Medicinal Plant Research 2024, Vol.14, No.6, 345-357
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Review Article Open Access

Screening of Disease and Pest Resistant Hangbaiju (*Chrysanthemum morifolium*) Varieties and Their Application Prospects in Green Cultivation

Jianli Lu [1], Chuchu Liu [2]

1 Traditional Chinese Medicine Research Center, Cuixi Academy of Biotechnology, Zhuji, 311800, China
2 Institute of Life Sciences, Jiyang Colloge of Zhejiang A&F University, Zhuji, 311800, Zhejiang, China
Corresponding author: chuchu.liu@jicat.org

Medicinal Plant Research, 2024, Vol.14, No.6 doi: 10.5376/mpr.2024.14.0029
Received: 30 Oct., 2024
Accepted: 02 Dec., 2024
Published: 18 Dec., 2024

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Preferred citation for this article:
Lu J.L., and Liu C.C., 2024, Screening of disease and pest resistant Hangbaiju (*Chrysanthemum morifolium*) varieties and their application prospects in green cultivation, Medicinal Plant Research, 14(6): 345-357 (doi: 10.5376/mpr.2024.14.0029)

Abstract Hangbaiju (*Chrysanthemum morifolium*) is popular among consumers because of its anti-inflammatory, antioxidant and liver-protecting effects, and it has both medicinal and ornamental value. With the expansion of planting scale, pests and diseases have become the main obstacles affecting yield and quality. Although chemical pesticides are still the main means of prevention and control, there are problems such as increased resistance and environmental pollution. In order to promote green planting, this study screened out a number of resistant chrysanthemum varieties, and combined field natural infection experimental analysis, artificial inoculation experiments and molecular marker analysis to clarify the role of resistance genes, like *CmWD40* and *CmWRKY8-1* in the defense mechanism. The results showed that, these varieties can effectively reduce the incidence of pests and diseases while maintaining yield and quality, and adapt to the green prevention and control system. This study provides strong germplasm support and theoretical basis for the sustainable cultivation of Hangbaiju, and helps its promotion and application in ecological agriculture and organic certification paths.

Keywords Hangbaiju (*Chrysanthemum morifolium*); Disease and insect resistance; Green cultivation; Molecular markers; Resistance screening; Sustainable agriculture

1 Introduction

Hangbaiju (*Chrysanthemum morifolium*) plays an important role in both traditional Chinese medicine and horticulture. It can be used as medicine, make tea, decorate courtyards, or be exported as cut flowers. It is a common choice for both medicine and food and garden landscape in many places (Wang et al., 2018; 2021). In particular, the anti-inflammatory, antioxidant and liver-protecting effects of chrysanthemum have always made it useful in health products and traditional formulas (Xu et al., 2021; Xia et al., 2023). In recent years, with the increase in people's demand for health and the market's preference for ornamental flowers, the planting area of chrysanthemum has expanded rapidly and the degree of commercialization has continued to deepen.

But, when planting areas get bigger, problems with the soil usually show up too. Farmers often run into things like tired soil, trouble from growing the same crop over and over, and pests or diseases that are hard to deal with(Chen et al., 2018; Li et al., 2024a). Among the diseases, wilt and black spot are the most common. Wilt is caused by *Fusarium oxysporum*, and black spot comes from *Alternaria alternata*. These diseases not only hurt the plants and cut down the harvest, but also lower the quality of the medicine they're used for (Xu et al., 2021; Zhang et al., 2019). As for pests, aphids and the larvae of *Spodoptera litura* are the main ones that attack Hangbaiju. When there's an outbreak, farmers might lose part of their crop, or in bad cases, all of it (Li et al., 2024a; Zhang et al., 2025).

At present, the most commonly used pesticides are chemical pesticides, which are effective quickly, but of course there are many problems. On the one hand, the resistance of pests and diseases is increasing; on the other hand, the problem of chemical residues and damage to the environment has also attracted more and more attention (Chen et al., 2018). Long-term reliance on pesticides will not only pollute the land and increase its burden, but also affect the stability of the medicinal quality of Hangbaiju, and may even threaten the health of consumers (Burketová et al., 2015).

A greener and more sustainable solution is urgently needed. This study aims to solve the problem at the source - by systematically screening pest-resistant Hangbaiju varieties and clarifying their resistance basis. Whether it is at the molecular level, field performance, or actual pest and disease resistance, we hope to find several good varieties to provide strong support for subsequent green planting. Only by starting with variety improvement can we reduce dependence on pesticides and truly achieve the sustainable development of Hangbaiju in terms of its dual value of medicinal and ornamental use.

2 Overview of Major Diseases and Pests in Hangbaiju

2.1 Fungal and bacterial diseases

Hangbaiju (*Chrysanthemum morifolium*) is highly susceptible to a variety of fungal and bacterial diseases, which seriously affect its yield and quality. Leaf spot is one of the most common diseases, mainly caused by pathogens such as *Alternaria* spp. and *Stagonosporopsis chrysanthemi*, which manifests as necrotic spots on the leaves, followed by early leaf fall and reduced photosynthesis capacity (Liu et al., 2020). Root rot and wilt caused by *Fusarium oxysporum* will cause root rot, plant wilting, and eventually death, especially under conditions of poor soil health or long-term continuous cropping (Guo et al., 2014).

