

From Wild to Cultivated: The Domestication Pathways of Asian Cultivated Rice (*Oryza sativa* L.)

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Abstract The domestication of rice (commonly known as Asian cultivated rice) is a pivotal event in agricultural history, significantly impacting global food security. This review synthesizes current research on the pathways of rice domestication, with a focus on genetic and geographic origins, the role of wild ancestors, and the evolutionary processes involved. Multiple studies indicate that *Oryza sativa* was independently domesticated from different populations of its wild ancestor, *Oryza rufipogon*, in various regions of Asia, including southern China, India, and Indochina. Genetic analyses reveal that the two main subspecies, indica and japonica, underwent separate domestication events, followed by gene flow between them. Additionally, the domestication process involved significant genetic changes, such as reduced seed shattering and dormancy, which are crucial for effective cultivation and harvest. This study also explores the impact of human-directed breeding and introgression on the genetic diversity of domesticated rice.

Keywords Rice (*Oryza sativa* L.); Wild rice; Domestication; Phylogeography; Genomic variation

1 Introduction

Rice (hereafter referring to Asian cultivated rice, *Oryza sativa* L.) is one of the world's most important staple crops, feeding more than half of the global population. Its significance extends beyond nutrition, playing a crucial role in the cultural, economic, and social aspects of many societies, particularly in Asia. The domestication of rice from its wild ancestors was a pivotal event in agricultural history, facilitating the development of stable and high-yielding agricultural systems that support large populations (Hoyos et al., 2020).

Understanding the pathways of rice domestication is essential for several reasons, as it provides insights into the evolutionary processes shaping the genetic diversity of this critical crop. Research indicates that rice was independently domesticated at least twice from different populations of its wild ancestor, *Oryza rufipogon*, leading to the formation of two major rice varieties: indica (*Oryza sativa* subsp. *Indica*) and japonica (*Oryza sativa* subsp. *Japonica*) (Hoyos et al., 2020). This knowledge is vital for breeding programs aimed at improving rice varieties, as it highlights the genetic resources available in wild populations that can be used to enhance traits such as yield, disease resistance, and stress tolerance (Zhao et al., 2010). Additionally, understanding the pathways of domestication aids in the conservation of wild rice species, which are valuable reservoirs of genetic diversity.

This study aims to comprehensively examine the pathways of rice domestication from historical, genetic, environmental, and cultural perspectives. By delving into archaeological findings, genetic research, and case studies, with a particular focus on the Yangtze River basin, it seeks to narrate the story of rice domestication in detail. The goal is to elucidate the key processes and milestones in rice domestication, highlight significant genetic changes, and explore how traditional agricultural practices and cultural influences have shaped rice cultivation. Furthermore, the study will discuss modern breeding techniques and future challenges, providing a comprehensive understanding of the journey of rice from a wild grass to a cultivated staple food.

2 The origin and Early History of Rice

2.1 The geographical origins of wild rice

The domestication of rice (particularly *Oryza sativa*) is a significant milestone in agricultural history, with origins deeply rooted in the geographical distribution and evolution of wild rice species. The genus *Oryza* includes both cultivated and wild species, believed to have originated approximately 130 million years ago on the ancient supercontinent Gondwana. As Gondwana split apart, different types of rice dispersed across various continents.

The primary wild ancestors of Asian cultivated rice (*Oryza sativa*) are *Oryza rufipogon* and *Oryza nivara*. These species are distributed throughout Asia, with *Oryza rufipogon* being particularly important as it is considered the direct ancestor of cultivated rice. Genetic studies suggest that japonica rice was first domesticated from *O. rufipogon* populations in the central region of the Pearl River in southern China. Subsequently, as the initial varieties spread to Southeast Asia and South Asia, japonica (*Oryza sativa* subsp. *Japonica*) hybridized with local wild rice, leading to the development of indica rice (*Oryza sativa* subsp. *Indica*) (Wang et al., 2017).

