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Linkage Drag and Domestication Syndrome: The Genetic Lessons from Rice Evolution

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Abstract The domestication of rice (*Oryza sativa*) from its wild relatives has been a pivotal event in agricultural history, leading to significant genetic changes known as domestication syndrome. This study synthesizes current knowledge on the genetic mechanisms underlying these changes, with a focus on linkage drag and its implications for rice breeding. The severe bottleneck during domestication resulted in a dramatic reduction in genetic diversity in cultivated rice compared to its wild progenitors, *O. rufipogon* and *O. nivara*. Multiple independent domestication events have been identified, contributing to the genetic differentiation between the *indica* and *japonica* subspeicies. The identification of quantitative trait loci (QTLs) and candidate genes associated with domestication-related traits has provided insights into the clustered distribution of these genes, which may explain the phenomenon of linkage drag. Furthermore, the study of de-domestication in weedy rice has revealed the complexity of genetic changes during the domestication process. This study highlights the importance of understanding the genetic basis of domestication syndrome and linkage drag to improve rice breeding strategies and harness the genetic potential of wild rice species for crop improvement.

Keywords Rice domestication; Linkage drag; Genetic diversity; Quantitative trait loci; De-domestication

1 Introduction

Rice (*Oryza sativa* L.) is one of the most important staple crops globally, providing a primary food source for over half of the world's population. The domestication of rice from its wild progenitors, such as *O. rufipogon*, has been a complex process involving significant genetic changes that have resulted in the cultivated varieties we see today. This process has led to the development of numerous domestication-related traits, including reduced seed shattering, increased grain size, and changes in plant architecture (Xiong et al., 1999; Izawa et al., 2009; Voss-Fels et al., 2017). The genetic basis of these traits has been extensively studied, revealing that both major and minor effect genes are involved, often clustered in specific chromosomal regions (Xiong et al., 1999; Hasan et al., 2023). The domestication of rice has also been characterized by multiple selection steps and introgression events, which have shaped the genetic diversity of modern rice cultivars (Vaughan et al., 2008; Voss-Fels et al., 2017).

Linkage drag refers to the phenomenon where undesirable traits are co-inherited with desirable traits due to their physical proximity on the chromosome. This can pose significant challenges in breeding programs, as it can hinder the introduction of beneficial traits from wild relatives into cultivated varieties (Voss-Fels et al., 2017). Understanding the genetic basis of linkage drag is crucial for developing strategies to overcome these challenges and improve crop performance. Domestication syndrome, a collection of traits that distinguish domesticated plants from their wild ancestors, provides insights into the evolutionary processes that have shaped crop genomes. Studying these traits can reveal the underlying genetic mechanisms and help in the identification of key genes involved in domestication (Xiong et al., 1999; Wang et al., 2008; Hasan et al., 2023). This knowledge is essential for crop improvement and for addressing the challenges posed by changing environmental conditions and increasing food demand.

The objective of this study is to synthesize current knowledge on the genetic lessons learned from rice evolution, with a particular focus on linkage drag and domestication syndrome. By examining the genetic factors controlling domestication-related traits and the impact of linkage drag on breeding programs, this study aims to provide a comprehensive understanding of the genetic mechanisms underlying rice domestication. Additionally, this study will explore the implications of these findings for future rice breeding efforts and crop improvement strategies. Through this synthesis, we hope to highlight the importance of integrating genetic insights into practical breeding programs to enhance rice productivity and sustainability in the face of global challenges.

2 The Concept of Linkage Drag

2.1 Definition and mechanisms

Linkage drag refers to the phenomenon where undesirable traits are co-inherited with desirable traits due to their close proximity on the same chromosome. This occurs because the genes for these traits are physically linked, making it difficult to separate them through traditional breeding methods. In the context of plant breeding, linkage drag can significantly hinder the improvement of crop varieties by introducing unwanted characteristics alongside beneficial ones (Giovannoni et al., 2018; Fuentes et al., 2021; Egorova et al., 2022).

2.2 Historical context and examples in plant breeding

Historically, linkage drag has been a major challenge in the breeding of various crops. For instance, in potato breeding, the introgression of traits such as pathogen resistance from wild germplasm is often accompanied by undesirable features like high steroidal glycoalkaloid content and long stolons, which complicate the breeding process (Egorova et al., 2022). Similarly, in tomato, the breeding of modern varieties has inadvertently included alleles affecting metabolic quality due to linkage drag, demonstrating the pervasive nature of this issue across differentcrops (Giovannoni et al., 2018).