The infection cycle of these pathogens is closely related to environmental conditions. For example, warm and humid climates and dense planting patterns are conducive to the reproduction and spread of fungal spores, while soil-borne pathogens such as *Fusarium oxysporum* can survive for a long time in contaminated soil, leading to repeated occurrence of diseases (Guo et al., 2014). Continuous monoculture, lack of crop rotation system and improper field management often provide favorable conditions for the survival and spread of pathogens, which can easily induce outbreaks of diseases.

2.2 Insect pests affecting Hangbaiju

Aphids (*Macrosiphoniella sanbourni*) are one of the worst pests for Hangbaiju. They suck the juice from the plant, which makes it grow slowly. The leaves may curl up, and the flowers don't look as good (Chen et al., 2018; Wang et al., 2021). Other bugs like thrips and leaf miners also cause damage. They eat the leaves and flower parts, making the plant look worse and grow poorly (Zhan et al., 2025). So far, people have found at least 14 kinds of insects that harm Hangbaiju. These bugs affect how healthy the plant is and how much it can produce, though the level of damage is not the same for each one.

In addition to the damage caused by direct feeding, pests such as aphids and thrips often act as vectors for viral and bacterial pathogens, causing the disease to spread rapidly in the field and even across plots (Gong et al., 2019). This mode of transmission caused by vector insects makes disease prevention and control more complicated and often leads to mixed infections, which in turn increases the difficulty of governance (Gong et al., 2019; Zhan et al., 2025).

2.3 Current control strategies and limitations

Right now, farmers mainly use chemical pesticides to deal with diseases and pests when growing Hangbaiju. But using these chemicals too much has made some bugs and germs harder to kill, so the pesticides don't work as well over time (Chen et al., 2018; Zhan et al., 2025). Also, there's worry that the chemicals left in the flowers might not be safe. This makes people question if the product is healthy and could hurt how well it sells (Guo et al., 2014).

In recent years, some eco-friendly methods have started to show promise. For example, using rice straw biochar can make the soil better, lower the number of harmful germs, and help plants stay healthy (Guo et al., 2014). People are also paying more attention to integrated pest management (IPM). This includes things like rotating crops, planting different kinds of plants together, using helpful bugs to fight bad ones, and choosing stronger plant types that resist disease (Zhan et al., 2025). These ways try to fix the problems that come from using too many chemicals.

As more people want green and chemical-free products, it's important to grow plants in ways that are safer and better for the environment. But switching to these green methods isn't easy. There are still a lot of problems, like farmers not knowing enough, the costs being too high, and the lack of strong, pest-resistant plant types (Guo et al., 2014).

3 Genetic Resources and Resistance Traits in Hangbaiju

3.1 Germplasm diversity and resistant gene pools

Hangbaiju has significant genetic diversity, which provides an important basis for breeding disease-resistant and insect-resistant varieties. Studies using ISSR and SSR molecular markers have shown that there is a high degree of polymorphism between local varieties, wild relatives and breeding lines of Hangbaiju, showing rich resistance allele resources (Luo et al., 2018; Hodaei et al., 2019). For instance, ISSR analysis of 20 *Chrysanthemum* materials found that they could be classified into three major genetic groups, and the leaf spot resistance performance of these groups was highly consistent with field observations (Guo et al., 2014). SSR-based studies further confirmed the genetic differences between wild species, large-flowered varieties and local varieties, supporting the rational use of diverse germplasm resources in resistance breeding (Luo et al., 2018; Hao et al., 2022). Wild relatives and traditional landraces, such as 'Hangbaiju', 'Gongju', and 'Chuju', are particularly valuable for introducing novel resistance traits into breeding programs (Hodaei et al., 2019; Hao et al., 2022).

Molecular markers have become an important tool for screening resistant genotypes. For example, ISSR markers have been successfully used for early identification of leaf spot resistant varieties (Guo et al., 2014); while SSR and SNP markers are associated with aphid resistance and white rust resistance, providing technical support for marker-assisted selection (MAS) in resistance breeding (Luo et al., 2018; Fu et al., 2018; Sumitomo et al., 2021). Besides, transcriptome analysis has identified multiple differentially expressed genes (DEGs) and candidate resistance genes, most of which are involved in secondary metabolite synthesis, plant hormone signal transduction, and plant-pathogen interaction processes, and are significantly upregulated in resistant materials or under stress conditions (Zhang et al., 2019; Li et al., 2024a; Wang et al., 2024; Zhang et al., 2025).