Further genetic analysis indicates that modern wild rice populations have extensively mixed with domesticated rice through gene flow mediated by pollen and seeds. This extensive gene flow suggests that many assumed wild rice varieties may actually represent different stages of feral domesticated rice. The gene flow from domesticated to wild rice forms a hybrid swarm, indicating ongoing and dynamic interactions between wild and cultivated rice populations.

Debates about the origins of domesticated rice have led to two major hypotheses: the single-origin model and the multiple independent domestications model. The single-origin model posits that both indica and japonica subspecies were domesticated from *O. rufipogon*. In contrast, the multiple independent domestications model suggests different domestication events for indica and japonica in different regions. However, recent molecular evidence supports the single-origin model, indicating that rice was first cultivated in the Yangtze River basin in China around 8 200 to 13 500 years ago (Choi et al., 2017).

2.2 Early evidence of rice cultivation

The domestication of rice (*Oryza sativa*) marks a pivotal event in agricultural history, signifying a major shift from foraging societies to agricultural ones. The earliest evidence of rice cultivation dates back to the middle reaches of the Yangtze River, where archaeological and archaeobotanical findings suggest that rice cultivation began around 8500 to 8000 years ago. This region is considered one of the primary centers of rice domestication, from which it spread to southern China and Southeast Asia (Wu et al., 2016).

In the lower Yangtze River region of China, early rice farming projects identified a critical turning point around 4600 BC, when the number of domesticated rice varieties began to surpass wild varieties. This period marks the beginning of systematic rice cultivation, where rice was grown in small, irregularly shaped paddies, allowing for precise water management and control (Zhao, 2010). The Shangshan site, dating back approximately 10 000 years, provides some of the earliest direct evidence of rice cultivation, though it remains unclear whether the rice at that time was fully domesticated (Gross and Zhao, 2014).

Further evidence from the Kuahuqiao site in eastern China, dating to about 7 700 years ago, indicates that early Neolithic communities selected lowland marshes for rice cultivation. These communities used fire to clear wetland shrubs and maintain vegetation suitable for rice paddies, demonstrating a sophisticated level of environmental management. Additionally, the Hemudu culture, around 5 000 BCE, is noted for its advanced rice cultivation techniques, including the use of seedbeds and transplantation into flooded fields (Wang et al., 2022).

The domestication process of rice in China was lengthy, with significant developments occurring approximately 6 500 to 6 000 years ago. This period marked the peak of early domestication traits in Yangtze japonica rice, which later hybridized with proto-indica varieties from India. The transition from wild rice to domesticated rice

was not linear; instead, it involved a pre-domestication cultivation phase where wild and domesticated forms coexisted and were cultivated simultaneously (Fuller and Weisskopf, 2011).

Rice (*Oryza sativa*) domestication is a crucial event in agricultural history with significant implications for human civilization. Recent archaeological and genetic studies have provided a clearer picture of the timeline and process of rice domestication. Archaeological evidence indicates that rice cultivation began around 8 000 years ago in the Yangtze River basin in southern China. However, the critical domestication trait of non-shattering was not fixed until around 7 000 years ago, suggesting a prolonged early cultivation phase before achieving full domestication (Choi et al., 2017). This timeline is supported by phytolith evidence from Hainan Island, indicating the presence of domesticated rice as early as 5 600 years ago, implying the spread of rice agriculture from the Yangtze River basin.

Genetic studies have further elucidated the domestication process. The genetic differentiation between the two major subspecies of Asian rice, indica and japonica, has been a topic of debate. Recent findings support the single-origin hypothesis of rice domestication, with japonica being the first variety to diverge from its wild ancestor *O. rufipogon*, approximately 13 100 to 24 100 years ago. This predates the earliest archaeological evidence of domestication, suggesting that early management practices of wild rice may have preceded full domestication (Choi et al., 2017). Additionally, genetic evidence indicates significant gene flow from japonica to indica, facilitating the transfer of domestication alleles and leading to the development of indica rice.

