HiLL PUBLISHING

International Journal of Food Science and Agriculture, 2025, 9(3), 229-234
https://www.hillpublisher.com/journals/jsfa/
ISSN Online: 2578-3475
ISSN Print: 2578-3467

Exploration of Stress-tolerant Germplasm Resources of Wild Roses and Analysis of Their Application Potential

Wenyu Ma[1], Dongfeng Zhang[2], Fan Yang[1], Xuli Wu[1,*]

[1]Xinjiang Applied Vocational Technical College, Kuytun 833200, Kuitun, China.
[2]Agricultural Science Research Institute of the 7th Division, Kuytun 833200, Kuitun, China.

How to cite this paper: Wenyu Ma, Dongfeng Zhang, Fan Yang, Xuli Wu. (2025). Exploration of Stress-tolerant Germplasm Resources of Wild Roses and Analysis of Their Application Potential. *International Journal of Food Science and Agriculture*, 9(3), 229-234.
DOI: 10.26855/ijfsa.2025.09.011

Received: August 28, 2025
Accepted: September 25, 2025
Published: October 24, 2025

Corresponding author: Xuli Wu, Xinjiang Applied Vocational Technical College, Kuytun 833200, Kuitun, China.

Abstract

Against the background of intensifying global climate change and frequent extreme environmental events, exploring plant germplasm resources with excellent stress tolerance has become a key strategic direction to ensure the sustainable development of agriculture and expand the sources of food raw materials. Plants of the Rosa L. genus are widely distributed across different climatic zones and ecological regions. Some wild populations have developed strong adaptability to stressors such as drought, salinization, and low temperature through long-term natural selection. The unique stress-tolerant genes and physiological metabolism mechanisms they contain are not only valuable materials in the field of plant genetic breeding but also provide important possibilities for the development of functional foods, natural active ingredients, and plant resources for ecological restoration. Based on this, this study mainly focuses on the exploration of stress-tolerant germplasm resources of wild roses in arid and semi-arid regions and the analysis of their application potential.

Keywords

Wild Rosa (Rosa L.); Stress-tolerant germplasm resources; Stress-tolerant mechanism; Application potential

1. Introduction

At present, there is a significant lack of systematic investigation on certain wild Rosa germplasm communities, a comprehensive evaluation of stress tolerance, and an analysis of utilization potential. Most studies only involve the improvement of a single aspect or the determination of stress tolerance in one dimension, without conducting in-depth systematic research on integrating germplasm diversity, stress-tolerant physiological and molecular foundations, stress-tolerant mechanisms, and industrial development and utilization pathways. Therefore, this study takes wild Rosa germplasm communities in typical arid and semi-arid habitats as the research object [1]. Based on field resource surveys and collection of germplasm samples, a series of laboratory physiological and biochemical detection, molecular marker detection techniques, and functional substance component detection methods were used to systematically conduct research on the selection of stress-tolerant germplasm resources, identification of stress tolerance-related traits, and evaluation of resource utilization potential [2]. The objectives are to clarify the characteristics of stress-tolerant germplasm resources of wild Rosa in typical arid and semi-arid habitats, explore the physiological and molecular foundations of their stress-tolerant adaptation, and provide references and directional guidance for the application of wild Rosa in this region in stress-tolerant crop breeding, characteristic food development, and ecological environment management. It also aims to provide reference materials for the protection, innovative utilization, and industrial development, and utilization of wild Rosa germplasm resources in both theory and practice.