3.2 Inheritance patterns of resistance traits

The resistance traits of chrysanthemum can be controlled by a single gene or regulated by multiple genes. For example, the resistance of the 'Southern Pegasus' variety to white rust (*Puccinia horiana*) is controlled by a single gene, and linkage analysis of SNP markers has verified this (Sumitomo et al., 2021). In contrast, resistance to aphids and wilt caused by *Fusarium oxysporum* often belongs to a polygenic inheritance pattern, involving multiple loci and their regulatory pathways. Association analysis found that multiple markers were associated with the aphid resistance trait, which can explain a large proportion of phenotypic variation, and have high heritability and moderate genetic gain, indicating that the trait has the genetic characteristics of a quantitative trait (Fu et al., 2018). Transcriptome studies also revealed that resistance to *Fusarium wilt* and black spot caused by *Alternaria alternata* involves complex transcription factor regulatory networks (like WRKY, bHLH, MYB), plant hormone signaling pathways, and metabolic pathways, further supporting its multi-gene control characteristics (Zhao et al., 2020; Li et al., 2024a; Ding et al., 2023; Miao et al., 2023a; b).

The expression of resistance traits is also affected by the interaction between genotype and environment. Field and greenhouse studies have shown that environmental factors such as temperature, humidity, and soil conditions can modulate the actual effectiveness of resistance genes (Guo et al., 2014; Hodaei et al., 2019). Taking aphid resistant varieties as an example, they exhibit stability in different seasons, but certain traits such as persistent metabolite accumulation during flowering are influenced by both genotype and environment (Hodaei et al., 2019; Long et al., 2022).

3.3 Screening indicators for disease and pest resistance

The resistance screening of Hangbaiju usually combines phenotype evaluation under field and control conditions, mainly examining indicators such as lesion size, disease severity, pest infection level, and plant growth potential (Guo et al., 2014; Fu et al., 2018; Li et al., 2024a). The results of grouping germplasm resources based on field performance often match molecular marker data, indicating that combining molecular screening with phenotype screening is a reliable method (Guo et al., 2014; Luo et al., 2018; Hodaei et al., 2019). In the evaluation of aphid resistance, commonly used indicators include aphid damage index and physiological and biochemical indicators (such as flavonoid content, enzyme activity, etc.) (Zhang et al., 2019; Wang et al., 2024) (Figure 1).

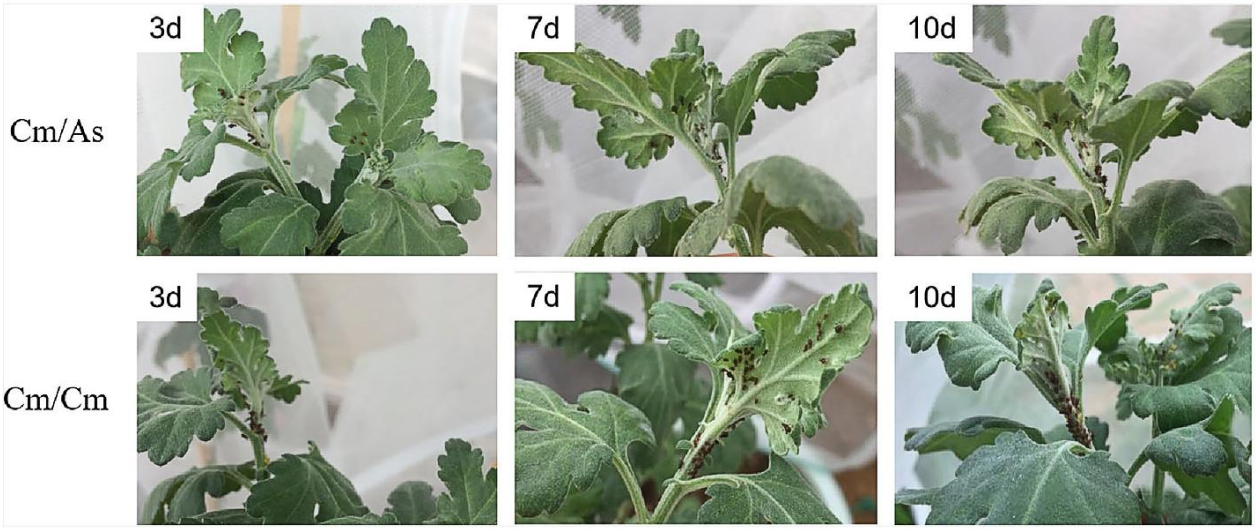


Figure 1 Representative pictures for aphid settlement at 3 d, 7 d and 10 d after aphid inoculation on selfrooted grafted chrysanthemum (Cm / Cm) and the grafted *Artermisia*-chrysanthemum (Cm / As) (Adopted from Wang et al., 2024)

Image caption: The figure shows the comparison of aphid colonization on leaves of self-rooted chrysanthemum (Cm/Cm) and chrysanthemum grafted on *Artermisia* (Cm/As) at 3, 7, and 10 days after aphid inoculation. The results show that over time, the number of aphids on Cm/Cm plants increased significantly, while the aphid expansion on Cm/As plants was limited and showed a slow growth trend (Adapted from Wang et al., 2024)

In terms of biochemical markers, flavonoid and phenolic acid content, antioxidant enzyme activity, and secondary metabolite composition can serve as important resistance response indicators when attacked by pests and diseases (Gong et al., 2019; Lu et al., 2024; Wang et al., 2024). Molecular resistance indicators include the expression of defense-related genes (e.g., *WRKY*, *bHLH*, *NPR1*, *CmWD40*), differentially expressed genes (DEGs) identified in transcriptome analysis, and resistance-related alleles detected by SSR, ISSR or SNP markers (Guo et al., 2014; Zhang et al., 2019; Ding et al., 2023; Miao et al., 2023a;b; Li et al., 2024a). The application of these markers not only helps early screening, but also accelerates the breeding process of resistant varieties.

