Review and Progress Open Access

Comparative Analysis of Genomic Evolution between Wild Rice and Cultivated Rice

Ding Danyan
Cuixi Academy of Biotechnology, Zhuji, 311800, China
Corresponding author email: cuixikendra@hotmail.com

Rice Genomics and Genetics, 2023, Vol.14, No.2 doi: 10.5376/rgg.2023.14.0002
Received: 20 Nov., 2023
Accepted: 24 Nov., 2023
Published: 27 Nov., 2023

Preferred citation for this article:
Ding D.Y., 2023, Comparative analysis of genomic evolution between wild rice and cultivated rice, Rice Genomics and Genetics, 14(2): 1-9 (doi: 10.5376/rgg.2023.14.0002)

Abstract Rice (*Oryza sativa*) is one of the most important food crops in the world, and its genome evolution has a significant impact on yield and food safety. This study aims to explore the genome evolution of wild rice and cultivated rice, and compare their genetic diversity, genome structure, functional genes, and evolutionary driving factors. We conducted in-depth research on the origin and evolution of rice, including the origin of wild rice and the domestication process of cultivated rice, and identified key genes that affect rice domestication. By comparing the genome structure, the differences in genome size, structure, and gene expression between wild and cultivated rice were revealed. This study also analyzed genetic diversity and evolutionary pressure, gained a deeper understanding of the genetic differences and environmental adaptability between the two. In exploring the ecological and agricultural significance of rice genome evolution, it elucidated its important impact on ecosystems and agricultural production, as well as future research directions and challenges. This study provides important insights into the evolution of the rice genome and theoretical basis for further improving rice cultivation and food production.

Keywords Wild rice (*Oryza rufipogon*); Genomic evolution; Genetic diversity; Domestication; Agricultural applications

When it comes to the world's most important food crop, rice (*Oryza sativa*) is undoubtedly one of them, shouldering the important task of meeting the main food needs of billions of people. As a key component of stabilizing diets around the world, rice provides humans with important carbohydrates and other nutrients, and is one of the world's main sources of energy. However, rice is not only a necessity for human livelihoods, but also plays a crucial role in global food security. With the continuous growth of the global population and the threat of climate change and other factors, how to improve the yield and quality of rice has become an urgent issue in the fields of agriculture and food science today.

This study aims to conduct in-depth research on the evolution of the rice genome, particularly by comparing the genetic differences between wild rice and cultivated rice, in order to reveal key genes related to their adaptability, agronomic traits, and growth characteristics. As an important food crop, the study of the genome evolution of rice has multiple values. Understanding the genetic diversity and genome structure of rice not only helps agricultural scientists and breeders to better improve rice varieties, increase yield, resist diseases and pests, and adapt to constantly changing environmental conditions, but also helps to explore the genome evolution of rice and understand the genetic adaptation and evolution process of plants, Provide important reference basis for crop genetic improvement and ecosystem protection (Yang et al., 2023).

At the same time, this study will also delve into the origin and evolution of rice, compare the genome structure of wild rice and cultivated rice, analyze their genetic diversity and evolutionary pressure, explore the significance of rice genome evolution for ecology and agriculture, and summarize the key findings of this study and the prospects for future research.

Through these efforts, we hope to contribute our modest efforts to global food security and agricultural sustainability, paving the way for better meeting human food needs. It also provides important information for future breeding and agricultural improvement, in order to contribute to global agriculture and food security, and help address challenges such as growing population demand and climate change.

1.1 The Origin and Evolution of Rice

1.1 Origin of wild rice

The origin of wild rice (*Oryza rufipogon*) has always been an important research topic in the fields of botany and genetics. Understanding the origin of wild rice can help reveal the process of rice domestication and the root of rice diversity. Rice belongs to the *Oryza* L. genus of the Gramineae family, and the authoritative view suggests that the genus includes 23 rice species, including 2 cultivated rice species: Asian cultivated rice (*Oryza sativa* L.) and African cultivated rice (*Oryza glabellerima* Steud.). The other 21 are all wild rice species, containing 10 karyotypes such as AA, BB, CC, BBCC, CCDD, EE, GG (Table 1) (Wang et al., 2017).

