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Genetic Diversity and Adaptability Analysis of Wild Rice Germplasm Resources

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Abstract The study delves into the genetic diversity and adaptability of wild rice, revealing its immense potential in rice breeding. Utilizing molecular marker techniques, we gained profound insights into the genetic diversity of the wild rice genome, providing a valuable genetic foundation for breeding. Wild rice exhibits exceptional adaptability, and its performance in terms of stress resistance and environmental adaptation lends theoretical support to its application in breeding. Particularly in rice breeding, harnessing wild rice genes has emerged as a crucial avenue for enhancing both crop yield and stress resistance. The utilization of gene-editing and transgenic technologies presents innovative possibilities in this regard. On the conservation front, emphasis is placed on strengthening the protection of the native habitats of wild rice, advocating for the establishment of a global wild rice gene bank, and fostering public awareness through education and outreach. This comprehensive understanding provides scientific guidance and a sustainable development path for future rice breeding and the preservation of wild rice germplasm resources.
Keywords Wild rice (*Oryza rufipogon*); Genetic diversity; Adaptability; Rice breeding

Oryza rufipogon is a close ancestor of cultivated rice and is a national level II protected plant. During the long evolutionary process of wild rice, due to the complex geographical environment and various ecological factors, rich genetic diversity has been formed, which contains abundant excellent gene resources, such as disease and insect resistance, stress resistance genes, efficient nutrition, high yield and quality, male infertility and other genes. These excellent genes are the important material basis and "resource treasure trove" for solving the many problems in current rice production (Yang et al., 2022).

Wild rice germplasm resources, as a member of the rice family, have unique genomic composition and biological characteristics. In this study, we will provide a detailed definition and overview of the germplasm resources of wild rice, clarify its position in the rice family, and its relationship with cultivated rice. On this basis, we will use modern genetic methods such as molecular marker technology to systematically determine the genetic diversity of wild rice germplasm resources and analyze their genetic structure in different populations. This will provide necessary data support for us to gain a deeper understanding of the wild rice genome.

This study conducts a detailed analysis of the genetic diversity of wild rice and uses molecular marker technology to deeply study the genetic differences between different populations of wild rice, thereby revealing their adaptive strategies in the evolutionary process. In addition, we will also focus on the impact of genetic diversity on the stress resistance of wild rice and explore its adaptability in different ecological environments. On the one hand, this will help us better understand the ecological significance of wild rice, and on the other hand, it will provide a theoretical basis for its potential application in stress resistant breeding of cultivated rice.

By studying its ecological adaptability, we can understand the growth and reproduction strategies of wild rice under different habitat conditions, providing reference for its application in cultivation environments. Examining the impact of human factors on its adaptability, especially the impact of human activities on the habitat of wild rice, is crucial for developing effective protection and utilization strategies.

In addition, we will focus on the application of wild rice germplasm resources in rice breeding. By utilizing the genes of wild rice, we have the potential to improve the stress resistance of cultivated rice, enabling it to better adapt to constantly changing environmental conditions. At the same time, we will also explore the potential value of wild rice in improving rice yield and quality, in order to provide strong support for future rice breeding work.

1 Wild Rice Germplasm Resources

1.1 Definition and Overview

Wild rice germplasm resources, as an important component of the rice family, refer to rice related populations that grow and evolve in the natural environment. Compared with cultivated rice, wild rice exhibits more primitiveness and diversity in morphology, biological characteristics, and genetic genes. These wild populations are widely distributed near wetlands, swamps, and rivers on various continents around the world, adapting to different climate and soil conditions (Shi et al., 2020).

The overview of wild rice germplasm resources includes its close relationship with cultivated rice. Although wild rice plays an important role in nature reserves in ecosystems, its close relationship with cultivated rice makes it an important gene pool for rice genetic improvement. This natural genetic relationship endows wild rice germplasm resources with a richer genome compared to cultivated varieties, and has stronger survival and stress resistance. Therefore, in-depth research on wild rice germplasm resources not only helps to understand the origin and evolution of rice, but also provides potential genetic resources for improving the resistance, adaptability, and productivity of cultivated rice (Xing et al., 2021).