4 Methods for Screening Disease and Pest Resistant Varieties

4.1 Field-based evaluation under natural infection

Field evaluation is still one of the core methods for screening disease and insect resistance of *Chrysanthemum morifolium*. Multi-location trials usually plant candidate varieties in different ecological and environmental regions to expose their true performance under diverse pathogens and pests. This method can capture the interaction effect between genotype and environment, thereby screening out resistant varieties with stable performance under different climatic conditions and pathogen groups. For example, a large-scale field trial conducted by Sidhya et al. (2024) on 40 *Chrysanthemum* genotypes showed that there were large differences in the degree of infestation of aphids, mealybugs and mites among different varieties, and it was mainly due to genetic differences. Similarly, resistance to white rust and leaf blight is often verified through cross-regional and cross-season field evaluations to ensure that the selected varieties have broad-spectrum and stable resistance (Sumitomo et al., 2021; Seliem et al., 2024).

To be closer to the challenges in actual planting environments, resistance screening is often combined with other environmental stresses such as drought, salinity or poor soil. This helps to identify varieties with multiple stress resistance, as environmental stress often affects the susceptibility of plants to diseases and insects. Studies have found that under combined stress conditions, some anatomical traits (like cuticle thickness and stem thickness) and the physiological responses of plants are closely related to their enhanced resistance to diseases such as bacterial blight (Li et al., 2024b; Seliem et al., 2024).

4.2 Artificial inoculation and pest challenge assays

Artificial inoculation and pest challenge experiments are usually conducted in a greenhouse or laboratory environment to ensure that plant materials are exposed to specific pathogens or pests under uniform and reproducible conditions. By controlling the inoculation concentration, time and environmental factors, this method can accurately compare the resistance performance of various varieties. For instance, standardized inoculation with *Alternaria alternata* or *Fusarium oxysporum* and uniform release of aphids have been widely used in the study of resistance mechanisms and the screening of resistant varieties (Ding et al., 2023; Miao et al., 2023a; Li et al., 2024a; Seliem et al., 2024). Transgenic and gene-edited materials are also often tested under artificial inoculation for pest and disease stress to verify the effect of specific resistance genes (Shinoyama et al., 2015; Pak et al., 2020).

Standardized scoring systems are key to quantifying disease severity and insect damage. Common scoring methods include numerical scoring or grading, examining indicators such as lesion size, leaf yellowing, insect population density or plant growth potential. Based on the scoring results, resistance levels can be assigned, allowing objective comparisons and facilitating early identification of resistant materials (Fu et al., 2018; Seliem et al., 2024). For example, white rust resistance testing uses obvious susceptible/resistant phenotypes, while aphid resistance is quantified by damage index and population growth rate (Kos et al., 2014; Nabeshima et al., 2014; Fu et al., 2018).

4.3 Molecular and biochemical validation

Molecular validation mainly studies the expression of candidate resistance genes through techniques such as RNA-Seq, qRT-PCR or transcriptome analysis. These methods can identify differentially expressed genes (DEGs) activated under pest and disease infestation conditions and their regulatory pathways. For example, overexpression or silencing of genes such as *CmWRKY8*-1, *CmMYB15* and *CmNAC083* have been shown to regulate the resistance of Hangbaiju to wilt, aphids and black spot, respectively (An et al., 2019; Ding et al., 2023; Miao et al., 2023a; Huang et al., 2023; Zhang et al., 2025). Expression profiling can also help reveal the key roles of plant hormone signaling, secondary metabolism synthesis and defense enzyme activity in resistance responses (Liu et al., 2020; 2021; Zhang et al., 2023; Li et al., 2024a; b).

Marker-assisted selection (MAS) uses molecular markers (e.g., SSR, ISSR, and SNP) that are closely linked to resistance loci to achieve early screening of resistant materials and efficient breeding. ISSR markers have been used to distinguish leaf spot-resistant Hangbaiju varieties, and SNP markers have been associated with white rust resistance in parental populations (Fu et al., 2018; Sumitomo et al., 2021; 2022). Association analysis and genome-wide association analysis (GWAS) have also identified markers associated with aphid and white rust resistance, enabling the application of MAS in resistance breeding (Fu et al., 2018; Xu et al., 2021). Currently, MAS strategies are being combined with field and laboratory screening to accelerate the development and application of resistant varieties.

5 Case Studies

5.1 Analysis of *CmWD40*-mediated disease-resistant Hangbaiju

In the process of screening disease- and insect-resistant Hangbaiju varieties, the study of immune regulation mechanisms at the molecular level provides precise targets for the breeding of superior germplasm. Zhang et al. (2025) reported an effector protein AaAlta1 derived from *Alternaria alternata*, which can recognize and activate the WD40 repeat protein *CmWD40* in *Chrysanthemum morifolium*, thereby activating the plant's jasmonic acid (JA) signaling pathway and inducing programmed cell death and defense responses.