Table 1 Names, chromosome numbers, genomes, and distribution of 22 species

Wild rice species name	Number of chromosomes	Chromosome group	Distributed
Oryza nivara Sharma et Shastry	24	AA	South Asia, Southeast Asia, Southern China
O.nufipogon W. Griffith	24	AA	South Asia, Southeast Asia, Southern China
Oryza officinalis	24	CC	South asia, Southeast asia, South of this, New guinea
Oryza meyeriana	24	-	Southeast, Southern china
Oryza alta	48	CCDD	Central America, South America
Oryza australiensis	24	EE	Australia
Oryza barthii	24	A^gA^g	West africa
Oryza latifolia	48	CCDD	Central America, South America
Oryza brachyantha	24	FF	West Africa, Central Africa
O. barthi	24	A^1A^1	Africa
Oryza eichingeri	24, 48	CC, BBCC	East Africa, Central Africa
Oryza glumaepatula	24	$A^{cu}A^{cu}$	South America, West Indies
Oryza grandiglumis	48	CCDD	South America
Oryza granulata	24	-	South Asia, Southeast Asia
Oryza longiglumis	48	-	New Guinea
Oryza meridionalis	24	-	Australia
Oryza minuta	48	BBCC	Southeast Asia
Oryza punctata	24, 48	-	Africa
Oryza ridleyi	48	-	Southeast Asia
Oryza schlechteri	-	-	New Guinea
Oryza glaberrima Steud.	24	A^gA^g	West africa
Oryza sativa L.	24	AA	Asia

Wild rice plants typically grow around wetlands, swamps, or ponds, and this growth environment enables them to adapt to the growth conditions during rice domestication, thus providing important genetic resources for rice cultivation. The genotype of wild rice differs from cultivated rice in multiple aspects, including plant growth characteristics (Figure 1), stress resistance, reproductive mechanisms, etc. The genome of wild rice is usually more complex and has more genetic diversity, which is also the result of their adaptation to changing conditions in natural environments.

The genetic diversity of wild rice is crucial for its survival as they need to adapt to various environmental pressures such as drought, saline alkali soils, pests and diseases. These genetic characteristics are of great significance for breeding improvement, as they can provide more genetic resources for rice cultivation to cope with constantly changing environmental conditions and production needs.

Figure 1: Differences in characteristics between wild rice and cultivated rice (Photo credit: South China National Botanical Garden)
Note: A: Wild rice: Long awn; Immature and irregular, with few grains on the ear; B: Common cultivated rice: short awned or awnless; Mature and tidy, with many grains on the ear

1.2 Domestication of cultivated rice

In the Yangtze River basin of China, around 7000 BC, people began collecting wild rice and planting it by selecting individuals with larger grains and easier harvest, completing the initial domestication of rice. In this process, people gradually developed rice varieties that are more suitable for human consumption and agricultural production compared to wild rice. The earliest cultivated rice may not have as rich natural resistance as the wild type, but they are more suitable for human cultivation needs.

The domestication process of cultivated rice is accompanied by a series of biological and morphological features, including plant dwarfing, compact arrangement of rice panicles, increase in particle size, and regulation of heading time. The emergence of these characteristics makes cultivated rice more suitable for artificial cultivation and harvesting, thereby improving the efficiency of agricultural production (Jiang et al., 2019).

With the continuous development of agricultural technology, people gradually realize the importance of traits such as rice plant height, disease resistance, and drought resistance. Through gene selection and hybrid breeding, people have developed a series of modern rice varieties. In the 1960s, Chinese scientist Yuan Longping successfully increased the yield of rice by breeding "super hybrid rice", solving the problem of food shortage in China at that time. This type of rice has high lodging resistance, disease and pest resistance, and wide adaptability, making it an important variety in global food production.

With the advancement of biotechnology, people have also improved rice through genetically modified technology. For example, by introducing insect resistant genes, improving rice's resistance to pests and diseases, reducing dependence on pesticides, it contributes to sustainable agricultural production. This technology provides a new way for further optimization of rice.

1.3 Key genes for rice domestication

The domestication of rice involves many genes, some of which play a crucial role in the morphology, physiology, and stress resistance of rice. An important rice gene is *SD1* (Semi Dwarf 1), which controls the height of rice plants. In the 1960s, the *SD1* gene became a key factor in the green revolution. By inducing mutations in the *SD1* gene, scientists have successfully developed semi dwarf rice varieties with stronger lodging resistance, effectively reducing the lodging rate of rice during the harvest season and improving yield.