From an ecological perspective, wild rice germplasm resources play an important role in maintaining ecological balance between wetlands and rivers. It adapts to diverse habitat conditions, including high temperature, high humidity, and different soil types, allowing wild rice to survive and reproduce in complex and ever-changing natural environments. This adaptability makes it an important component of the ecosystem, maintaining the health of wetland ecosystems.

Wild rice germplasm resources cover their growth and evolutionary characteristics in the natural environment, as well as their genetic relationships with cultivated rice. This resource not only provides abundant materials for the study of rice genetic diversity, but also provides important genetic resources for the agricultural field, with important scientific research and practical application value.

1.2 Methods for measuring genetic diversity

China has abundant resources of *O. rufipogon*, and Chen (2001) analyzed the genetic diversity of *O. rufipogon* distributed on the Tropic of Cancer in Guangxi from a morphological perspective. The results indicate that common wild rice has rich genetic diversity in morphology. Among all common wild rice varieties, the creeping type accounts for 45.11%, the tilting type accounts for 35.00%, the semi upright type accounts for 9.78%, and the upright type accounts for 2.97%. The plant height of ordinary wild rice ranges from 1.30 to 2.50 meters.

The DNA extraction of wild rice is the first step in determining genetic diversity, which typically utilizes modern molecular biology techniques such as CTAB or commercial DNA extraction kits to extract high-quality genomic DNA from wild rice samples. The extracted DNA serves as the basis for subsequent analysis, ensuring the accuracy and reliability of the study.

The application of molecular marker technology plays an important role in the study of genetic diversity in wild rice. Common molecular marker technologies include randomly amplified polymorphisms (RAPD), microsatellite markers (SSR), single nucleotide polymorphisms (SNP), etc. These technologies reveal the level of genetic diversity among different populations and individuals of wild rice by detecting the differences in DNA molecules among different individuals. Microsatellite markers have become one of the preferred methods for studying the genetic diversity of wild rice due to their high variability and polymorphism. They provide highly variable molecular markers by analyzing simple repetitive sequence units in DNA sequences.

In addition, population genetic structure analysis is also an important means to determine the genetic diversity of wild rice. This method reveals the genetic and phylogenetic relationships between different wild rice populations by studying the distribution of gene frequencies in different populations. The main analytical tools include principal component analysis (PCA), cluster analysis, and model independent population structure analysis. These analysis methods can effectively determine the genetic connections between wild rice populations, providing strong support for further research (Banaticla-Hilario and Sajise, 2022).

The impact of genetic diversity on the stress resistance of wild rice is also an important aspect of measurement methods. By combining genetic diversity data with the growth status of wild rice under different environmental conditions, researchers can analyze the performance of different genotypes in stress resistance, further revealing their potential mechanisms for adapting to different habitats. The determination method of genetic diversity of wild rice germplasm resources combines DNA molecular level analysis and population level research, comprehensively and deeply revealing the richness and complexity of genetic diversity of wild rice through modern molecular marker technology and population genetics methods.

1.3 Genetic diversity of wild rice germplasm resources

The existence of genetic diversity in wild rice germplasm resources is reflected in different populations and geographical distributions. Due to the widespread distribution of wild rice in wetlands, rivers, and swampy areas around the world, they face different climate and soil conditions, which promote the adaptive differentiation of genotypes. This difference is not only manifested in morphological characteristics, but also includes genetic differences at the genomic level, providing a genetic basis for their survival and reproduction in different habitats.

Molecular marker technology has played a crucial role in studying the genetic diversity of wild rice germplasm resources. By using molecular marker techniques such as Random Amplified Polymorphism (RAPD), Microsatellite Markers (SSR), and Single Nucleotide Polymorphism (SNP), researchers can gain a deeper understanding of genetic differences within wild rice populations and the genetic relationships between different populations. The application of these technologies reveals the diversity of wild rice at the genetic level, providing researchers with tools to gain a more comprehensive and in-depth understanding of its adaptability and evolutionary process.