The study showed that in Hangbaiju expressing AaAlta1, JA pathway-related genes were upregulated, indicating that this effector has the potential to induce host disease resistance. At the same time, *CmWD40* was expressed in a circadian rhythm under normal conditions, and its overexpression significantly enhanced the resistance of chrysanthemums to black spot disease, while gene silencing reduced resistance, verifying its positive regulatory role in the disease response (Figure 2). The study also used subcellular localization and bimolecular fluorescence complementation (BiFC) technology to confirm that AaAlta1 interacts with *CmWD40* in the cell nucleus.

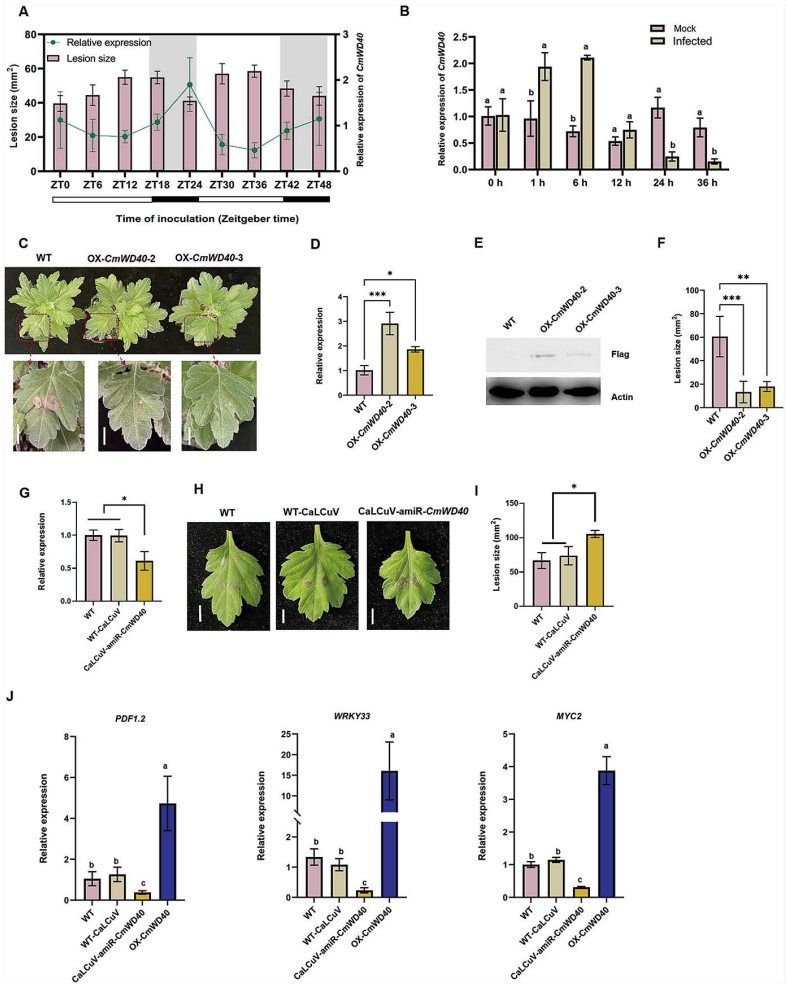


Figure 2 *CmWD40* regulates the resistance of chrysanthemum plants to *Alternaria alternata*. (A) The rhythmic expression pattern of *CmWD40* and the temporal variation in chrysanthemum susceptibility to *A. alternata*. The line chart represents the rhythmic expression pattern of *CmWD40* in wild-type (WT) plants under long-day (LD) conditions. Leaves were collected every 6h at the indicated times, and gene expression levels were assessed using quantitative reverse transcriptase polymerase chain reaction (qRT-PCR). The bar chart represents the mean lesion size on chrysanthemum leaves inoculated with *A. alternata* at dawn, i.e., at zeitgeber time (ZT)0 and every 6 h for 48 h under LD conditions. The size of the lesions was statistically analyzed at 48 hpi. Data are presented as the mean ± standard error of three biological replicates. (B) Relative expression levels of the *CmWD40* gene during infection were assessed using qRT-PCR. Data are presented as the mean ± standard error of three biological replicates. Different letters at the top of error bars indicate significant differences ($P < 0.05$, Tukey's test). (C) Disease symptoms caused by *A. alternata* infection in chrysanthemum leaves. Leaves of WT and *CmWD40* transgenic lines were inoculated with *A. alternata*, and images were captured at 48 hpi; scale bar=1 cm. (D) Identification of the *CmWD40* overexpression (OX) transgenic line (OX-*CmWD40*) at the transcript level using qRT-PCR. Samples were collected at dawn. Different letters at the top of error bars indicate significant differences ($P < 0.05$, Tukey's test). (E) Immunoblot analysis of *CmWD40* in two transgenic lines overexpressing *CmWD40*. Samples were collected at dawn. Total proteins of transgenic seedlings were extracted and detected with anti-Flag antibodies. Actin was used as an equal loading control. (F) Mean lesion size on WT and OX-*CmWD40* chrysanthemum leaves inoculated with *A. alternata* at 48 hpi. Data are presented as the mean ± standard error of three biological replicates. * $P \leq 0.05$ compared with control, as calculated by one-way analysis of variance (ANOVA). (G) Expression of *CmWD40* in CaLCuV-amiR-*CmWD40* transgenic lines. Samples were collected at dawn. Different letters at the top of error bars indicate significant differences ($P < 0.05$, Tukey's test).