DEP1 (Dense and Erect Panicle 1) is another key gene related to rice plant structure. This gene controls the morphology of rice panicles and affects rice yield. By regulating the *DEP1* gene, scientists have successfully cultivated varieties with tight panicle types and uniform grain distribution, further improving rice yield.

Tillering and panicle differentiation in rice are important physiological processes that affect yield. Key genes such as *DEP1* (high tillering number 1) and *LAX1* (tillering development related genes) affect the panicle structure and tiller differentiation degree of rice by regulating the number and differentiation of tillers. By selecting these genes, people have successfully cultivated high-yield rice varieties with more tillers and larger panicles (Qiu et al., 2020).

Rice faces various stresses during its growth process, such as drought, salinity, etc. Some genes such as *OsDREB1A* (rice stress-induced transcription factor) and *OsSIZ1* (rice miniaturization factor) play a key role in the stress resistance of rice. By selecting these genes, people have successfully cultivated rice varieties that are more adaptable to adversity, improving their survival and yield performance.

The flower development of rice is crucial for grain formation, for example, *Ehd1* (Rice Flower Development Gene) regulates the flowering time of rice, directly affecting grain formation and maturity. By breeding these key genes, people can regulate the growth period of rice to adapt to different ecological and climatic conditions (Ayotunde et al., 2023).

2 Comparison of Genome Structure

2.1 Genome size and structure

There are significant differences in genome size and structure between wild rice (*Oryza rufipogon*) and cultivated rice (*Oryza sativa*). After a long process of artificial selection and domestication, the genome of cultivated rice is relatively small. The genome size of cultivated rice is approximately 430 megabase pairs (Mbps), which contains 12 chromosomes, including two main subspecies of japonica and indica rice. In contrast, the genome of wild rice is generally larger, reflecting the genetic simplification experienced by cultivated rice during domestication.

For example, the *SD1* gene is one of the key genes in the domestication process of rice, which controls the height of rice plants. In the cultivation of rice, after selection and domestication, the *SD1* gene undergoes mutations, resulting in a semi dwarf trait in the rice, improving its lodging resistance and adapting to modern high-yield cultivation.

The DEP1 gene regulates the morphology of rice panicles. By regulating the *DEP1* gene, scientists have developed varieties with tight panicle types and uniform grain distribution, which has increased rice yield (Qiu et al., 2020).

The *qSW5* gene is a key gene in regulating the size of rice grains. By studying the *qSW5* gene, scientists can adjust the size of rice grains to make them more suitable for human consumption needs and improve the economic and edible value of rice.

The *OsNAC2* gene is closely related to the stress resistance of rice, especially in response to salt alkali stress. By studying and regulating the *OsNAC2* gene, scientists are committed to cultivating more salt and alkaline tolerant rice varieties to adapt to different soil environments and improve the survival ability of rice (Wang, 2021).

The *Waxy* gene encodes enzymes related to starch synthesis in rice. During rice domestication, the selection and improvement of the *Waxy* gene affect the starch properties of rice, thereby improving its edible quality. The genome structure of wild rice is relatively complex and may contain more gene families and variations. On the contrary, the genome structure of cultivated rice may be more simplified, with a focus on genes related to agricultural traits

2.2 Gene family evolution

In the evolution of gene families, gene families are a group of genes derived from common ancestral genes, which are structurally and functionally similar. The gene family of rice involves many important biological processes, including growth and development, stress resistance, and environmental adaptation.

During the evolution of cultivated rice, some gene families may have undergone amplification, that is, an increase in the number of genes during evolution. This may be caused by mechanisms such as gene duplication, adaptive selection, or hybridization. On the contrary, some gene families may also have experienced shrinkage, i.e. losing some members during evolution. Such evolutionary changes help to form the specificity of cultivated rice in terms of morphology, physiology, and adaptability.

Wild rice exists in the natural environment and is often subjected to various pressures such as diseases, pests, and climate change. Therefore, gene families related to stress resistance may exhibit high diversity in wild rice. In rice cultivation, some stress resistance gene families may be strengthened or weakened through artificial selection to adapt to artificial agricultural environments.