The integration of archaeological and genetic data provides a comprehensive understanding of rice domestication. For example, ancient DNA recovered from prehistoric rice remains in Thailand and India reveals the presence of early japonica in these regions, supporting the hypothesis of hybridization between japonica and proto-indica populations (Li et al., 2017). This gene exchange likely played a crucial role in the spread and diversification of domesticated rice.

Moreover, the early Holocene climate conditions characterized by an active East Asian summer monsoon may have facilitated the natural expansion of wild rice's distribution range, aligning with the earliest known domestication sites in the middle and lower Yangtze River. This climatic backdrop supports the hypothesis that initial domestication occurred in areas where wild ancestors were naturally abundant (Figure 1) (Dodson et al., 2021).

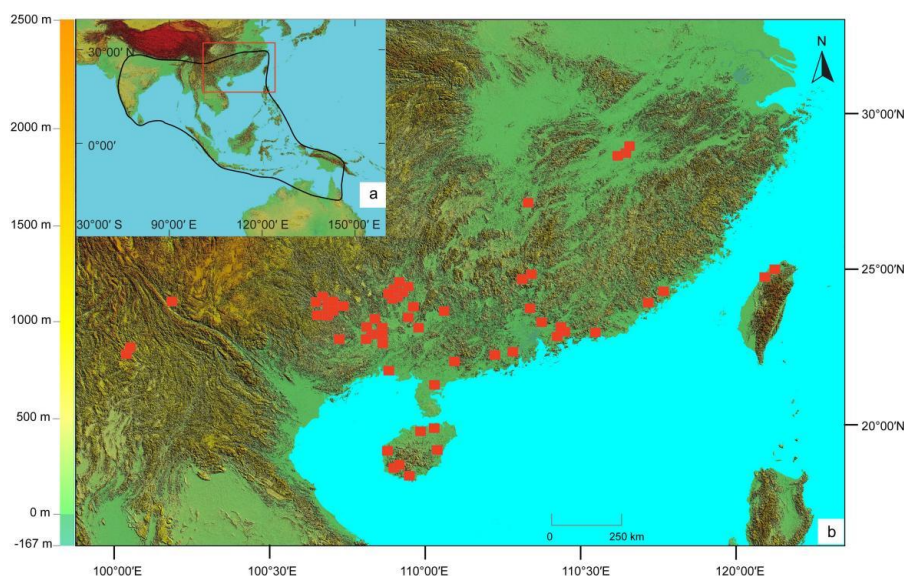


Figure 1 Natural distribution of *Oryza rufipogon*. Inset shows full natural distribution (Adopted from Dodson et al., 2021)

Image caption: On the mainland, the distribution includes Yunnan, Guangxi, Guangdong, Hunan, and Jiangxi provinces, as well as the offshore islands of Hainan and Taiwan, natural populations in Jiangxi and Taiwan have become extinct due to habitat destruction (Adopted from Dodson et al., 2021)

3 Insights from Genetics and Genomics of Domestication

3.1 Key genetic changes associated with domestication

The domestication of rice is a complex process involving significant genetic changes. Recent studies have provided valuable insights into the genetic and genomic alterations that occurred during the domestication of rice. One of the key genetic changes associated with rice domestication is the reduction in seed shattering and seed dormancy, which are crucial for effective harvesting and cultivation. Quantitative trait locus (QTL) analysis has identified several loci associated with these traits, including a cluster of QTLs on chromosome 7, which can significantly improve the plant architecture and panicle structure of cultivated rice (Li et al., 2006). This suggests that selection for high yield played a crucial role in the fixation of beneficial mutations.

Whole-genome studies have shown that the two main subspecies of rice, *indica* and *japonica*, originated from genetically distinct gene pools within their wild ancestor, *Oryza rufipogon*, indicating multiple domestication events. However, the presence of common domestication alleles in all cultivated varieties suggests limited introgression of key domestication genes between different gene pools (Kovach et al., 2007; Wei et al., 2012).