(H) Disease symptoms caused by *A. alternata* infection in chrysanthemum leaves. Leaves of the WT and cabbage leaf-curl geminivirus vector (CaLCuV)-amiR-*CmWD40* lines were inoculated with A. alternata, and images were captured at 48 hpi; scale bar=1 cm. (I) Mean lesion size on WT and *CmWD40* silenced chrysanthemum leaves inoculated with *A. alternata* at 48 hpi. Data are presented as the mean ± standard error of three biological replicates. * $P \leq 0.05$ compared with control, as calculated by one-way ANOVA. (J) qRT-PCR analysis for expression of *PDF1.2*, *WRKY33*, and *MYC2* genes reveals that their transcript levels are upregulated in OX-*CmWD40* and CaLCuV-amiR-*CmWD40* transgenic lines, respectively, upon infection with *A. alternata*. Data are presented as the mean ± standard error of three biological replicates. Different letters at the top of error bars indicate significant differences ($P < 0.05$, Tukey's test) (Adopted from Zhang et al., 2025)

This discovery reveals the key nodes of the natural resistance of Hangbaiju, and also provides theoretical support for green planting conditions without over-reliance on pesticide intervention. By screening materials with high *CmWD40* expression levels or enhanced functions in natural populations, it is expected that this resistance pathway will be introduced into actual breeding, thereby cultivating Hangbaiju varieties that are more adaptable to the green prevention and control system.

5.2 The *CmWRKY8-1* gene of Hangbaiju negatively regulates resistance to wilt disease

Hangbaiju wilt disease is caused by the fungus *Fusarium oxysporum*, which seriously affects its ornamental and economic value. WRKY transcription factors in plants play a key regulatory role in disease resistance signaling pathways, especially closely related to the defense mechanism related to salicylic acid (SA). Miao et al. (2023a) found that the gene *CmWRKY8-1* in the WRKY transcription factor family plays an important role in regulating disease resistance. Through gene cloning and transgenic technology, the researchers constructed a chrysanthemum transgenic line overexpressing the *CmWRKY8-1-VP64* fusion protein.

The results showed that these transgenic plants were more susceptible to *F. oxysporum* infection than the wild type (Figure 3). Further studies showed that the expression of this fusion protein inhibited the expression of multiple key genes in the salicylic acid (SA) signaling pathway (e.g., PAL, EDS1, NPR1, etc.), resulting in a decrease in endogenous SA content and the expression levels of related disease resistance genes *PR1*, *PR2*, and *PR5*, thereby weakening the plant's systemic acquired resistance.