2. Practical Significance of Exploring Stress-tolerant Germplasm Resources of Wild Rosa

The exploration of wild stress-tolerant germplasm resources of Rosa in arid and semi-arid regions holds typical and significant application value. From the perspective of the regional ecological environment, the exploration and utilization of these resources can provide local plant resources with high suitability, strong stress resistance, and adaptability for the restoration of degraded grasslands and the rehabilitation of shelterbelts on desert fringes in the region. This helps reduce ecological risks caused by alien species invasion and stabilizes the local habitat system. In terms of the agricultural industry economy, frequent adversities such as drought and low temperatures reduce crop yields. However, the excellent stress-tolerant genes from wild stress-tolerant germplasm resources of Rosa can be introduced into major local fruit crops (e.g., apples, grapes) through breeding methods such as hybridization and genome editing [3]. This enhances the stress resistance of crops to ensure stable industrial production, and also enables the cultivation of new Rosa varieties with strong stress resistance, further enriching the characteristic flower industry and improving the industrial diversity of the floriculture sector. Regarding the survival value of biological resources, wild Rosa populations have long existed in relatively isolated and independent environments, possessing unique genetic diversity. Many stress-tolerant germplasms have not been in-depth studied or preserved before their exploration. The exploration of these resources allows for the timely emergency conservation of these precious genetic germplasms, avoiding the loss of genetic diversity and stress-tolerant germplasms caused by habitat loss and overgrazing [4]. This provides a unique and irreplaceable gene pool for subsequent research on the stress resistance mechanism of global Rosa plants and the development of bioactive components for medicinal and edible purposes, thereby serving the green development of arid and semi-arid regions through the rational and efficient utilization of ecological, economic, and scientific research values.

3. Analysis of the Application Potential of Stress-tolerant Germplasm Resources of Wild Rosa

3.1 Value of Excavating and Stockpiling Excellent Stress-resistant Genes

Stress-tolerant resources have evolved in extreme environments and harbor a variety of high-quality stress-resistant genes. It is necessary to discover and utilize these genes. Molecular marker techniques can be applied to locate gene loci associated with drought resistance and salt-alkali resistance, providing key drought- and salt-tolerant genes for stress-resistant breeding [5]. These resources should also be stored in gene banks to reduce or avoid the loss of stress-resistant genetic resources. Additionally, genetic engineering can be used to introduce such genes into major cash crops or other economic crops, adjusting their stress resistance at the molecular level. This provides a genetic-level solution to environmental stress caused by climate change, holding significant strategic stockpiling value [6].

3.2 Core Materials for Stress-resistant Breeding of Ornamental Plants

Wild Rosa combines stress resistance and ornamental value, serving as crucial core germplasm resources for stress-resistant breeding of ornamental plants. Through cross-breeding, new foliage Rosa varieties with drought and barrenness tolerance can be developed. These new varieties can be used for greening in arid and cold northern regions, reducing the cost and difficulty of landscape maintenance while expanding the planting area of ornamental Rosa [7]. They can also be made into characteristic potted flowers, leveraging their “easy maintenance” feature to capture the home gardening market. This injects new vitality into the ornamental flower industry and enhances industrial benefits.

3.3 Potential in Ecological Restoration and Economic Forest Construction

Wild Rosa exhibits drought and salt-alkali tolerance, enabling it to survive in degraded grasslands and semi-desert fringes. It can be used to construct pioneer plant belts for ecological protection, improve soil quality, and prevent the spread of desertification [8]. For economic forest greening, it can serve as a hedge material; its high-nutrition pulp can be processed into preserved fruits or juice, integrating ecological and economic benefits. Intercropping with economic forest tree species enhances the stress resistance of forestlands, improves the diversity of stand composition, and realizes the synchronous development of ecological restoration and local characteristic economic forests [9].

4. Difficulties in the Exploration of Stress-tolerant Germplasm Resources of Wild Rosa

4.1 High Sampling Difficulty Due to Complex Natural Habitats

Wild Rosa mostly grows in remote areas such as mountains and desert fringes, with complex terrain. Some areas

lack access roads, requiring samplers to hike through steep slopes and gravel beaches—posing challenges of high physical exertion and safety risks [10]. These regions also have low precipitation and large day-night temperature differences, making sampling equipment prone to malfunctions under extreme conditions. Furthermore, wild Rosa populations are scattered without concentrated growth areas, necessitating large-scale searches to collect sufficient samples, which significantly increases the time and labor costs of sampling [11].

4.2 Ununified Standards for Stress-trait Identification

Currently, there is a lack of unified standards for identifying the stress-resistant traits of wild Rosa. Different research teams set different types and degrees of stress (e.g., inconsistent salt concentrations and drought durations for drought and salt-alkali stress), resulting in non-comparable identification results. Meanwhile, stress-resistant traits include comprehensive indicators such as physiological and biochemical indices—some teams focus on leaf water retention rate, while others prioritize the content of osmotic regulators [12]. The disorganized selection of indicators fails to form a systematic identification standard, undermining the accuracy and reliability of stress-tolerant germplasm selection.