In rice, the domestication process has led to the fixation of certain alleles that are beneficial for cultivation but also brought along linked undesirable traits. For example, the seed shattering genes in wild rice populations are functional, while domesticated rice has dysfunctional alleles, indicating a trade-off between ease of harvest and seed dispersal mechanisms (Hasan et al., 2023). Additionally, the modification of plant architecture in rice through the selection of the *TIG1* gene has been crucial for domestication, but it also highlights the complexity of managing linked traits during the breeding process (Zhang et al., 2019).

2.3 Implications for crop improvement

The implications of linkage drag for crop improvement are profound. It necessitates the development of advanced breeding techniques to break the linkage between desirable and undesirable traits. One promising approach is the *de novo* domestication strategy, which involves using gene editing technologies to modify candidate genes responsible for undesirable traits before hybridization with cultivated varieties. This method has been proposed for crops like potato and tomato, offering a potential solution to the linkage drag problem (Giovannoni et al., 2018; Egorova et al., 2022).

Moreover, understanding the genetic mechanisms underlying domestication and the associated linkage drag can inform breeding strategies. For example, the identification of genes responsible for seed dormancy and their selection across multiple crop families, such as the stay-green *G* gene in soybean, rice, and tomato, provides insights into parallel domestication processes and potential targets for genetic improvement (Wang et al., 2018). Additionally, the study of recombination patterns in crops like tomato reveals how domestication shapes genetic diversity and linkage disequilibrium, further emphasizing the need for targeted breeding interventions to mitigate linkage drag (Fuentes et al., 2021).

Recently, by using a very large rice genetic population (18K), research has found that the superposition of two genes does not necessarily result in the sum of their effects. Therefore, it is proposed that there is a phenomenon of epistasis between genes, such as mutual “suppression” and “masking”. In rice breeding, introducing a gene into the parent may not work, and this gene is influenced by genetic background and belongs to gene epistasis (Wei et al., 2024). Researchers have identified 170 pairs of masked epistasis that determine genetic background effects.

For example, *Ghd8* affects grain protein content in the background of *Ehd1* (wild-type allele), but is masked in the background of *ehd1* (mutant allele) due to the epistasis of *Ehd1*×*Ghd8* (Wei et al., 2024). The study provides comprehensive gene interaction information for quantitative traits for rice genetic research and will provide theoretical support for rice molecular design breeding, offering significant insights into linkage drag and domestication syndrome.

In brief, addressing linkage drag is essential for the successful improvement of crop varieties. By leveraging modern genetic tools and a deeper understanding of domestication genetics, breeders can more effectively separate desirable traits from undesirable ones, ultimately enhancing crop performance and sustainability.

3 Domestication Syndrome in Rice

3.1 Defining domestication syndrome

Domestication syndrome refers to the suite of morphological and physiological traits that differentiate domesticated plants from their wild ancestors. In rice, these traits have been shaped by human selection to enhance agricultural productivity and ease of cultivation. The genetic basis of these traits often involves both major and minor effect genes, which are frequently clustered in specific chromosomal regions. This clustering can lead to “linkage drag”, where undesirable traits are co-inherited with desirable ones due to their proximity on the chromosome (Xiong et al., 1999).

3.2 Traits associated with domestication in rice

Seed shattering is a critical trait that has been significantly altered during the domestication of rice. Wild rice species typically exhibit high levels of seed shattering, which aids in natural seed dispersal. However, for cultivated rice, reduced seed shattering is a desirable trait as it prevents loss of grains before harvest. Genetic studies have identified several quantitative trait loci (QTLs) that control seed shattering, and these loci are often conserved across different cereal crops, including maize and sorghum (Poncet et al., 2002).

Plant architecture, including traits such as plant height, tiller number, and leaf angle, has been extensively modified during rice domestication. These changes have been driven by the need for higher yield and better adaptability to various growing conditions. The genetic factors controlling these traits are often located in specific chromosomal regions, and their manipulation can lead to significant improvements in plant architecture. For instance, loci on linkage groups 6 and 7 have been identified as central to the developmental control of plant architecture traits in cereals (Poncet et al., 2002).

A study found that using the high-quality *indica* rice variety HJX74 as the background and AA genome wild rice *O. rufipogon* and *O. nivara* as donors, the single segment substitution lines (SSSL) was constructed. By comparing chromosome interval and sequence alignment, the allelic variation of domesticated genes was analyzed. Among them, 7 genes have allelic variations with known genes (Table 1), and 4 genes are considered as newly discovered genes (Wang et al., 2023).