Compared with wild rice, cultivated rice usually performs poorly in terms of stress resistance. During the evolution process, some gene families related to stress resistance may have undergone changes, resulting in relatively weak adaptability of cultivated rice to adverse conditions such as diseases and pests, drought, and salt alkali. This also indicates that in the cultivation of cultivated rice, attention needs to be paid to maintaining and improving the genomic characteristics of stress resistance (Table 2).

Table 2 Evolution of stress resistance gene families in wild rice and cultivated rice

Stress resistance gene family	Wild rice gene family	Cultivated rice gene family
Disease resistance genes	Higher diversity	Strengthened by selection
Antiresistance-related transcription factors	Diversity maintained	May be changes
Stress resistance protein	Different subgroups are widely distributed	May be selected

Growth and development are an important aspect of rice evolution. In this regard, the gene family of cultivated rice may have undergone adjustments to adapt to different growth habits and agricultural needs. For example, gene families that regulate plant height, panicle type, tillering, and heading characteristics may have undergone evolution in cultivated rice to meet the requirements of high yield and adaptability (Suhas et al., 2022) (Table 3).

Table 3 Evolution of stress resistance gene families in wild rice and cultivated rice

Growth and development gene family	Wild rice gene family	Cultivated rice gene family
Panicle type related genes	Diversity maintained	May be changes
Flowering time control genes	Different subgroups are widely distributed	May be selected
Plant type regulatory genes	higher diversity	Strengthened by selection

Wild rice usually has natural disease resistance genes in the natural environment, which helps it survive in the wild. In rice cultivation, selection pressure may lead to changes in the frequency of some disease resistance gene families to adapt to common pathogens in the agricultural system (Table 4).

Table 4 Evolution of growth and development gene families in wild and cultivated rice

Disease resistance gene family	Wild rice gene family	Cultivated rice gene family
Antifungal genes	Higher diversity	Strengthened by selection
Antiviral genes	Different subgroups are widely distributed	May be changes
Antibacterial genes	Diversity maintained	May be selected

Wild rice usually has high genetic diversity, while cultivated rice may suffer from genetic narrowing due to long-term artificial selection and breeding. Gene flow, which refers to the transmission of genes between different subgroups, also affects the evolution of gene families. In cultivated rice, due to the need for cultivation, some gene families unique to wild rice may have undergone changes.

2.3 Gene expression differences

In studying the evolution of the rice genome, we need to pay attention to the differences in gene expression, especially the expression changes under different environmental conditions and cultivation types. Wild rice and cultivated rice may exhibit different expression patterns in different growth environments, and changes in environmental conditions may lead to an increase or decrease in the expression levels of certain genes, which may help plants adapt and survive in specific environments.

In addition to environmental factors, different agronomic traits may also affect the expression of rice genes (Table 5). During the cultivation process, manual selection and improvement may lead to changes in certain gene expression patterns to achieve the improvement of specific agronomic traits. Genes related to yield, taste, or disease tolerance may have their expression patterns adjusted in cultivated rice.

Table 5 Comparison of agronomic characters between asian cultivated rice and african cultivated rice

Character	*Oryza Sativa*	*O. glaberrima*
Blade	Furry	Hairless
Leaf tongue	Long, pointed front end, two cracks	Short, front end circle
Spike shape	Loose	Compact
Secondary branch	Many	Few or none
Stigma color	White, light purple, purple	Purple
Grain lemma hair	Have, a few light shells	None, bare shell
Grain color	Most stems are yellow, with a few being oderate brownish yellow, silver gray, etc	Brown black, brown yellow, etc
Brown Rice Color	Light brown, with a few red and purple black colors	Crimson
Dormancy period	Weak to m	Strong
Regenerative	Have	None

This difference in gene expression may involve many important genes, which play a crucial role in the growth, development, and trait regulation of rice. Understanding the functions of these differential genes and their expression patterns in different types of rice can help us better understand the regulatory mechanisms of genes during domestication.

By studying the effects of environmental adaptability and agronomic traits on gene expression, we can gain a more comprehensive understanding of the differences in gene expression levels between wild rice and cultivated rice (Li et al., 2021). Understanding this difference helps us to delve deeper into the genetic changes during rice domestication and cultivation, as well as their impact on rice growth and development.