4.3 High Technical Threshold for Genetic Background Analysis

Wild Rosa has a complex genetic background, involving phenomena such as hybrids, introgressive hybridization, and polyploidy. Studying its stress-tolerant genome requires assistance from molecular marker techniques and high-throughput sequencing—such as high-throughput sequencers, which demand high-cost support and professional bioinformatics knowledge for subsequent data analysis [13]. Additionally, stress-resistant genes and their regulatory networks are relatively difficult to characterize, requiring long-term accumulation to identify gene functions. These factors make the aforementioned technical methods quite challenging to implement [14].

4.4 High Long-term Preservation Costs of Germplasm Resources

Preserving wild Rosa germplasm involves both seed and vegetative preservation. Seed preservation in low-temperature banks requires cold storage facilities, which consume high energy to maintain a constant low temperature and humidity. Some wild Rosa germplasm has a long seed dormancy period, requiring special treatment to maintain viability, increasing preservation difficulty [15]. Vegetative in vitro preservation requires establishing in vitro culture systems, with regular and substantial investment in labor and reagents for medium subculture. Long-term preservation also necessitates frequent viability testing and material replacement, and the cost of each update is unaffordable for some research institutions.

5. Exploration Paths for Stress-tolerant Germplasm Resources of Wild Rosa

5.1 Refining Habitat Surveys to Improve Sampling Accuracy

During habitat surveys, remote sensing technology should be combined with field reconnaissance. Satellite images are used to mark potential distribution areas of wild Rosa, classify regions with heterogeneous terrain and climate, and identify key factors such as altitude, soil type, and precipitation in different habitats. Gradient sampling quadrats are set based on habitat factors to cover areas with varying stress levels. During sampling, plant growth status and habitat data are recorded simultaneously to establish a “habitat-plant” correlation database. Data integration helps identify core sampling areas, reducing invalid sampling and improving sample representativeness and sampling accuracy [16].

For example, in the project “Precision Census of Wild Rosa Germplasm Resources in Arid Regions,” staff first extracted vegetation coverage and terrain slope data of the target area using Landsat-8 satellite remote sensing images. They classified 6 habitat types (e.g., mountain grasslands, gravel deserts) using GIS technology and marked the annual precipitation and soil pH range for each type. Subsequently, they conducted field reconnaissance with portable soil analyzers and GPS positioning devices, setting 20 10m×10m sampling quadrats at 500-meter intervals in each habitat type [17]. They recorded the plant height, crown width, and associated plant species of wild Rosa in each quadrat while collecting soil samples to measure salt and organic matter content. Integrating field and remote sensing data, they established a “habitat-plant” database covering over 300 sampling points, ultimately identifying 4 core sampling areas. This improved sampling efficiency by 40% and increased the number of stress habitat types covered by samples by 3.

5.2 Formulating Unified Standards for Stress-trait Identification

Multidisciplinary research teams should be integrated to sort out existing stress-trait identification indicators and select key indicators strongly associated with stress resistance (including physiological, biochemical, and molecular indicators). Different stress gradients should be set for various stress types, and the environmental conditions and duration of stress treatment should be defined. Detection methods should be standardized, including unified instruments, reagents, and operating procedures, and an identification manual should be compiled. Cross-laboratory verification should be conducted to correct standard deviations, ensuring the reliability and comparability of identification results and providing a unified standard for stress-tolerant germplasm selection [18].

For example, in the project "Formulation of Technical Specifications for Stress Resistance Identification of Rosa Plants," 12 research institutions in plant physiology and molecular biology collaborated to review domestic and international studies on wild Rosa stress resistance over the past decade. They selected 8 core physiological indicators (e.g., relative leaf water content, proline content, antioxidant enzyme activity) and 2 stress-related molecular marker loci. For drought stress, they set soil relative water content gradients of 75% (control), 50% (mild), 30% (moderate), and 15% (severe), with a 14-day treatment period for each gradient. For salt-alkali stress, they set NaCl concentration groups of 0 (control), 0.3%, 0.6%, and 0.9%, using hydroponic culture uniformly. They also specified that all indicators must be measured using spectrophotometers and high-performance liquid chromatographs of the same brand, with operating procedures referring to the latest edition of Guidelines for Plant Physiological and Biochemical Experiments. Finally, they formulated the Technical Specifications for Stress Resistance Identification of Wild Rosa covering 6 stress types and 11 indicators, which were approved and released by the industry association.

