nucleotide polymorphisms (SNPs), and random amplified polymorphic DNA (RAPD) are widely used. SSRs, also known as microsatellites, are DNA repeat sequences composed of 1 to 6 base pairs, featuring high variability and dominance, which makes them very useful in genetic diversity research and the construction of linkage maps. On the other hand, SNP is a single-base pair variation at a specific site in a DNA sequence. Due to its large quantity and wide distribution in the genome, it can provide a high-resolution genetic map (El-Hack et al., 2018).

RAPD markers are generated by amplifying random fragments of genomic DNA with a single primer (any nucleotide sequence). They belong to explicit markers, meaning that it is impossible to distinguish between homozygous and heterozygous states, which might be a limitation. However, RAPD can rapidly generate a large number of markers without prior understanding of the genome. Each marker has its advantages and disadvantages. The specific choice depends on the requirements of the breeding plan, such as the required polymorphism level, cost and ease of operation (El-Hack et al., 2018; Hu et al., 2024).

### 3.2 Selection criteria for molecular markers of Qingchuan Wu

To screen the molecular markers of Qingchuan Wu, it is necessary to identify the genetic markers closely related to important characteristics such as growth conditions, appearance, and medicinal components. Single nucleotide polymorphisms (SNPS) are particularly crucial because they are numerous and widely distributed in genes. In Qingchuan Wu, scientists discovered that the SNPS of *SIRT1, SIRT2* and *LPL* genes are useful markers related to these characteristics, which laid the foundation for marker-assisted breeding (MAS) (El-Hack et al., 2018). Facts have proved that these marks play a significant role in increasing the content of medicinal components, optimizing plant growth, and predicting the quality (Xu et al., 2012).

In addition, proteomics provides us with a new approach to understanding the biological processes that affect the characteristic expression of plants. Studies have found that proteins such as actin, myosin and heat shock protein can be used as biomarkers and linked to medicinal properties. These proteomic markers can help us understand the molecular principles that affect the quality of Qingchuan Wu more clearly and are of great value for screening and breeding Qingchuan Wu varieties (Figure 1) (Hasan et al., 2021). Other studies have shown that combining proteomics and genomics can significantly improve the efficiency of screening markers (Zhao et al., 2018).