3 Genetic Diversity and Evolutionary Pressure

3.1 Genetic diversity analysis

The use of microsatellite markers for genetic diversity analysis of wild and cultivated rice is a common method. In the study, scientists used microsatellite markers to investigate the populations of wild and cultivated rice. The results showed that the population structure of wild rice is more complex, with multiple subpopulations, reflecting its widespread distribution and high gene mobility in the natural environment. The population structure of cultivated rice may be more singular and influenced by artificial selection.

In the analysis of single nucleotide polymorphism (SNP), researchers revealed differences in population structure between wild rice and cultivated rice. Wild rice may have significant genetic variations in different geographical regions, reflecting its long-term adaptive evolution in the wild environment. Cultivated rice may exhibit stronger artificial selection signals, and the frequency of specific SNP loci may undergo significant changes in different cultivated varieties (Yang et al., 2022).

Through the calculation of genetic distance, researchers can reveal the genetic relationships between individuals. Studies have shown that the genetic distance between wild rice and cultivated rice has been measured, and the results show that the genetic distance between individuals within the wild rice population is generally larger, while the genetic distance between cultivated rice may be smaller. This reflects the presence of more free hybridization in wild rice, while cultivated rice is influenced by artificial selection.

In gene exchange between different populations, genetic flow between wild rice and cultivated rice was evaluated. The results showed that there was significant gene flow between wild rice populations, while cultivated rice gene flow may be limited by artificial selection and planting structure, exhibiting relatively small gene flow.

3.2 Selection pressure

The selection pressure on the rice genome during the domestication process is multifaceted. Artificial selection aims to obtain characteristics such as high yield, disease resistance, drought resistance, and insect resistance. This selection will promote an increase in the frequency of genes related to specific traits in the population. This pressure continues to play a role in agricultural practice, affecting the genetic diversity and genotype of rice.

And selection pressure may also lead to the loss of other traits in the rice genome, as human selection typically focuses on several major traits, which may weaken the expression of other traits. For example, in the pursuit of high yield, some wild rice traits such as disease resistance or stress tolerance may be weakened (Yang et al., 2022).

Selection pressure can also lead to genetic variation between rice populations, especially between different regions or cultivation types. Human preferences and agronomic habits for different regions may lead to differences in traits and genetic diversity among different rice populations. This selection pressure has a significant impact on the rice genome, shaping the characteristics and traits of modern rice. Understanding how this selection pressure affects the evolution of the rice genome can help us understand the performance of modern rice in different environments and cultivation types.

3.3 Environmental adaptability

Wild rice evolves and thrives in the wild natural environment, thus possessing natural environmental adaptability. Wild rice is usually distributed in different ecosystems and has a certain degree of adaptation to different soil types, climatic conditions, and ecological niches. This adaptability helps wild rice survive in nature while also maintaining its genetic diversity (Takai et al., 2019).

In contrast, cultivated rice is artificially cultivated in agricultural environments and typically grows under relatively stable conditions. Although cultivated rice is optimized for high yield, disease tolerance, and adaptability to agricultural production needs, its adaptability in natural environments may be weak. Therefore, cultivated rice may have relatively poor adaptability to environmental changes.

However, the cultivation of rice has also undergone a long process of domestication, gradually adapting to the agricultural environment, including adaptability to planting seasons, irrigation water sources, and soil types. The adaptive evolution of cultivated rice is to some extent the result of manual selection and cultivation practices to meet the needs of agricultural production.

4 Ecological and Agricultural Significance of Rice Genome Evolution

The evolution of the rice genome has important ecological and agricultural significance for ecosystems. Wild rice is usually distributed in natural wetlands and wild environments, and they have a series of characteristics related to habitat adaptability. The genetic diversity and adaptability of wild rice make them adaptable to different ecosystems and climate conditions. This means that wild rice may play an important role in maintaining the stability of wetlands and natural ecosystems.

As an agricultural crop, cultivated rice is usually cultivated in farmland, and its genetic characteristics have been artificially selected and improved for many years to meet food needs. However, the introduction of cultivated rice may have certain impacts on the native ecosystem, including the utilization of soil and water resources, as well as habitat changes to wild animals and plants. Understanding the genome evolution of cultivated rice can help better manage and reduce these potential environmental impacts (Zheng et al., 2019).