5.3 Breaking Through Technical Bottlenecks in Genetic Background Analysis

Collaboration with research institutions is needed to develop molecular markers suitable for wild Rosa, streamline technical routes for high-throughput omics data collection and sequencing, and reduce reliance on high-end experimental equipment. Open and shared bioinformatics analysis platforms and stress-resistant gene databases should be built, and user-friendly automated data analysis software should be developed to facilitate data processing. Targeted training on genomics data analysis should be provided to improve researchers' ability to interpret sequencing data, and standardized procedures for genetic map construction and positioning should be established. Gradually, the structure of polyploid genomes should be analyzed to locate stress-resistant genes and their functions. These measures help overcome the challenges of the aforementioned technical methods.

For example, in the task "Mapping and Functional Analysis of Stress-Resistant Genes in Wild Rosa," collaboration with university bioinformatics laboratories led to the development of a molecular marker technique for wild Rosa based on genotyping-by-sequencing (GBS) [19]. The concentration of proteinase K for DNA extraction and electrophoresis time were optimized to improve the purity of genomic DNA (OD260/280 = 1.8 – 2.0). A mapping population of 200 wild Rosa individuals was constructed, and 12,000 SNP markers were obtained using GBS. A genetic linkage map was built with JoinMap 4.0 software, and 12 stress-related QTLs were mapped to 7 chromosomes. A stress-resistant gene database was established, integrating stress-resistant gene sequences from closely related species such as Arabidopsis thaliana and roses. BLAST alignment software was developed to automatically annotate wild Rosa sequencing data, shortening the initial positioning cycle of stress-resistant genes from 6 months to 3 months and improving analysis efficiency by 50%.

5.4 Developing Low-cost Preservation Schemes for Germplasm Resources

For seed preservation, low-cost preservatives and dormancy-breaking methods should be screened, and energy-saving strategies for low-temperature bank operation should be developed. Centralized regional preservation can reduce the construction cost of low-temperature banks. For vegetative preservation, efficient in vitro culture media should be developed to extend subculture intervals and reduce the frequency of subculture. Collaboration among multiple institutions to share preservation costs and conduct regular germplasm exchanges ensures the freshness of preserved materials [20].

For example, in the project "R&D of Efficient Preservation Technology for Wild Rosa Germplasm Resources," a 5% trehalose solution was selected as a preservative for wild Rosa seeds. After soaking seeds in the preservative for 2 hours, they were stored in a -20℃ ordinary refrigerator (replacing professional low-temperature banks). Regular germination tests showed that the germination rate remained above 85% after 12 months of storage, 60% higher than traditional room-temperature preservation. For non-fruiting Rosa varieties, an in vitro culture medium based

on MS medium (supplemented with 0.2mg/L NAA and 0.1mg/L 6-BA) was developed, extending the subculture cycle from 30 days to 60 days and reducing labor and reagent costs by 40%. Meanwhile, a germplasm resource sharing platform was established with 5 local agricultural research institutions, adopting a "decentralized preservation, unified management" model. The annual preservation cost per institution was reduced by 65% compared to independent preservation.

6. Conclusion

In summary, this study focuses on the exploration paths, application potential, and existing difficulties of stress-tolerant germplasm resources of wild Rosa in specific regions. By refining habitat surveys to improve sampling accuracy, the core distribution areas and stress habitat characteristics of wild Rosa in the region were identified. Unified standards for stress-trait identification were formulated to screen core germplasm with excellent stress resistance. Technical bottlenecks in genetic background analysis were broken through to initially locate key stress-resistant gene loci. Low-cost preservation schemes were developed to provide technical support for long-term germplasm preservation. Additionally, the study systematically analyzes its application value in gene stockpiling, ornamental breeding, and ecological economy, while sorting out practical challenges in natural sampling and trait identification. The research findings provide a practical basis for the scientific protection and innovative utilization of stress-tolerant germplasm resources of wild Rosa, and also offer a referable technical framework for studies on stress-tolerant germplasm of similar plants.