For example, SSR markers are a co dominant marker with good stability and have been widely used in the detection of genetic diversity between species, construction of genetic maps, and other fields. Zhu et al. (2002) used SSR markers to conduct genetic research on common wild rice in Guangdong, Guangxi, Jiangxi, and Yunnan, and found that the differentiation degree of common wild rice in Guangdong and Guangxi was high. Jiangxi and Yunnan common wild rice were primitive types that did not undergo indica japonica differentiation, and there were genetic differences between common wild rice in different regions.

Genetic diversity not only plays a crucial role in the ecological adaptability of wild rice, but also has significant implications for rice breeding and improvement. In the face of increasingly changing climate and ecological environment, utilizing the genetic diversity of wild rice and breeding cultivated rice varieties with stronger stress resistance and higher yields is expected to improve the sustainability of agriculture and ensure global food security.

However, with the continuous expansion of human activities, the natural habitat of wild rice is gradually being threatened, which also poses a challenge to its genetic diversity and survival status. Therefore, in-depth research on the genetic diversity of wild rice germplasm resources not only helps scientists better understand the ecological balance of nature, but also provides scientific basis for the protection and sustainable utilization of this precious resource. By comprehensively considering the expression of genetic diversity at different levels, we can have a more comprehensive understanding of the ecological and genetic characteristics of wild rice, and provide more targeted measures for its protection and sustainable utilization.

2 Genetic diversity analysis

2.1 Application of molecular marker technology in the study of genetic diversity in wild rice

In the study of genetic diversity in wild rice, molecular marker technology is a powerful tool that provides scientists with a deeper understanding of its genomic characteristics and genetic relationships. The main applications of molecular marker technology include randomly amplified polymorphisms (RAPD), microsatellite markers (SSR), and single nucleotide polymorphisms (SNPs). The application of these technologies not only reveals genetic differences between wild rice populations, but also provides important information for revealing their adaptability and ecological evolution (Wu et al., 2021).

Random Amplified Polymorphism (RAPD) is a PCR amplification technique based on random primer guidance, which reveals genetic diversity by identifying polymorphisms in different regions of DNA. In wild rice, RAPD technology is widely used to evaluate genetic variations between different individuals and populations. Due to its advantages of simplicity, speed, and low cost, RAPD technology has become a powerful tool for preliminary screening of genetic diversity in wild rice.

Microsatellite marker (SSR) is a highly polymorphic molecular marker technique that reveals genetic diversity at the genomic level by detecting short and repetitive sequence units in DNA. In the study of genetic diversity in wild rice, SSR technology has been widely applied in population genetic structure analysis and genetic relationship research. Its high polymorphism and locus richness enable it to provide high-resolution genetic information, providing an ideal means to reveal small differences between wild rice populations (Yang et al., 2022).

In addition, with the development of single nucleotide polymorphism (SNP) technology, more and more studies have begun to use SNP markers in genetic diversity analysis of wild rice. SNP markers have the characteristics of high stability and high throughput, enabling them to cover the entire genome more comprehensively and provide more accurate genetic information. By analyzing the distribution of SNPs, researchers can gain a more detailed understanding of the genetic differences between wild rice populations, providing a more accurate genetic background for further research on their adaptability.

It can be seen that the application of molecular marker technology in the study of genetic diversity in wild rice provides researchers with a comprehensive and in-depth perspective. The different characteristics of these technologies enable researchers to choose the most suitable method based on research objectives and needs, further revealing the mysteries of the wild rice genome, and providing scientific basis for its protection, utilization, and breeding improvement.

2.2 Analysis of population genetic structure

The genetic structure analysis of wild rice populations is a crucial research task aimed at revealing the genotype frequency distribution, genetic relationships, and genetic differences within different wild rice populations. This analysis helps to understand the evolutionary process, ecological adaptability, and genetic variation of wild rice populations, providing useful information for their application in breeding and conservation.

By collecting wild rice samples from different geographical locations or ecological environments to form populations, such geographical or ecological differences may lead to genetic differences between different populations. Then, using molecular marker techniques such as microsatellite markers (SSR) or single nucleotide polymorphisms (SNPs), genetic markers were applied to the wild rice population (Chen et al., 2021).