Gene introgression from wild relatives has also played an important role in rice domestication. For instance, the *Pi-cd* blast resistance gene found in *japonica* varieties was introgressed from the southern wild rice, highlighting the importance of gene flow from wild species in enhancing the disease resistance of cultivated rice (Fujino et al., 2019). Additionally, whole-genome analyses have identified numerous structural variations and loss/gain of genes that differentiate cultivated rice from its wild ancestors. These genetic changes are associated with phenotypic and physiological adaptations, such as improved photosynthetic and oxidative phosphorylation systems, enabling cultivated rice to thrive in diverse environments (Zhang et al., 2016).

3.2 The role of selective breeding in shaping modern rice varieties

Selective breeding has played a crucial role in the domestication and evolution of modern rice varieties. The domestication process involved both natural and artificial selection, leading to significant genetic changes that distinguish cultivated rice (*Oryza sativa*) from its wild ancestors. Recent studies have highlighted the impact of selective breeding on the genetic diversity and structure of rice populations (Chen et al., 2019). For example, analyses of genome-wide polymorphism patterns in rice have shown that selective breeding has resulted in the introgression of beneficial traits from different subspecies, creating genetic mosaics that enhance the adaptability and productivity of cultivated rice. This genetic introgression is evident in the genetic coherence around key domestication genes in different subgroups, indicating that ancient farmers exchanged genetic material to improve crop traits (Chen et al., 2019).

Quantitative Trait Locus (QTL) analysis has further elucidated the genetic basis of domestication traits. Studies involving crosses between cultivated rice and wild species such as *O. nivara* have identified QTLs associated with reduced seed shattering, decreased seed dormancy, and synchronized seed maturation-traits essential for effective harvesting and cultivation. These findings emphasize the role of selective breeding in fixing beneficial mutations, thereby improving yield and enhancing plant architecture, such as fewer erect tillers and more branched panicles.

Genomic sequencing and analysis of a large number of wild and cultivated rice varieties have provided insights into the genomic characteristics of domestication. For instance, selective sweeps identified in the genomes of *indica* and *japonica* rice varieties have pinpointed regions that underwent strong selection during domestication. These selective sweeps are associated with traits conferring advantages in agricultural environments, such as disease resistance and improved grain quality (Yuan et al., 2017).

Combining genome-wide association studies (GWAS) with genomic scans has also highlighted the interaction between artificial and natural selection. These approaches effectively identify valuable alleles from both cultivated and wild species, which can be used in breeding programs aimed at improving rice varieties. The accumulation and appropriate sampling of germplasm collections are crucial for expanding the pool of useful alleles, potentially leading to the re-domestication of rice varieties for sustainable food production.

3.3 Advances in genomic technologies and their impact on understanding domestication

Recent advances in genomic technologies have significantly enhanced our understanding of rice domestication pathways. The application of genomic sequencing and analysis is crucial for identifying the genome-wide characteristics of rice domestication. For instance, studies on wild rice (*Oryza rufipogon*) and Asian cultivated rice (*Oryza sativa*) have elucidated the genetic diversity and evolutionary history of these species, providing insights into the domestication process (Londo et al., 2006).

One of the key breakthroughs is the use of genome-wide association studies (GWAS) and single nucleotide polymorphism (SNP) combinations. These tools enable researchers to map complex traits and understand the genetic structure of rice. For example, a study utilizing 1 536 SNP sets from 395 diverse rice varieties revealed significant genetic differences between the indica and japonica subspecies, supporting the theory of at least two independent domestication events. Similarly, another GWAS involving 44 100 SNP variations in 413 germplasms discovered numerous common variations affecting various complex traits, highlighting the rich genetic structure of *O. sativa* (Zhao et al., 2010).