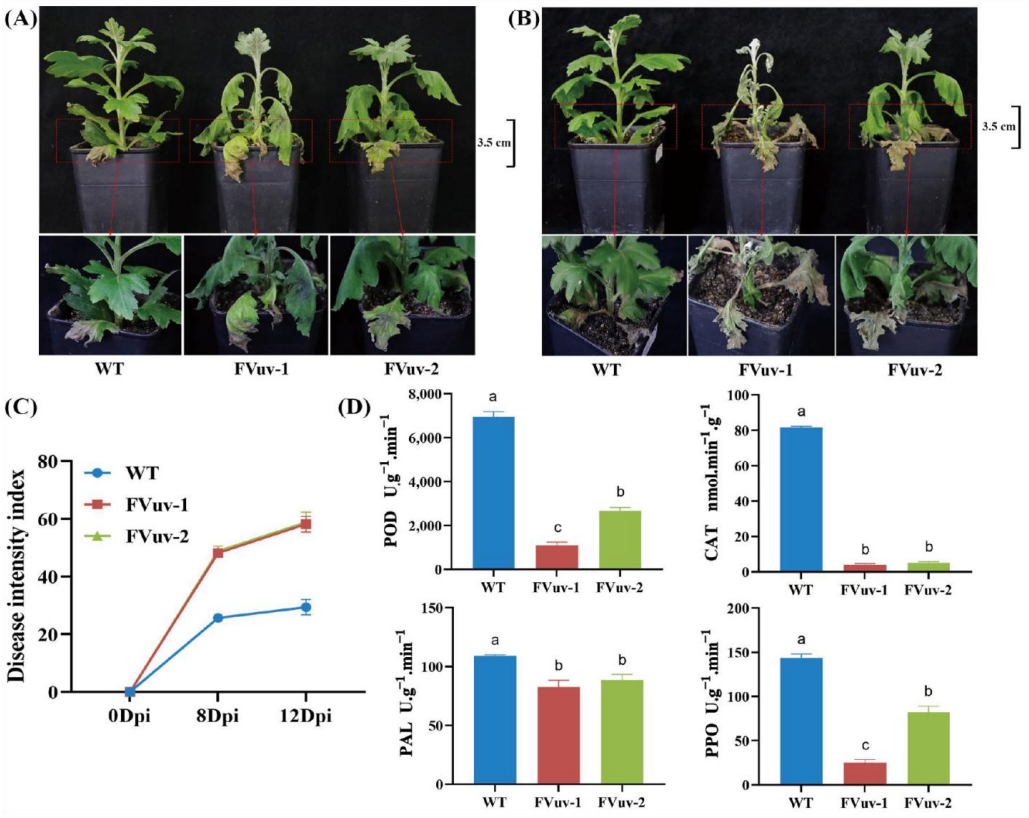


Figure 3 Physiological phenotypes after inoculation with *F. oxysporum*. (A) Phenotypes at the eighth day after inoculation with *F. oxysporum*. (B) Phenotypes at the twelfth day after inoculation with *F. oxysporum*. (C) Disease severity index of plants. (D) The content of POD, CAT, PAL, and PPO on the 8th day of inoculation (Adopted from Miao et al., 2023a)

Image caption: The figure systematically demonstrates that transgenic chrysanthemums overexpressing the *CmWRKY8-1-VP64* fusion protein have enhanced susceptibility to *Fusarium oxysporum* infection. Images on the 8th and 12th days (A, B) show that transgenic plants wilt and die severely, while the wild type is only slightly affected; disease index analysis (C) quantifies the difference, with transgenic plants significantly higher than wild types; defense-related enzyme activity assays (D) show that POD, CAT, PAL, and PPO activities in transgenic plants are all reduced. The results verify that overexpression of *CmWRKY8-1* weakens plant disease resistance (Adapted from Miao et al., 2023a)

The study revealed the molecular mechanism by which *CmWRKY8-1* negatively regulates Hangbaiju disease resistance by regulating the SA signaling pathway, and also suggested the dual regulatory role of WRKY family members in plant stress resistance. The research results have important application value for the breeding of disease-resistant Hangbaiju varieties, and provide a new molecular basis for in-depth exploration of the hormone signaling network in plant-pathogen interactions.

5.3 Field performance and agronomic traits

Field trials conducted under conditions of high pest and disease pressure have verified the comprehensive performance of resistant Hangbaiju varieties. For example, virus-free "Hangju" maintained high yield and medicinal quality after natural reinfection with B/R virus, outperforming the infected control plants (Bi et al., 2016). Similarly, in soils supplemented with biochar, the incidence of *Fusarium oxysporum* was significantly reduced, while yield and flower quality were also improved, indicating that resistant varieties can maintain good agronomic performance even under adverse conditions (Zhang et al., 2020).

A key question in resistance breeding is whether there is a “trade-off” between disease resistance and yield or flower quality. But, several studies have shown that some resistant Hangbaiju lines can combine high yield with high-quality flowers. For example, the application of 10% rice straw biochar not only reduced the incidence of diseases, but also increased yield by 23.9%, and the total flavonoid content in flowers also increased significantly (Zhang et al., 2020). Virus-free and resistant lines also showed improvements in yield and medicinal ingredients, indicating that resistance traits can be bred in conjunction with excellent agronomic traits and quality indicators (Bi et al., 2016).

6 Application Prospects in Green Cultivation Systems

6.1 Role in pesticide reduction and ecological balance

Promoting pest-resistant varieties of *Chrysanthemum morifolium* is a key step in achieving green cultivation systems by reducing chemical pesticide inputs. Field studies have shown that combining resistant strains with soil improvement measures such as rice straw biochar can inhibit the incidence of soil-borne pathogens such as *Fusarium oxysporum* by 42%-54%, while increasing yields by 23.9% compared to conventional planting methods (Chen et al., 2018). This model not only reduces dependence on synthetic pesticides, but also promotes the transition to low-input, environmentally friendly production methods, which is in line with the basic principles of sustainable agriculture (Munir and Bashir, 2019 ; Ikram et al., 2024).

In green cultivation practices, the combination of resistant Hangbaiju varieties and organic soil conditioners has been shown to improve soil microbial diversity, increase the number of beneficial bacteria and actinomycetes, and inhibit the growth of harmful fungi (Chen et al., 2018). Improved soil health helps build a more resilient agricultural ecosystem and indirectly promotes the development of pollinator populations by reducing pesticide residues and creating an ecologically balanced planting environment. Although direct research on the number of pollinators in chrysanthemum systems is still limited, extensive research in the field of sustainable horticulture supports the positive ecological effects of "reducing pesticide use and increasing biodiversity" (Munir and Bashir, 2019 ; Chadfield et al., 2022).