Principal Component Analysis (PCA) is a commonly used statistical method that can reveal genetic similarity and differences between samples through dimensionality reduction techniques. Through PCA, multidimensional genetic data can be transformed into a few principal components, so that the distribution of samples on the principal components reflects their relative positions in the genetic space. This helps to identify genetic relationships among different populations of wild rice.

Cluster analysis is another commonly used method that divides samples into different groups based on genetic similarity. This analysis can help determine which individuals or populations are more genetically similar, thereby identifying the genetic relationships within the group. Model independent population structure analysis is a method of determining population structure by calculating genetic variation within a population and genetic differences between populations. This method does not rely on prior assumptions and can more flexibly identify genetic differentiation between different populations.

By integrating these analysis methods, the study of the genetic structure of wild rice populations can reveal genotype differences between different populations, providing important clues for understanding the evolutionary process, adaptability, and genetic diversity of wild rice. These pieces of information are of great significance for scientists in rice breeding, ecological research, and the protection and sustainable use of wild rice germplasm resources.

2.3 The impact of genetic diversity on stress resistance of wild rice

Genetic diversity plays an important role in the stress resistance of wild rice. The genetic diversity within the wild rice population reflects the richness and variability of genotypes, providing a genetic basis for their adaptability under different environmental conditions. This diversity not only helps the wild rice population adapt to changes in the natural environment, but also has a significant impact on its stress resistance performance.

Genetic diversity provides wild rice with stronger adaptability to ecological pressures. In wild habitats, different genotypes may exhibit different resistance to adversity such as drought, salinity, and pests and diseases. This difference stems from genetic diversity, which through adaptive evolution enables individuals in a population to better adapt to specific environmental pressures, maintain survival and reproduction (Zhang et al., 2019).

The impact of genetic diversity on the stress resistance of wild rice is reflected at the genetic level. Through molecular marker technology, genetic variation between different genotypes can be studied, and key genes related to stress resistance can be identified. This provides important information for breeding improvement, allowing scientists to enhance the resistance of cultivated rice to adversity by selecting hybrid combinations with specific resistance genotypes.

In addition, genetic diversity also affects the interspecific and intra specific relationships of wild rice populations, thereby affecting their role in the ecosystem. Relatively high genetic diversity helps populations better adapt to different ecological niches, improving their stability and stress resistance in ecosystems. However, due to the continuous changes in the environment and interference from human activities, the wild rice population is gradually threatened, and the reduction of its genetic diversity may lead to a decrease in stress resistance, making the population more vulnerable. Therefore, protecting and maintaining the genetic diversity of wild rice is crucial for ensuring its stress resistance and survival in the natural environment.

3 Adaptability analysis

3.1 Impact on ecological environment

The adaptability analysis of wild rice involves its survival and reproduction strategies in different ecological environments, examining their adaptability to various ecological factors. The impact of ecological factors on wild rice is an important aspect of adaptability analysis. The impact of ecological environment is reflected in climate and geographical conditions. Wild rice is distributed globally and faces challenges from different climate and geographical conditions. Some wild rice populations exist in hot and humid tropical regions, while others may live in cold and dry temperate or plateau areas. By studying the wild rice populations in these different ecological environments, their adaptive mechanisms in temperature, humidity, light, and other aspects can be revealed, providing insights for cultivating cultivated rice that is more adaptable to different climate conditions (Chen et al., 2021).

Water quality and soil type are also key factors affecting the adaptability of wild rice. Some wild rice grows in saline alkali areas and has strong salt alkali resistance, while others grow near wetlands or freshwater lakes and show adaptability to different water qualities. The fertility and drainage of soil also play a crucial role in the distribution and survival of wild rice. Therefore, studying the ecological adaptability of wild rice in different soil types can help understand its growth status in agricultural environments.

The impact of ecological environment on the adaptability of wild rice also involves interactions with other plants and animals. There are complex interrelationships between wild rice and other organisms in the surrounding ecosystem, which may have an impact on its growth and reproduction. For example, symbiosis with specific microorganisms may help wild rice absorb nutrients or resist diseases, and this symbiotic relationship is crucial for its adaptability in natural ecosystems.