Integrated genomic approaches have facilitated the study of hybrid vigor loci in hybrid rice, which are crucial for yield heterosis. These studies have revealed the genomic structure behind rice heterosis, further enhancing rice breeding programs. The use of multi-locus analyses and population genomics has also provided deeper insights into the domestication and evolution of Chinese rice, indicating independent domestication events for the indica and japonica subspecies from different rice populations (Wei et al., 2012). In addition to these advances, biotechnological tools have facilitated the transfer of beneficial genes from wild species into cultivated rice. For example, genes conferring resistance to biotic and abiotic stresses have been successfully introgressed from wild species into rice, demonstrating the potential of wild species as reservoirs of beneficial traits. The introduction of the bacterial blight resistance gene (*Xa21*) from *O. longistaminata* into various rice varieties exemplifies this potential (Zhao et al., 2011).

4 Environmental and Ecological Factors

4.1 Influence of climate and geography on domestication

The domestication of rice (*Oryza sativa*) has been significantly influenced by climatic and geographical factors. Phylogeographic analyses of the wild ancestors of cultivated rice (*Oryza rufipogon*) indicate that domestication events occurred in different geographical regions. Indica rice is believed to have been domesticated south of the Himalayas, including regions of eastern India, Myanmar, and Thailand, while japonica rice was domesticated in southern China. This geographical distribution underscores the role of regional climates in shaping the pathways of rice domestication (Londo et al., 2006). Global climate change, particularly the increase in nighttime temperatures, has also affected rice yields. High nighttime temperature (HNT) stress has been shown to reduce rice yields, with the impact being more pronounced during the rainy season compared to the dry season. This demonstrates that climatic factors continue to influence rice cultivation and productivity (Jia et al., 2017).

4.2 Adaptation of rice to different environments

Rice exhibits exceptional adaptability to a wide range of environmental conditions, which is crucial for its extensive cultivation. Genetic analysis of domestication traits in rice has shown that selection for traits such as reduced seed shattering, seed dormancy, and synchronized seed maturation has enabled rice to thrive in diverse agricultural environments. Additionally, adaptation to different thermal conditions, including cold and heat tolerance, is essential for the geographic expansion of rice cultivation (Schaarschmidt et al., 2020).

The application of compounds such as gamma-aminobutyric acid (GABA), glutamic acid (Glu), and calcium chloride (CaCl₂) has been proven to enhance the cold tolerance of rice seedlings, further demonstrating the species' ability to adapt to various environmental stresses. These adaptations allow rice to be grown in both temperate and tropical regions, making it a versatile crop (Zhu et al., 2007).

4.3 Ecological impacts of rice cultivation

The ecological impacts of rice cultivation are multifaceted, affecting both the environment and the microbial communities associated with rice. The rhizosphere microbiome, or the microbial community in the rice root zone, is significantly influenced by rice cultivation practices. Studies indicate that the rhizosphere microbiome of cultivated rice is more sensitive to environmental changes compared to wild rice. This sensitivity is reflected in the higher diversity and more complex microbial networks observed in cultivated rice.

Additionally, the domestication and subsequent cultivation of rice have led to a reduction in genetic diversity. Severe bottlenecks during the domestication process have resulted in a significant loss of nucleotide diversity in cultivated rice compared to its wild relatives. The reduction in genetic diversity may have long-term ecological impacts, potentially affecting the resilience of rice to environmental changes and diseases (Li et al., 2006). Climate and geography have shaped the pathways of domestication, while the adaptation of rice to different environments has facilitated its global cultivation. However, these processes have also led to ecological impacts, including changes in microbial communities and a reduction in genetic diversity. These impacts require further investigation to ensure sustainable rice production.

5 Agricultural Practices and Cultural Influences

Traditional rice cultivation methods have been shaped by centuries of agricultural practices and cultural traditions. In many regions, rice farming relies on manual labor and simple tools, with practices varying significantly across different geographical areas. For instance, in southern China, traditional methods involve transplanting rice seedlings into flooded fields, a technique that helps control weeds and pests while ensuring ample water supply for the growing plants. In contrast, in parts of India and Southeast Asia, direct seeding is more common, where seeds are sown directly into the fields, reducing labor but requiring more careful water management (Izawa et al., 2008).