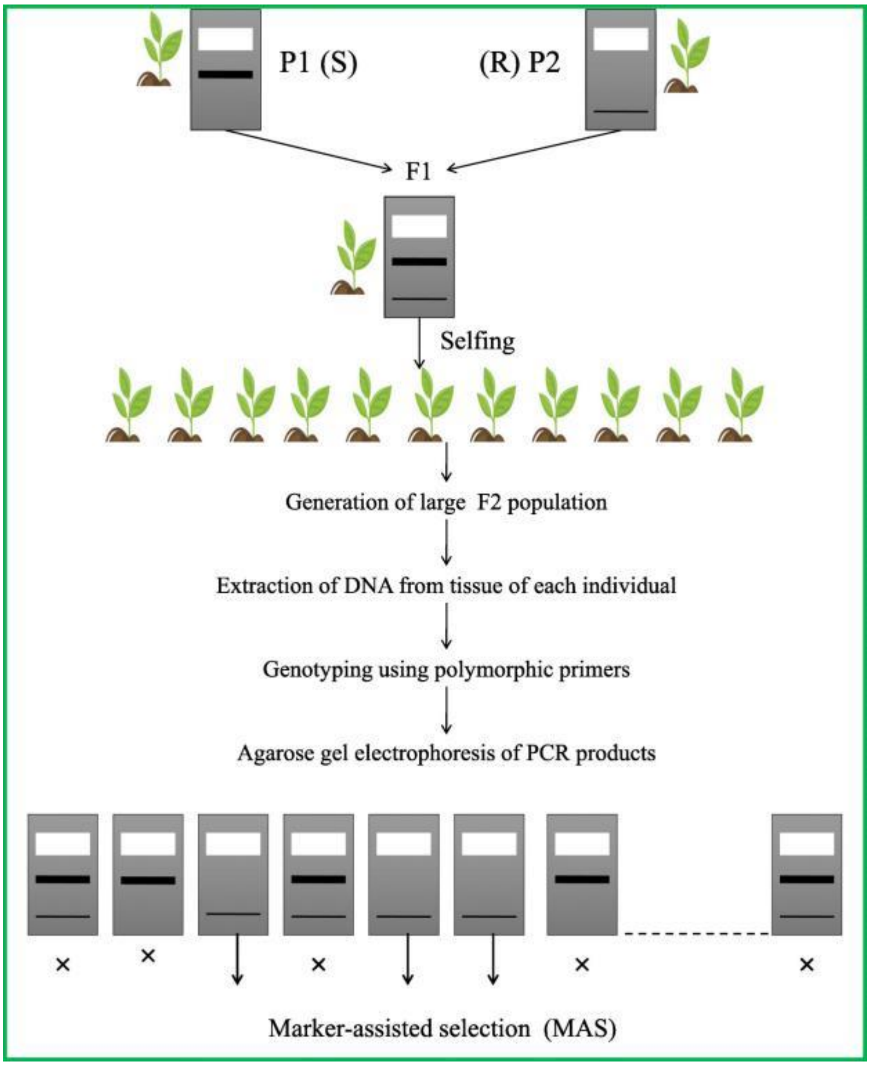

Figure 1 The figure explains the basic procedure of marker-assisted selection (Adopted from Hasan et al., 2021)

### 3.3 How molecular markers aid in selecting traits for medicinal plants

When selecting the important characteristics of medicinal plants, molecular markers can precisely identify the genetic traits related to medicinal characteristics and play a very crucial role. With it, breeders can distinguish which plants have specific genetic maps, and these maps are related to high levels of active ingredients, disease resistance or other good characteristics. This is particularly important for medicinal plants because the content and composition of active ingredients in different plants vary greatly. With these markers related to characteristics, breeders can select plants that consistently produce high-quality medicinal components (El-Hack et al., 2018).

The method of screening genetic characteristics can also promote the progress of gene-assisted breeding technology. By using this method, the varieties that have grown can be picked out when the plants are still small. This advantage is particularly obvious when cultivating medicinal plants, because the previous methods of cultivating medicinal plants not only took a long time but were also not very accurate. With gene-assisted breeding technology, breeders can specifically cultivate plants that are more likely to have excellent characteristics, making the work of cultivating better medicinal plant varieties fast and effective (El-Hack et al., 2018).

### 3.4 Previous studies demonstrating the success of molecular markers in medicinal herb breeding

From the findings of previous studies, the gene screening method is particularly useful in the cultivation of traditional Chinese medicinal materials. By this method, plants that are less prone to illness and can produce more active ingredients can be selected. For instance, by using specific genetic markers, genetic changes that enable medicinal plants to produce more alkaloids can be identified. Breeders can select plants with a high content of active ingredients and the ability to withstand harsh environments through these markers. In this way, the quality of the Chinese medicinal materials grown is better and the yield is more stable (El-Hack et al., 2018).

Some studies have found that SSR markers can well evaluate the genetic differences and structures of medicinal plant populations. This information is crucial for the protection and rational use of genetic resources, and can help breeders maintain genetic diversity while selecting specific traits. The use of SSR markers in the breeding process has successfully cultivated new varieties with better medicinal effects, which also indicates that applying molecular markers to traditional breeding methods does have great benefits (El-Hack et al., 2018).

## 4 Genetic Diversity and Marker Analysis

### 4.1 Genetic diversity of Qingchuan Wu varieties

Genetic diversity is of great significance for the cultivation and selection of plant varieties. It is the prerequisite for plants to adapt to the environment and optimize varieties. When studying the varieties of Qingchuan Wu, multiple molecular marker techniques can be used to evaluate genetic diversity. For example, simple sequence repetition (SSR) markers can easily distinguish different varieties by detecting genetic differences. The genetic situation of Qingchuan Wu was analyzed using SSR markers, and it was found that its genetic characteristics were diverse. Similarly, scientists also used randomly amplified polymorphic DNA (RAPD) and ISSR markers to study the genetic differences of Qingchuan Wu and its similar varieties. The results showed that there were significant genetic differences among different populations (Pin et al., 2014).

The genetic differences within the same population and among different populations of Qingchuan Wu are the key to its ability to adapt to the environment and maintain vitality. This genetic difference is not only related to the survival of species, but also enables people to improve specific traits of plants through screening and cultivation. Studies have shown that evaluating genetic diversity with molecular markers can strongly promote the breeding and optimization of new varieties of Qingchuan Wu (Zhao et al., 2015).