6.2 Compatibility with organic and GAP standards

Resistant Hangbaiju lines cultivated with minimal chemical inputs and sustainable soil management practices are well-suited for organic and Good Agricultural Practice (GAP) certification. The use of biochar and biostimulants, such as arbuscular mycorrhizal fungi (AMF), further enhances compliance with organic standards by improving plant health and stress tolerance without synthetic chemicals (Nelson et al., 2017; Chen et al., 2018). These practices facilitate the certification process and add value to the final product, making resistant lines attractive for organic and eco-labeled markets (Sniezko and Koch, 2017; Ahmad et al., 2020).

Hangbaiju produced under green cultivation systems demonstrates higher yield, improved flavonoid content, and better overall quality, which are highly valued in health-conscious and premium markets (Sniezko and Koch, 2017; Chen et al., 2018; Ahmad et al., 2020). Certification and quality improvements can increase market

competitiveness, open new sales channels, and provide economic incentives for growers to adopt resistant varieties and sustainable practices.

6.3 Strategy for integrating resistance breeding in sustainable systems

A holistic strategy that links resistance breeding, sustainable cultivation, and targeted marketing is essential for the success of green Hangbaiju production. Breeding programs should prioritize resistance traits compatible with organic and low-input systems, while extension services and technical support can guide farmers in adopting best practices and accessing high-value markets (Nelson et al., 2017; Ikram et al., 2024). This integrated pipeline ensures that resistant varieties are not only developed but also effectively utilized and marketed.

Government and industry support, including technical training, subsidies for sustainable inputs (e.g., biochar, AMF), and streamlined certification processes, are crucial for scaling up green Hangbaiju cultivation. Policy frameworks that encourage the adoption of resistant varieties and sustainable practices can help farmers transition to green systems while maintaining profitability and environmental stewardship (Wigboldus et al., 2016; Nelson et al., 2017; Ikram et al., 2024).

7 Challenges and Future Directions

7.1 Limitations in current screening and breeding efforts

One of the main challenges in breeding Hangbaiju for disease and insect resistance is that the genetic basis of cultivated varieties is narrow, which limits the scope of available resistance genes. Currently, most commercial varieties are derived from limited parental lines, resulting in genetic bottlenecks and lack of diversity in resistance traits (Su et al., 2019; Mekapogu et al., 2022). Efficient molecular markers for key resistance genes are still lacking, especially in complex polyploid crops such as chrysanthemum (Sumitomo et al., 2021; 2022). Although genomics and marker-assisted selection (MAS) have made some progress in recent years and identified some resistance loci, high-throughput and stable marker systems for multiple diseases and pests have not yet been perfected (Su et al., 2019; Sumitomo et al., 2021).

Now, breeding efforts focus on single pest and disease resistance, which may result in selected varieties showing poor resistance to other biotic stresses (Kos et al., 2014; Shinoyama et al., 2015; Li et al., 2020). It is technically difficult to integrate resistance traits to multiple pests and diseases, such as aphids, white rust, and alternaria, into one variety. This is mainly due to the complex inheritance patterns of resistance traits, potential negative linkage drag, and the lack of efficient trait aggregation strategies (Shinoyama et al., 2015; Mundt, 2018). The persistence of resistance is also threatened because pathogens and pest populations evolve rapidly and may break through the defenses of single-gene resistance (Mundt, 2018).

7.2 Gaps in cultivar adoption and dissemination

Although several resistant varieties of Hangbaiju have been introduced, the adoption rate among farmers in actual production is still low. The main obstacles include: insufficient awareness of the advantages of resistant varieties, lack of technical knowledge in integrated pest management (IPM), and concerns about the "compromise effect" of yield or quality (Sidhya et al., 2024). Due to the imperfect extension services and knowledge transfer mechanisms, there is a clear hesitation in the adoption of new varieties, especially among small farmers and traditional growers.

A stable seed supply system and an effective variety rights protection mechanism are key to the widespread use of resistant varieties. However, as an ornamental crop, Hangbaiju faces special challenges, such as widespread informal breeding, weak intellectual property protection, and difficulty in obtaining certified seedlings (Mekapogu et al., 2022).

7.3 Future prospects in integrated resistance breeding

The integrated application of multi-omics technologies, including genomics, transcriptomics, proteomics, and metabolomics, has brought new opportunities for analyzing complex resistance mechanisms and accelerating candidate gene screening (Mekapogu et al., 2022; Ding et al., 2023). In recent years, gene editing technologies such as CRISPR/Cas9 have been established in Hangbaiju, which is expected to achieve precise modification of resistance genes and break through the limitations of traditional breeding (Chen et al., 2024).

In the future, breeding of Hangbaiju should focus on developing climate-resilient varieties that are resistant to multiple pests and diseases as well as drought and heat stresses. This will rely on the combination of advanced phenotyping platforms, high-throughput screening technologies, and predictive breeding models. Interdisciplinary collaboration between breeders, plant pathologists, entomologists, and farmers will also be the key to the successful development and application of new varieties adapted to green cultivation and sustainable production systems.

Acknowledgments

The authors sincerely thank Dr. Zhang for reviewing the manuscript and providing valuable suggestions, which contributed to its improvement. Additionally, heartfelt gratitude is extended to the two anonymous peer reviewers for their comprehensive evaluation of the manuscript.

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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