In adaptability analysis, understanding the phenotypic and genotype variations of wild rice in different ecological environments, as well as its interactions with the environment, is of great significance for revealing the mechanisms of adaptability of wild rice. This information helps us better utilize the genetic resources of wild rice, improve the stress resistance and productivity of cultivated rice, and provide scientific basis for protecting and maintaining wild rice germplasm resources.

3.2 Adaptability of biological characteristics

The biological characteristics of wild rice reflect its adaptive evolution in the natural environment, and through these characteristics, wild rice has successfully adapted to diverse and complex ecosystems. The growth cycle and reproductive strategy of wild rice demonstrate its flexible adaptation to changing environments. Some wild rice populations exhibit shorter growth cycles, allowing them to complete the reproductive process in environments with significant seasonal changes. Other populations may exhibit longer growth cycles and adapt to relatively more stable ecosystems. This difference in growth cycle provides flexibility for wild rice to find the most suitable breeding time in different ecological environments.

For example, we know that rice is a cold sensitive crop originating from tropical or subtropical regions, and encountering low temperatures during the booting stage can lead to abnormal rice development and severe yield reduction. Li et al. (2021) conducted a genome-wide association analysis using cold tolerant near isogenic lines to construct isolated populations. Based on linkage mapping, they further utilized the cold tolerant phenotypes at the booting stage of 54 japonica and 67 indica rice germplasm resources to identify a new cold tolerant gene, CTB2. CTB2 encodes a glucosyltransferase that is highly expressed in the tapetum, pollen grains, and anthers. Under low temperature stress, CTB2 maintains cell membrane permeability by affecting the content of sterol glycosides and acetylated sterol glycosides, protects pollen grains and pollen outer wall structure, and ultimately improves the cold tolerance of rice (Figure 1).

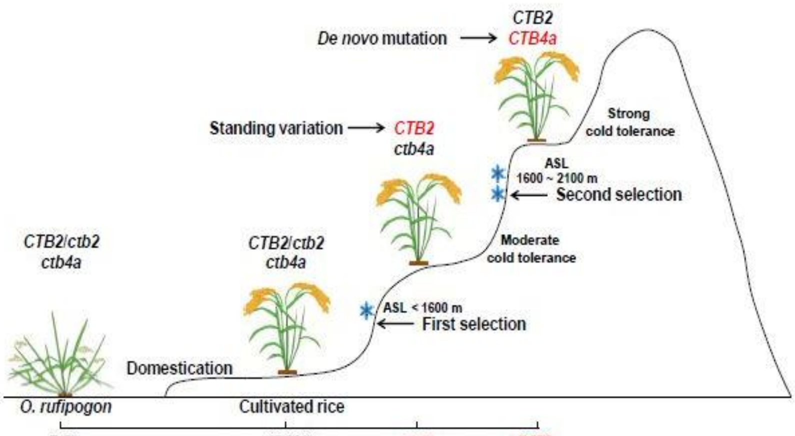

Figure 1 Evolutionary model of CTB4a and CTB2 during cold adaptation of japonica (Li et al., 2021)

This study found that during the domestication process of japonica rice, the cold tolerance can be improved by gradually selecting existing and new variations. Not only does it provide important genetic resources for cold tolerance breeding in rice, but it also provides another theoretical example for plant adaptive evolution. This research result is of great significance for effectively ensuring the high and stable yield of rice under low temperature or cold planting conditions, promoting the further development of rice cultivation in high-altitude and high latitude areas, and addressing the growing demand for rice in China (Li et al., 2021).

The stress tolerance and disease resistance of wild rice are significant adaptations in its biological characteristics. Wild rice populations typically exhibit stronger resistance to adverse conditions in their growth environment, such as drought, salinity, and diverse pests and diseases. This resilience reflects its adaptation to complex ecological pressures during long-term evolution, providing advantages for its wider distribution and survival in the natural environment.

The genetic diversity in biological characteristics is also an important manifestation of the adaptability of wild rice. The genotype differences within the wild rice population enable a group of individuals to respond differently to environmental changes. This diversity not only ensures the overall survival of the population, but also provides a material basis for its continuous adaptation to constantly changing environments during the evolutionary process.