Grain size and shape are among the most important traits selected during rice domestication. Larger and more uniform grains are preferred for their higher market value and ease of processing. The genetic basis of these traits involves multiple QTLs, with some loci explaining a significant portion of the phenotypic variation. Studies have shown that both major and minor effect genes contribute to the differences in grain size and shape between wild and cultivated rice (Xiong et al., 1999).

In summary, the domestication of rice has involved the selection of multiple traits that enhance its suitability for human use. These traits are controlled by a complex interplay of genetic factors, many of which are clustered in specific chromosomal regions, leading to phenomena such as domestication syndrome and linkage drag. Understanding these genetic underpinnings can provide valuable insights for rice breeding programs aimed at improving crop performance and resilience.

Table 1 Domestication genes detected in RUF-SSSLs and NIV-SSSLs (Adapted from Wang et al., 2023)

Trait	SSSLs	Identifed genes	Chr	Region	Known genes	References
Tiller angle	SR59, SR60, SR61, SR63	*TA7-RUF*	7	RM515-RM195	*PROG1*	Jin et al. (2008); Tan et al. (2008)
	SR72, SR77, SR76, SR75 SR78, SR79, SR80	*TA8-RUF*	8	RM515-RM195	*TIG1*	Zhang et al. (2019)
	SN136, SN139, SN143	*TA11-NIV*	11	RM332-PSM175	-	-
Spreading panicle	SN22, SN28, SN29, SN33	*SPR3-NIV*	3	RM569-RM231	-	-
	SN57, SN58	*SPR4-NIV*	4	OSR15-PSM361	*OsLG1*	Zhu et al. (2013)
Awn	SN34, SN39	*AN3-NIV*	3	PSM428-RM218	-	-
	SN54, SN56	*AN4-NIV*	4	RM273-RM252	-	-
	SR118, SR119	*AN4-RUF*	4	RM4835-PSM326	*An-1*	-
Seed shattering	SN58	*SH4-NIV*	4	PSM361-RM559	*SH4*	Li et al. (2006)
Red pericarp	SR64, SR65	*RC7-RUF*	7	PSM144-RM214	*Rc*	Sweeney et al. (2006)
	SN79, SN82, SN85	*RC7-NIV*	7	RM180-RM6728		

4 Genetic Basis of Domestication Traits

4.1 Key genes involved in domestication

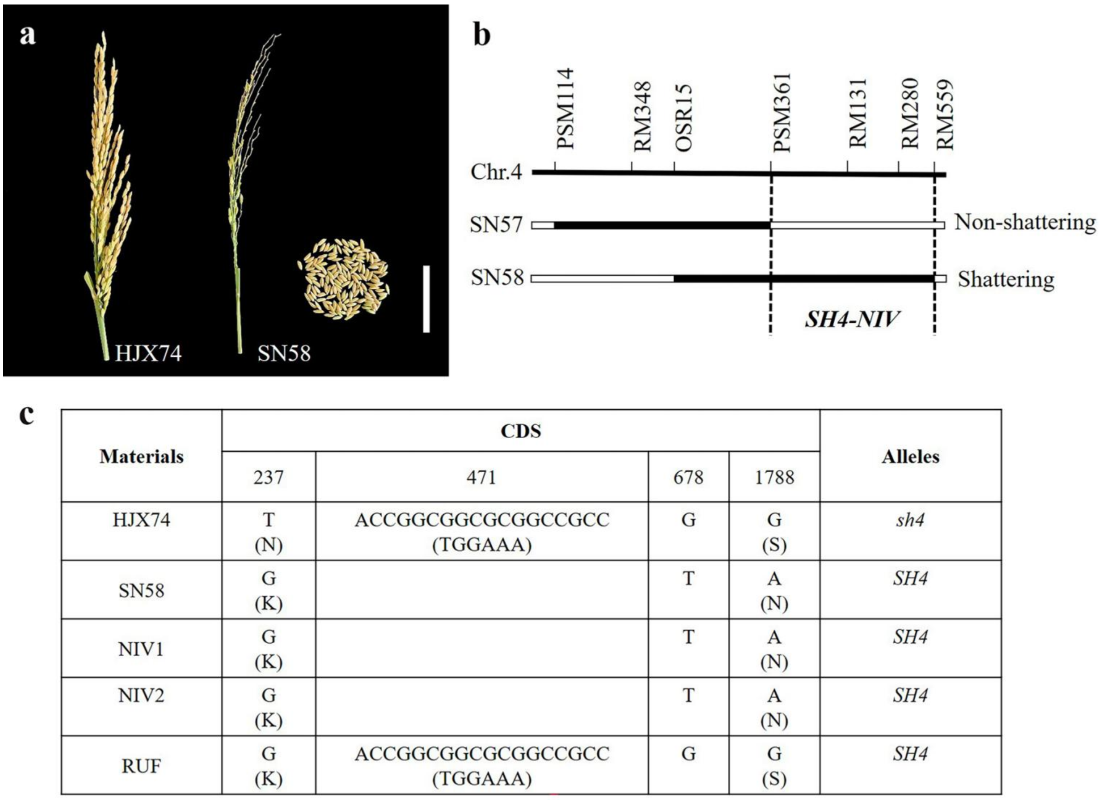
The *Sh4* gene plays a crucial role in the domestication of rice by controlling seed shattering. The nonshattering *sh4* allele was fixed in all rice cultivars, significantly reducing sequence polymorphism compared to wild progenitors (Zhang et al., 2009). The gene encodes a YABBY transcription factor, and its mutations lead to the loss of seed shattering, facilitating easier harvest (Lin et al., 2012; Lv et al., 2018). Additionally, the *sh4* gene has been shown to have a single origin and was fixed by artificial selection during rice domestication (Zhang et al., 2009). However, some studies suggest that the *sh4* locus might have played a minor role in Asian rice domestication, indicating the presence of other unidentified shattering loci (Zhu et al., 2012).