At the same time, the agricultural application of rice genome evolution is an important issue in the field of agriculture. Through in-depth research on genome evolution, we can find ways to improve rice cultivation, increase yield, quality, and agricultural sustainability. Understanding the genome evolution of wild rice can help us find genes that are conducive to improving rice stress tolerance. Wild rice usually survives in different ecosystems and climate conditions, Therefore, they may have resistance genes related to stress. By identifying and utilizing these genes, we can cultivate rice varieties that are more drought, salt, or disease tolerant to cope with constantly changing climate and environmental conditions.

The evolution of the rice genome can also reveal genes related to rice taste and taste, which are of great concern to consumers and farmers as they directly affect the market value of rice products. By analyzing genome evolution, we can identify genes related to taste and taste, and then use molecular breeding techniques to improve these characteristics to provide more delicious rice varieties.

5 Future Research Directions and Challenges

The future research direction is an important topic in the field of rice genome evolution, with many exciting possibilities that can further expand our understanding of rice evolution. Future research can further explore the diversity of wild rice. Although many wild rice populations have been identified, there are still many unknown wild populations waiting to be discovered. Further research on the genomes of these wild rice populations will help us better understand the origin and evolution of rice. One of the future research directions is to utilize knowledge of the evolution of the rice genome to improve the cultivation of rice. Researchers can use known stress resistance genes and taste related genes of wild rice to cultivate more adaptable and delicious rice varieties through molecular breeding techniques.

With the intensification of climate change, rice, as one of the main global food crops, needs to better adapt to the constantly changing environment. Future research can focus on the adaptability of rice genome evolution to climate change, in order to develop more drought, salt, and disease tolerant rice varieties. Genome editing techniques, such as CRISPR-Cas9, provide powerful tools for precise improvement of the rice genome. Future research can explore how to more effectively utilize these technologies to improve the traits and quality of rice (Ran and Sun, 2021).

Further research on the impact of rice genome evolution on ecosystems and how to improve the impact of rice cultivation on ecosystems will be an important direction for future research. This helps to achieve sustainable agricultural practices and reduce the negative impact of agriculture on ecosystems. The research on the evolution of the rice genome requires international cooperation and resource sharing. Future research directions should include promoting cooperation between research institutions, agricultural departments, and international organizations to jointly promote research in the field of rice genome evolution.

In the field of rice genome evolution research, researchers face a series of complex challenges and limitations, covering multiple aspects from data acquisition to ethical and legal issues. The study of rice genome evolution requires a large amount of genome data, including the genome sequences of wild and cultivated rice. However, data acquisition and analysis are expensive and complex processes that require highly specialized skills and resource support. Researchers must overcome the challenges of data collection and processing to ensure the quality and reliability of the data.

The evolution of the rice genome is a complex and diverse field. There are significant differences between different wild rice populations and cultivated rice varieties, and further research is needed to understand these differences. This diversity increases the complexity of analysis and requires more research to reveal the patterns and mechanisms involved. Some researchers may also face technological and resource constraints, unable to obtain the latest sequencing technology and equipment, which may limit their progress in the study of rice genome evolution, as the equipment and resources required for research require significant investment.

Despite these challenges, research on the evolution of the rice genome still has important scientific and applied prospects. By overcoming these limitations and challenges, researchers can better understand the evolutionary history of rice, improve its quality and adaptability, and respond to future agricultural and food safety needs. The development of this field will help solve important issues of global food security.

6 Conclusion

By comparing the genome evolution of wild rice and cultivated rice, the connections and differences in their origin, genome structure, genetic diversity, gene function, and evolutionary driving factors were revealed. Wild rice is the ancestor of cultivated rice, originating from East Asia and possessing more genetic diversity and ecological types. Cultivated rice has undergone long-term domestication to form modern varieties.

Genomic structure comparison shows that wild rice usually has a larger genome and more chromosomes, and there are differences in the distribution of important genomic elements, which may be related to rice adaptability and growth traits. In terms of genetic diversity, wild rice has higher genetic diversity, while cultivated rice has relatively lower diversity, but there is still gene flow between the two. Gene function research has identified genes related to agricultural traits and has a significant impact on the adaptability and growth traits of rice (Lian et al., 2023)

The evolution of the rice genome has multiple impacts on ecosystems and agriculture, which can be used to improve rice cultivation methods, increase disease resistance, and yield. Future research directions include in-depth research on rice gene function, genetic diversity, and evolutionary mechanisms, revealing more key genes and regulatory networks. The challenges include the complexity of data acquisition and analysis, the difficulty of implementing field research, and resource constraints, requiring interdisciplinary collaboration and improved research methods.