The biological characteristics of wild rice reflect its adaptability in the natural environment in multiple aspects. This adaptability not only lays the foundation for the survival of wild rice in various ecosystems, but also provides rich genetic resources for the stress resistance and productivity of cultivated rice. By conducting in-depth research on these biological characteristics, we can better understand the ecological and evolutionary characteristics of wild rice, providing scientific basis for its protection and sustainable utilization.

3.3 The impact of human factors on adaptability

Human factors have a profound impact on the adaptability of wild rice, and these factors to some extent shape the living environment and genetic characteristics of wild rice. Human activities have altered the habitat and ecosystem of wild rice. The development of land, expansion of farmland, and construction of water conservancy projects have all led to the destruction and alteration of the original habitat of wild rice. This human intervention poses new challenges to the adaptability of wild rice populations in artificial environments, requiring adaptation to new environmental factors.

Agricultural activities have had an impact on the genetic diversity of wild rice. Selective cultivation of rice by humans, selecting specific varieties that are high-yielding and easy to manage, may lead to a decrease in genetic diversity of wild rice populations. This reduction may lead to a decrease in the adaptability of wild rice to cope with new ecological pressures and climate change, as lower genetic diversity limits its variation at the genetic level (Chen et al., 2022).

In addition, the use of pesticides and fertilizers has a direct impact on the adaptability of wild rice. The use of these chemicals may lead to changes in sensitivity or resistance to these substances in wild rice populations, thereby affecting their survival ability in agricultural environments. This human intervention may to some extent alter the interaction between wild rice and other plants and organisms, and have complex and multi-level impacts on its ecological adaptability.

The application of artificial introduction and genetic engineering technology has also brought new possibilities for the adaptability of wild rice. By introducing specific genotypes or genes, scientists attempt to improve the stress resistance, yield, and quality of rice. However, such artificial selection and modification may also bring some potential risks and impacts, and it is necessary to carefully evaluate their long-term effects on the adaptability of wild rice populations.

The impact of human factors on the adaptability of wild rice is complex and multifaceted. Understanding these impacts helps us better balance the relationship between human agricultural activities and natural ecosystems, ensuring the sustainable utilization of wild rice germplasm resources and the stability of ecosystems.

4 Application of Wild Rice Germplasm Resources in Rice Breeding

4.1 Utilizing wild rice genes to improve the stress resistance of cultivated rice

Wild rice has many excellent traits that can be utilized in rice breeding. According to IRRI's research, the opportunity to search for resistance genes from wild rice is more than 50 times higher than from cultivated rice. Wild rice has strong insect resistance, is an excellent antigen for rice diseases and pests, and also has good stress resistance. The common wild rice in Dongxiang, Jiangxi, China is located at 24N° in January with an average temperature of 5.2 °C and a minimum temperature of -8 °C-5 °C can also safely survive the winter (Tiwari and Yadav, 2020).

There are materials with excellent quality in wild rice, mainly manifested as white belly, glassy texture, non easily broken rice grains, and high protein and lysine content. In medicinal wild rice, some materials not only have good appearance quality but also high protein content, up to 16%, making them good materials for high-quality breeding. At the same time, medicinal wild rice has high medicinal value.

Wild rice also has strong growth advantages, and its distant hybridization with cultivated rice has great potential for cultivating varieties with strong growth advantages. Especially, ordinary wild rice has fertility restoration genes, and its chromosomes are both AA type and have good affinity with cultivated rice. It has been widely used in the breeding of hybrid rice three lines. Wild rice also has strong regeneration ability, and many materials in China's perennial common wild rice have particularly strong regeneration ability.

Wild rice has evolved over a long period of time in the natural environment, forming resistance to various stresses. Among them, traits such as drought resistance, salt alkali resistance, and disease and pest resistance have been fully demonstrated in wild rice. Through in-depth research on the genome of wild rice, scientists can discover and understand the genetic mechanisms behind these stress resistance traits, including the localization and functional analysis of key genes.