Rice holds profound cultural significance in many societies, often symbolizing life, fertility, and prosperity. In China, rice is not only a staple food but also a central element in various cultural rituals and festivals, such as the Dragon Boat Festival, which commemorates the ancient poet Qu Yuan. Similarly, in Japan, rice is deeply embedded in cultural traditions, including the traditional tea ceremony and Shinto rituals, where rice is offered as a sacred food to the deities. In India, rice is an integral part of many religious ceremonies and is frequently used in offerings to gods and during weddings, symbolizing prosperity and fertility (Huang et al., 2012).

The evolution of rice farming practices has been driven by technological advancements and cultural exchanges. Initially, rice domestication involved simple selection processes by ancient farmers, leading to the development of distinct rice varieties such as indica and japonica. Over time, new agricultural technologies were introduced, such as the use of irrigation systems and the development of high-yielding rice varieties, significantly boosting productivity. The Green Revolution in the mid-20th century introduced high-yielding varieties and fertilizers, transforming rice farming methods and increasing yields in many parts of Asia (Huang et al., 2012; Wang et al., 2012).

Recent genomic studies have further enhanced our understanding of rice domestication and breeding. These studies have revealed the genetic basis of important traits such as disease resistance and grain quality, enabling the development of improved rice varieties through modern breeding techniques (Zhu et al., 2007). Additionally, the exchange of genetic material between ancient farmers played a crucial role in shaping the genetic diversity of rice varieties, as evidenced by gene flow between different rice subspecies (Wei et al., 2012).

The domestication of rice in the Yangtze River basin is a complex process that has been extensively studied through various archaeological and environmental analyses. Archaeobotanical evidence from the Tianluoshan site in the lower Yangtze region indicates that the proportion of unbroken domesticated rice spikelet bases increased from 27% to 39% between 6 900 and 6 600 years ago. During this period, the proportion of rice remains among all plant remains also increased from 8% to 24%, suggesting a growing reliance on rice cultivation over wild food gathering (Figure 2) (Fuller and Qin, 2010; Wang et al., 2022).

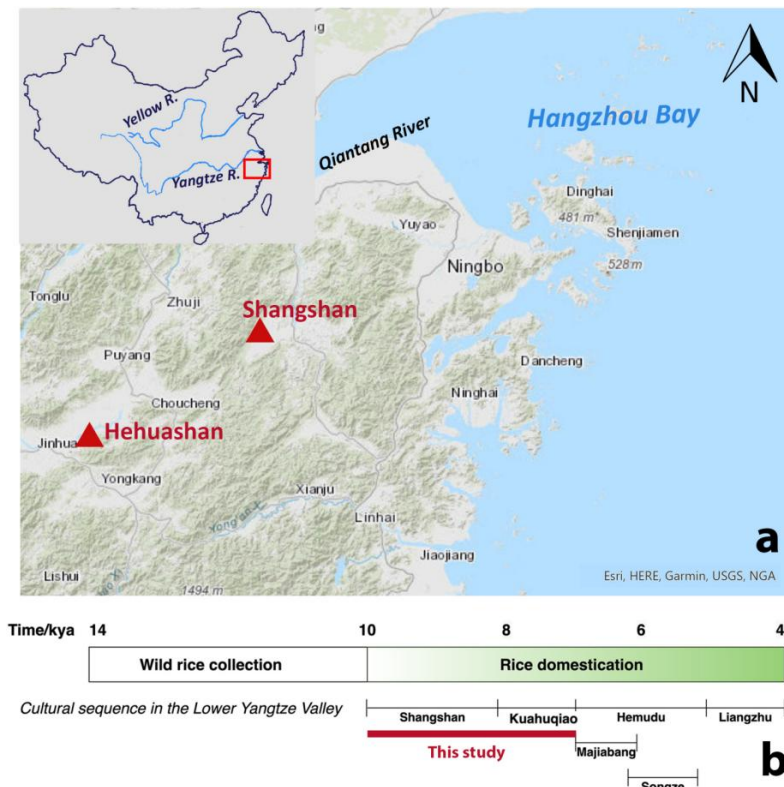


Figure 2 Archaeological background (Adopted from Wang et al., 2022)