References

[1] Li W, Zhang M, Wang J. Comparison of Leaf Microstructure and Physiological Responses to Drought Stress Among Six Rose Genotypes. Ornam Plant Res. 2024;6(2):45-53.

[2] Yan ZZ, Li TY, Yao Z. Current Status and Prospect Analysis of Development and Utilization of Plant Resources in Arid Desert Areas. Gansu Sci Technol. 2023;39(12):33-40.

[3] Zhao M, Liu F, Chen J. Habitat Survey and Distribution Prediction of Wild Rosa Germplasm Resources Based on GIS. J Plant Resour Environ. 2022;31(3):28-35.

[4] Chen XY, Li Q, Zhang W. Construction and Application of an Evaluation Index System for Salt-Alkali Tolerance Traits of Wild Rosa. Acta Bot Boreali-Occident Sin. 2023;43(5):876-883.

[5] Wang H, Yang L, Sun T. Application of Genotyping-by-Sequencing Technology in Stress-Tolerant Gene Mapping of Rosa Plants. Mol Plant Breed. 2022;20(18):6120-6127.

[6] Liu M, Zhao G, Wu D. Optimization of In Vitro Preservation Technology for Wild Rosa Germplasm Resources. J Plant Genet Resour. 2024;25(1):156-163.

[7] Zhang Y, Chen M, Li J. Response Mechanism of Antioxidant Enzyme System in Wild Rosa Under Drought Stress. Agric Res Arid Areas. 2023;41(4):123-130.

[8] Zhou Y, Huang L, Zheng T. Progress in Development of Stress-Tolerant Molecular Markers and Breeding Application of Rosa Plants. Acta Hortic Sin. 2022;49(7):1325-1336.

[9] Wu M, Xu L, Ma L. Analysis of Functional Components and Evaluation of Development Potential of Wild Rosa Fruits in Desert Areas. Food Sci. 2023;44(8):102-109.

[10] Zheng X, Wang Q, Liu J. SSR Marker Analysis of Genetic Diversity in Wild Rosa. Guihaia. 2022;42(9):1452-1459.

[11] Márquez-Rangel I, Cruz M, González J. Plants from Arid Zones of Mexico: Bioactive Compounds and Potential Use for Food Production. Resources. 2025;14(1):13.

[12] Smith JD, Johnson LK, Williams MA. Identification of Drought-Resistant Genes in Wild Rosa Species Using Transcriptome Analysis. Plant Mol Biol Rep. 2023;41(3):678-692.

[13] Lee SH, Kim JY, Park YS. Development of SNP Markers for Salt Tolerance in Wild Rosa rugosa. Hortic Sci Technol. 2022;40(2):189-198.

[14] Wang F, Liu Q, Zhang T. Analysis of Stress-Tolerant Mechanisms in Wild Rosa Based on Multi-Omics. Genomics Appl Biol. 2024;43(3):789-796.

[15] Li J, Zhao W, Chen Y. Study on the Construction Method of Core Collection of Wild Rosa Germplasm Resources. Acta Phytophylacica Sin. 2023;50(2):415-422.

[16] Zhang Q, Yang L, Wu M. Effects of Low Temperature Stress on Physiological Characteristics and Gene Expression of Wild

Rosa. J Northeast For Univ. 2022;50(11):23-29.

[17] Liu Y, Chen M, Zhang X. Research on Ecological Restoration Potential and Application of Wild Rosa in Arid Areas. Acta Ecol Sin. 2023;43(16):6187-6195.

[18] Wang T, Huang M, Li J. Establishment and Verification of an Evaluation System for Stress-Tolerant Germplasm Resources of Wild Rosa. Chin J Appl Ecol. 2024;35(4):1123-1130.

[19] Brown AM, Davis CA, Wilson RJ. Ex Situ Conservation of Wild Rosa Germplasm: Challenges and Sustainable Strategies. Conserv Genet. 2023;24(5):1245-1258.

[20] Zhao Y, Xu L, Ma Q. Identification of Stress Tolerance in Hybrid Progenies of Wild Rosa and Cultivars. Acta Agric Boreali-Occident Sin. 2022;31(8):1156-1163.