For example, researchers analyzed lncRNAs in rice using multiple recombination methods and found that compared to their ancestor species, common wild rice, 95% of lncRNAs in Asian cultivated rice were downregulated, and the downregulated lncRNAs exhibited population genetic characteristics consistent with the genome segments subjected to targeted selection during evolution. The target genes of these differentially expressed lncRNAs are enriched at sites related to carbon fixation ability and carbohydrate metabolism. Through experiments, it was verified that the decrease in expression levels of three lncRNAs directly leads to an increase in starch content and grain weight in rice seeds, revealing the multi-level regulatory mechanism of rice yield and quality. The downstream expression effects of these lncRNAs have a significant impact on various rice traits, and these effects may have been selected during the domestication process of japonica rice (Zheng et al., 2019) (Figure 2).

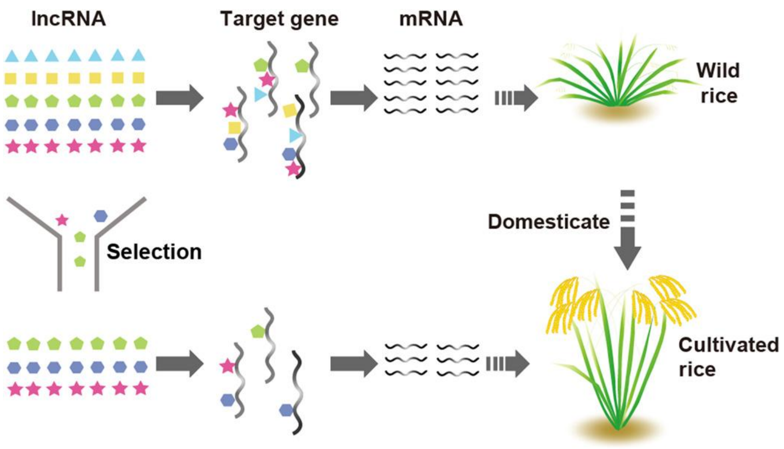

Figure 2 A model for the evolution of lncRNAs during rice domestication (Zheng et al., 2019)

Introducing stress resistant genes from wild rice into cultivated rice is an effective strategy in breeding practice. This involves molecular breeding techniques such as gene editing and transgenic technology. By accurately selecting and introducing specific genotypes from wild rice, cultivated rice can exhibit stronger survival ability under adverse conditions such as drought and salinity.

This breeding strategy can not only enhance the stress resistance of cultivated rice, but also help reduce dependence on chemical pesticides and fertilizers, and improve the sustainability of agricultural production. In addition, newly cultivated rice varieties can better adapt to constantly changing climate and environmental conditions, providing more reliable solutions for global agricultural production.

Overall, the application of wild rice germplasm resources has enormous potential for improving the stress resistance of cultivated rice. Through scientific and precise breeding methods, we can cultivate stronger and more adaptable rice varieties while maintaining high yield and quality, making a positive contribution to global food security and agricultural sustainability.

4.2 The potential value of wild rice in improving rice yield and quality

Wild rice has enormous potential value in improving rice yield and quality. Through in-depth research on the biological characteristics and genomics of wild rice, scientists can discover many beneficial genotypes and genes that can be applied in cultivated rice, thereby promoting the rice industry towards more efficient, high-yield, and high-quality directions.

There is rich genetic diversity within the population of wild rice, which means that there may be some genes that have a positive impact on yield and quality in different wild rice populations. By gaining a deeper understanding of these genotypes, it is possible to select and introduce some beneficial traits such as high yield, disease and pest resistance, and stress resistance, in order to improve the yield and resistance of cultivated rice.

During the process of adaptive evolution, wild rice has formed some special varieties with vigorous growth, excellent plant types, and resistance to pests and diseases. These characteristics can be introduced into cultivated rice through gene selection and genetic improvement to enhance its growth and development, stress resistance, and resistance to pests and diseases (Khanh et al, 2021).

Some genes in wild rice may be closely related to the yield of rice. For example, some genes that regulate plant growth may help improve the biomass and grain yield of rice. By gaining a deeper understanding of the functional mechanisms of these genes, targeted breeding work can be carried out to achieve greater yields in cultivated rice.