Image caption: a: Location of Shangshan and Hehuashan, with the base map modified from the USGS National Map Viewer; b: Overview of cultural history and the process of rice domestication in the Lower Yangtze River region (Adopted from Wang et al., 2022)

The use-wear and phytolith residue analysis of 52 flake tools from the Shangshan and Huguashan sites (dating back 10 000 to 7 000 years ago) provides the first evidence of rice harvesting. These tools reflect two harvesting methods: one involving cutting the panicles at the top and the other cutting the stems near the base. This reflects the early rice cultivation practices in the lower Yangtze River region (Figure 3) (Wang et al., 2022).

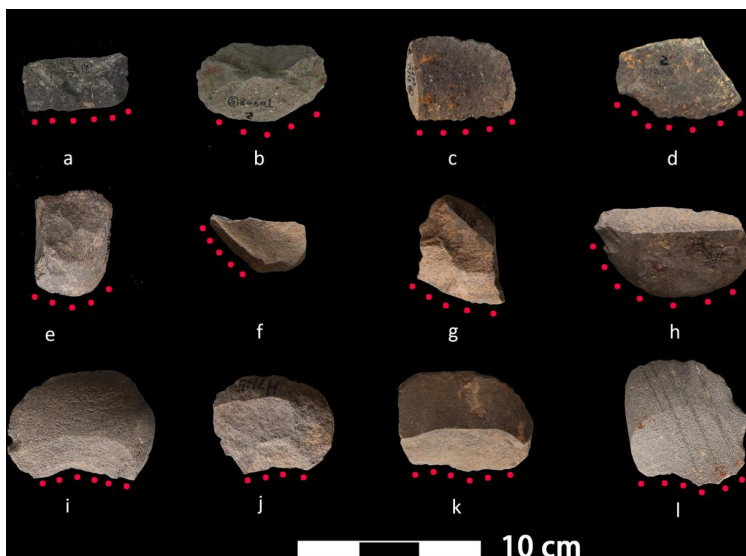


Figure 3 A selection of stone flakes analyzed in this study (Adopted from Wang et al., 2022)

Image caption: a-h represent flakes from the Shangshan culture, while i-l are flakes from the Kuahuqiao culture. The red dots indicate the working edges of these flakes (Adopted from Wang et al., 2022)

The Bashidang site, located in the middle reaches of the Yangtze River, provides microfossil evidence indicating that early Holocene groundwater fluctuations had a significant impact on rice domestication. The area evolved from a floodplain to a wetland, which facilitated rice domestication through practices of burning and clearing. However, due to rising groundwater levels, rice cultivation ceased around 8 000~7 900 years ago (Fuller et al., 2009; Ma et al., 2018).

Phytolith evidence from Diaotonghuan Cave in northern Jiangxi supports the hypothesis that the middle reaches of the Yangtze River were one of the centers of rice domestication. This evidence aligns with the broader understanding that domesticated rice first appeared in the Yangtze River basin. A comprehensive study of 38 archaeological samples from eight Neolithic sites in the lower Yangtze region suggests that the rice domestication process lasted approximately 6 000 years and can be divided into three stages (Ma et al., 2016). The study highlights the gradual and continuous development of domesticated rice traits, with significant turning points during the middle Hemudu culture, late Majiabang culture, and late Liangzhu culture periods (Liu et al., 2017).

Evidence from the early Neolithic Shishan site suggests that barnyard grass was a major staple alongside rice. This indicates that early managed wetland environments were initially harvested for multiple grain varieties, and the emergence of rice as a favored cultivated grass was a prolonged process. These case studies collectively illustrate the gradual and multifaceted nature of rice domestication in the Yangtze River basin, influenced by environmental changes and human agricultural practices. The transition from wild to domesticated rice involved different stages and strategies, reflecting the complex interplay between natural and cultural factors (Cheng et al., 2019).