### 4.2 Analysis of molecular marker results and their breeding significance

Molecular markers (such as single nucleotide polymorphisms [SNPs] and SSRs) play an important role in analyzing genetic diversity and screening ideal traits. For example, SNP markers have demonstrated practical value in the screening of growth characteristics and medicinal components of Qingchuan Wu. Furthermore, the SSR marker can be used to distinguish different varieties, which has also been verified in the research of Chinese cabbage and rice without panicles (Wang and Huang, 2024).

Studying these genetic characteristics not only makes the breeding of new varieties more efficient, but also helps us cultivate plant varieties with better efficacy, superior quality and greater resistance to harsh environments. As long as the genetic characteristics related to the ideal traits are found, the person responsible for breeding can make better decisions and accelerate the speed of breeding new varieties (Tian et al., 2007).

### 4.3 The relationship between genetic diversity and drug properties

The connection between the genetic differences of plant varieties and their medicinal properties is a very crucial research content. Researchers have found that the substances useful for medicinal purposes in plants, their generation and content are often affected by genetic differences, and these substances determine whether plants can be used for treating diseases or not (Zhao et al., 2017; Qin et al., 2024).

With the help of the technology of selecting varieties by looking at genes, researchers can identify specific genes related to the medicinal effects of plants. Such research results can help us cultivate new varieties with better efficacy and lay a solid foundation for the development of traditional Chinese medicine and the progress of the pharmaceutical industry (Pin et al., 2014).

## 5 Breeding Strategies of Qingchuan Wu

### 5.1 Review of traditional breeding methods and modern molecular breeding techniques

For a long time, traditional breeding methods have been the fundamental means of agriculture and plant cultivation. They rely on selecting plants with distinct appearance features and then optimizing the desired characteristics through hybridization. However, due to the complex genetic laws of plant characteristics and the influence of the environment, these methods often take a long time and are not accurate enough in seed selection. Unlike traditional methods, modern molecular breeding techniques, such as marker-assisted selection (MAS), can guide breeding work based on genetic information and have more specific goals. This technology can identify and select genes related to the ideal characteristics. As a result, the speed of breeding new varieties has increased and the accuracy has also improved (Jiang, 2013).

The application of techniques such as single nucleotide polymorphism (SNPs) and quantitative trait locus (QTL) localization in molecular breeding has brought significant changes to the field of breeding. Just as when screening varieties related to the medicinal components and growth characteristics of Qingchuan Wu, the use of SNP markers has demonstrated the potential of molecular markers to significantly enhance the breeding effect.

### 5.2 Marker-assisted selection (MAS) in breeding programs

Marker-assisted selection (MAS) is a powerful tool in modern breeding, which can precisely pick out plants with good genes. When cultivating Qingchuan Wu, MAS enhances the medicinal component content and growth status of Qingchuan Wu by identifying gene markers related to the target characteristics, such as SNPS of the *ACTL8* gene, providing a scientific basis for efficient breeding (Xu et al., 2012). The research finds that the use of MAS can reduce the uncertainty during seed selection and greatly increase the probability of successful variety improvement (Pin, 2014; Li et al., 2024).

Moreover, MAS can also solve the problems of breeding complex traits, such as those controlled by multiple genes. As long as breeders keep an eye on key genetic markers, they can make better decisions and cultivate high-quality varieties more quickly.

### 5.3 Improvement of target traits: quality and disease resistance of medicinal materials

Improving the medicinal quality of Qingchuan Wu is the main goal of breeding, which directly affects its efficacy and market sales. Breeders use molecular markers, such as SNP and QTL, to identify genetic differences related to the content and quality of medicinal components, and then select plants with good genes to improve the quality of medicinal materials (Zhao et al., 2017). There are also studies showing that this method is crucial for ensuring the continuous development of breeding work (Yang et al., 2015; Ouyang et al., 2024).

In addition to improving the medicinal quality, enhancing the disease resistance of Qingchuan Wu is also an important task in breeding. With the help of MAS, breeders can quickly select varieties with strong disease resistance, enabling them to grow well even in adverse environments and ensuring stable yields. This can not only meet the market demand, but also improve the overall health level of the variety (Xu et al., 2012; Yan, 2024).

## 6 The Application of Molecular Markers in Breeding

### 6.1 Successful cases of Qingchuan Wu marker-assisted breeding

The technology of selecting good varieties through genetic markers has been widely used in the cultivation of medicinal materials in Qingchuan, especially in enhancing the efficacy and quality of medicinal materials. Specific genetic markers are a good way to judge the medicinal value of medicinal materials. For instance, with the help of such genetic markers, breeders can accurately identify useful components like alkaloids in aconite, thereby enhancing the therapeutic effect of medicinal materials.