In terms of quality, wild rice may also provide some beneficial characteristics. Some wild rice may have higher antioxidant properties, higher nutritional content, or better taste. By introducing these characteristics into rice cultivation, the edible quality of rice can be improved, meeting people's demand for high-quality food.

4.3 Challenges of wild rice germplasm resources in rice breeding

Wild rice germplasm resources are facing increasingly severe habitat destruction and pressure from human activities. Urbanization, farmland expansion, and climate change have had a serious impact on its natural habitat. Therefore, protecting the natural habitat of wild rice and maintaining its population stability and diversity has become an urgent task. Establishing nature reserves, conducting monitoring of wild rice populations, and promoting environmental education are key steps in protecting wild rice germplasm resources.

Future research directions need to delve deeper into the genetic mechanisms, adaptive evolution, and ecological interactions of wild rice. By integrating research methods from multiple fields such as molecular biology, ecology, and genetics, a deeper understanding of the survival strategies and genetic variation mechanisms of wild rice under different ecological pressures will help to better utilize its abundant genetic resources.

It is particularly important to study the adaptability of wild rice under climate change conditions. With the increase in global temperatures and extreme weather events, the ecological adaptability of wild rice may face new challenges. Studying how to better adapt wild rice to climate change and understanding its genetic basis for adaptability in different climate backgrounds will provide useful information for the sustainability of future agriculture (Chen et al., 2021).

On the other hand, combining the genetic diversity of wild rice with the improvement of cultivated rice to cultivate more adaptable and stress resistant cultivated rice varieties is an important direction for future breeding. This requires a deep understanding of the relationship between genotype and phenotype of wild rice, and through precise gene editing techniques and genetic improvement methods, targeted introduction of target genes can be achieved to improve the overall quality of cultivated rice.

Strengthening international cooperation is also an important way to promote the protection and utilization of wild rice in future research. Sharing research results and integrating resources and experiences from various countries will help to gain a more comprehensive and in-depth understanding of the biological characteristics of wild rice, providing more scientific support for its protection and sustainable utilization. The key to challenges and prospects lies in protecting wild rice while fully realizing its potential value in sustainable agricultural development and food security. Future research needs to be conducted at multiple levels to provide scientific solutions to the problems faced by global agriculture.

5 Outlook

After conducting in-depth research on the genetic diversity and adaptability of wild rice, we have gained a more comprehensive understanding of the value of this precious resource. Wild rice, as the primitive form of the rice family, not only possesses rich genetic diversity, but also has formed outstanding adaptive characteristics over a long evolutionary process. Through a comprehensive understanding of its ecological environment, biological characteristics, and genetic mechanisms, we have gained a better understanding of the survival strategies of wild rice in the face of various natural and human pressures.

Future rice breeding and protection of wild rice germplasm resources require us to comprehensively apply various disciplinary knowledge and technological means. Firstly, we should strengthen our research on the genomics of wild rice and delve deeper into the beneficial genotypes to improve the stress resistance and productivity of cultivated rice. Secondly, it is recommended to strengthen international cooperation and jointly promote the monitoring and natural conservation of wild rice populations, protect their original ecological environment, and maintain the diversity and stability of their populations.

In rice breeding, we should focus on precision breeding and introduce beneficial genes from wild rice through molecular breeding techniques to improve the yield and quality of cultivated rice. This can not only contribute to global food security, but also help reduce dependence on pesticides and fertilizers, and promote the development of agriculture towards a more sustainable direction.

In terms of protection, it is recommended to strengthen the collection, preservation, and sharing of wild rice germplasm resources, and establish a global gene bank for wild rice. At the same time, through education and publicity, raise public awareness and importance of wild rice, and encourage society to pay more attention to and participate in the protection of wild rice.

A deeper understanding of the genetic diversity and adaptability of wild rice provides a theoretical basis for us to better utilize this important resource. In future research and practice, we should protect its original ecological environment, deepen genetic research, and strengthen international cooperation to promote more significant achievements in rice breeding and protection work. Such efforts will not only bring new breakthroughs in the field of agriculture, but also help maintain the rich biodiversity on Earth.

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