6 Key Archaeological Sites and Their Role in Understanding Rice Domestication

The domestication of rice has been extensively studied, with significant contributions from archaeological sites across Asia, providing crucial insights into the geographical and temporal aspects of rice domestication. One of the key regions identified is the area south of the Himalayas, encompassing eastern India, Myanmar, and Thailand (Huang et al., 2012). This region is considered a domestication center for one of the major rice varieties, *indica* (*Oryza sativa* subsp. *Indica*). Archaeological evidence from these areas supports the hypothesis of independent domestication events, highlighting the role of local wild rice populations in the development of cultivated rice (Londo et al., 2006).

Southern China, particularly the central region of the Pearl River, has also been identified as a significant location for rice domestication. Archaeological findings indicate that japonica rice was first domesticated from specific populations of wild rice ancestors (*Oryza rufipogon*) in this region. Following this domestication event, japonica rice spread to Southeast and South Asia, where it further hybridized with local wild rice populations, contributing to the genetic diversity of modern rice varieties (Zhu et al., 2007).

The domestication of rice involved significant genetic changes, which have been elucidated through various genomic studies. One major finding is the identification of selective sweeps, which are genomic regions that underwent strong selection during domestication. A comprehensive map of rice genome variation has revealed 55 such selective sweeps, providing insights into the genetic basis of domestication-related traits (Zhang et al., 2016).

Comparative genomic analyses between wild rice (*Oryza rufipogon*) and cultivated rice (*Oryza sativa*) have shown a drastic reduction in nucleotide diversity in the latter. This reduction indicates the presence of a severe domestication bottleneck, with only a small fraction of the genetic diversity in wild rice being retained in cultivated rice. It is estimated that the ancestral population of cultivated rice consisted of approximately 1,500 individuals, and the domestication process spanned about 3 000 years (Eizenga et al., 2017).

Further research has identified specific genes lost or gained during domestication. For example, structural variations between Dongxiang wild rice and the cultivated Nipponbare variety highlight the deletion or addition

of genes, leading to the phenotypic and physiological changes observed in cultivated rice. These genetic changes include adaptations to environmental conditions, such as improvements in photophosphorylation and oxidative phosphorylation systems (Zhou et al., 2022).

7 Summary

The domestication of cultivated rice (*Oryza sativa*) from its wild ancestor, *Oryza rufipogon*, was a complex and multifaceted process. The main findings of this study indicate that cultivated rice was domesticated at least twice from different populations of common wild rice, resulting in the two major rice varieties: indica and japonica. Genetic analysis suggests that japonica was first domesticated in southern China, particularly in the middle Pearl River region, while indica developed from a hybrid of japonica and local wild rice, subsequently spreading to Southeast and South Asia.

The domestication process faced severe bottlenecks, leading to a significant reduction in the genetic diversity of cultivated rice compared to its wild ancestors. Understanding the pathways of rice domestication has profound implications for agriculture and food security. Identifying multiple independent domestication events and the genetic diversity retained in wild rice populations provides valuable insights for rice breeding programs. These findings help develop new rice varieties that are more resilient to environmental stresses and diseases, thereby increasing crop yields and ensuring food security for the growing global population.

Utilizing the genetic resources of wild rice species can introduce beneficial traits into cultivated rice, further enhancing its adaptability and productivity. Research on rice domestication pathways is crucial for improving our understanding of crop evolution and advancing agricultural practices. By uncovering the genetic and geographic origins of cultivated rice, researchers can better understand the mechanisms of domestication and the factors influencing the genetic diversity of this major crop. This knowledge not only contributes to the scientific understanding of plant domestication but also has practical applications in strengthening rice cultivation and ensuring food security. As the global population continues to grow, the importance of such research cannot be overstated, as it provides the foundation for developing sustainable and resilient agricultural systems.

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Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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