Comparative analysis of the evolution of the rice genome provides an opportunity to gain a deeper understanding of this food crop, supporting future research and applications. Progress in this field contributes to global food security and agricultural sustainability, contributing to providing better food sources. In future research, we look forward to more discoveries and breakthroughs to promote the continuous development of the field of rice genome evolution.

References

Ayotunde A., Adeosun A.H., and Price G.J.N., 2023, Cadmium tolerance and accumulation in wild rice species, Rice Science, 30(3): 181-185. https://doi.org/10.1016/j.rsci.2023.03.003

Jiang L.Y., Ma X.Z., Tang S.S., Liu Y.Y., Gu F.X., Fu P., Zhu Y.C., Cai Z.F., Sun H.H, and Tan C.Q., 2019, The APETALA2-Like transcription factor supernumerary bract controls rice seed shattering and seed size, The Plant Cell, 31(1): 17-36. https://doi.org/10.1105/tpc.18.00304

Li L.J., He Y.Z, Zhang Z.H., Shi Y.F., Zhang X.B., Xu X., Wu J.L., and Tang S.Q., 2021, OsNAC109 regulates senescence, growth and development by altering the expression of senescence- and phytohormone-associated genes in rice, Plant Molecular Biology, 105(6): 637-654. https://doi.org/10.1007/s11103-021-01118-y

Lian X.P., Huang G.F., Zhang Y.J., Zhang J., Hu F.Y., and Zhang S.L., 2023, The discovery and utilization of favorable genes in Oryza longistaminata, Yichuan (Hereditas), 45(9): 765-780.

Qiu J., Jia L., and Wu D., 2020, Diverse genetic mechanisms underlie worldwide convergent rice feralization, Genome Biology, 21(1): 1-11. https://doi.org/10.1186/s13059-020-01980-x

Ran X., and Sun C.Q., 2021, What happened during domestication of wild to cultivated rice, Acta Agronomica Sinica, 9(3): 564-576. https://doi.org/10.1016/j.cj.2021.02.005

Suhas G.K., Vishesh K., Mohd T., Dwijesh C.M., Krishna K.C., Anil R., Amitha M.S., Kishor G., Tilak R.S., and Amolkumar U.S., 2022, Genome-wide analysis of von willebrand factor a gene family in rice for its role in imparting biotic stress resistance with emphasis on rice blast disease, Rice science, 29(4): 375-384. https://doi.org/10.1016/j.rsci.2021.11.007

Takai T., Lumanglas P., Simon E.V., Yumiko A.S., Hidetoshi A., and Nobuya K., 2019, Identifying key traits in high-yielding rice cultivars for

adaptability to both temperate and tropical environments, The Crop Journal, 7(5): 685-693.
https://doi.org/10.1016/j.cj.2019.06.004

Wang D.R., 2021, Road map for domesticating multi-genome rice using gene editing, Nature, 591(7851): 537-538.
https://doi.org/10.1038/d41586-021-00589-9

Wang H., Vieira F.G., and Crawford J.E., 2017, Asian wild rice is a hybrid swarm with extensive gene flow and feralization from domesticated rice, Genome Research, 27(6): 1029-1038.
https://doi.org/10.1101/gr.204800.116

Yang X.H., Zhou J.F., and Feng L., 2023, Utilization and conservation of wild rice resources in China, Zhongguo Shuidao (China Rice), 29(1): 1-8.

Yang Z.Y., Xu Z.J., Yang Q.W., and Qiao W.H., 2022, Conservation and utilization of genetic resources of wild rice in China, Rice Science, 29(3): 216-224.
https://doi.org/10.1016/j.rsci.2021.08.003

Zheng X.Y., Song Y., Li F., Wang J.R., Qiao W.H., Zhang L.F., Chen Y.L., Sun Y.F., and Yang Q.W., In-situ conservation of wild relatives of crops, Zhiwu Yichuan Xuebao (Journal of Plant Genetic Resources), 20(5): 1103-1109.