In addition, the technology of researching proteins has also been very successful in cultivating certain medicinal materials. Studies have found that analyzing the changes of proteins in medicinal materials can clarify the principles that affect the generation of useful components, which can help breeders improve the quality of medicinal materials higher (Zhao et al., 2018).

### 6.2 Genetic analysis techniques: DNA extraction, PCR amplification and software tools used

Several important techniques are needed to analyze the genes of Qingchuan Wu. First of all, the genetic material needs to be extracted from the collected samples. Then, using PCR amplification technology, the parts of the gene that we are concerned about are replicated multiple times, such as the places with specific gene markers. With these techniques can identify the differences in genes, and these differences can be used as genetic markers when breeding new varieties.

Software tools are particularly important in analyzing genetic data and helping researchers identify differences in genes. Methods such as restricted fragment length polymorphism and genome-wide association studies have been successfully used to identify changes in a certain gene. With these tools, the differences in genes can be linked to the external characteristics of plants, which is of great help in formulating the cultivation plan of Qingchuan Wu (Yang et al., 2015). Moreover, combining the measurement of gene sequences with large-scale observation of plant characteristics will make gene markers more useful in cultivation in the future (Xu et al., 2012).

### 6.3 The advantages of using molecular markers to enhance the accuracy and efficiency of breeding

Molecular markers, especially single nucleotide polymorphisms (SNPs), have greatly enhanced the accuracy and efficiency of the breeding of PseudoSouth rice. With the help of these markers, breeders can predict drug traits at an early stage through non-invasive methods such as DNA sampling, saving a lot of time and resources (Xu et al., 2012). Quantitative trait locus (QTL) analysis is helpful for determining the gene loci related to medicinal traits and laying the foundation for precise breeding.

### 6.4 Challenges of applying molecular markers in breeding

Although molecular marker technology has obvious advantages in breeding, there are still some challenges. The complexity of genetic interactions makes it difficult to isolate the influence of individual gene markers. This requires the construction of complex gene maps, which is both time-consuming and costly (Yang et al., 2015). In addition, integrating molecular markers into traditional breeding practices requires additional training and technical support to ensure that the technical investment is rewarding and effectively applied in practice (Hasan et al., 2021).

## 7 Conclusion and Future Directions

This study mainly investigates the application of gene marker selection technology in the cultivation of Qingchuan Wu. Research has found that methods such as specific gene markers are particularly effective in identifying and determining the medicinal components contained in Qingchuan Wu. With the help of these marks, breeders can pick out those varieties of Qingchuan Wu with good medicinal effects at the seedling stage, which greatly accelerates the speed of cultivating new varieties. In addition, by studying the changes in proteins in medicinal materials, we have gained new insights into how medicinal components are formed, which can help cultivators make better cultivation decisions. Overall, the application of gene marker selection technology has provided a new, accurate and rapid method for improving the varieties of Qingchuan Wu.

Although this research has set a good precedent for the variety cultivation of Qingchuan Wu medicinal herbs, there are still many areas that need in-depth study. Future research can expand the types of molecular markers. Besides SNPS, insertion and deletion mutations (indel) and gene expression can also be studied. In this way, a more comprehensive understanding of the genetic basis of the medicinal components and disease resistance of Qingchuan Wu can be achieved. In addition, the expression differences of genes such as *ACTL8* at different growth stages and in different parts of Qingchuan Wu can also be studied to figure out exactly what roles these genes play in medicine. Combining proteomics and metabolomics for research can provide a more thorough understanding of the generation process of medicinal components and offer useful information for optimizing breeding programs.

After the molecular marker technology was put into use, the speed of cultivating new varieties of Qingchuan Wu has become faster, and it can also bring long-term benefits in planting and medicinal use. If high-value varieties that can withstand harsh environments are cultivated, the harvest of Qingchuan Wu will be better and the quality higher, which can better meet market demands. Moreover, these research achievements can also be used to cultivate varieties with better efficacy, providing high-quality raw materials for the pharmaceutical industry. By combining molecular genetics with traditional breeding methods, Qingchuan Wu can continue to play a role in agricultural production and the medical field, and its important position in traditional medicine can be further consolidated.

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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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