Moreover, research has found that the single segment substitution lines (SSSL) have been developed using high-quality *indica* rice variety HJX74 as the background and wild rice varieties *O. rufipogon* and *O. nivara* as donors. In the SSSLs population, the broken grain domestication character *SH4* was identified by substitution mapping, and locate it on chromosome 4 (Figure 1). Through sequence comparison with known genes, it was found that *SH4-NIV* and *SH4* alleles, and SSSL became a valuable germplasm resource for understanding the regulation of character variation during domestication (Wang et al., 2023).

The *PROG1* gene is another significant gene involved in the domestication of rice, particularly influencing plant architecture. This gene affects the plant’s growth habit, transitioning from a prostrate to an erect form, which is more suitable for cultivation and harvesting. The domestication of rice involved selecting for mutations in the *PROG1* gene that resulted in an erect growth habit, thereby improving yield and ease of harvest (Lv et al., 2018). The *qSW5* gene is a quantitative trait locus (QTL) associated with grain width in rice. A deletion in this gene results in a significant increase in grain width, which was likely selected by ancient humans to increase rice yield (Shomura et al., 2008). This deletion increases the cell number in the outer glume of the rice flower, contributing to larger grain size and higher yield (Shomura et al., 2008).

4.2 Molecular pathways and networks

The domestication of crops involves complex molecular pathways and networks that regulate various agronomically important traits. For instance, the *Sh1* gene family, including *Sh1*, *OsSh1*, and *ZmSh1*, encodes YABBY transcription factors that control seed shattering in sorghum, rice, and maize, respectively (Lin et al., 2012). These genes were under parallel selection during the domestication of these cereals, indicating a conserved molecular pathway for seed shattering across different species (Lin et al., 2012). Additionally, the *SH3* gene in African rice also regulates seed shattering, highlighting the involvement of multiple genes and pathways in this trait (Lv et al., 2013).



Materials	CDS				Alleles
	237	471	678	1788	
HJX74	T (N)	ACCGGCGGCGCGGCCGCC (TGGAAA)	G	G (S)	*sh4*
SN58	G (K)		T	A (N)	*SH4*
NIV1	G (K)		T	A (N)	*SH4*
NIV2	G (K)		T	A (N)	*SH4*
RUF	G (K)	ACCGGCGGCGCGGCCGCC (TGGAAA)	G	G (S)	*SH4*

Figure 1 Seed shattering phenotype and the substitution mapping of *SH4-NIV*. a shows the shattered seeds and panicle of SN58, and panicles with non-shattered seeds in HJX74. b shows the substitution mapping of *SH4-NIV* for seed shattering. c shows the CDS variations of *SH4*. bar=10 cm (Adapted from Wang et al., 2023)

4.3 Evolutionary changes and selective pressures

The domestication of crops is driven by evolutionary changes and selective pressures that favor traits beneficial for cultivation and yield. For example, the fixation of the nonshattering *sh4* allele in rice cultivars was driven by strong artificial selection, which facilitated easier harvest and reduced seed loss (Zhang et al., 2009). Similarly, the *qSW5* deletion in rice was likely selected to increase grain size and yield, demonstrating the role of selective pressures in shaping domestication traits (Shomura et al., 2008). The presence of functional alleles of seed shattering genes in wild rice populations, such as *O. meridionalis*, indicates that these populations have remained genetically isolated from domesticated rice, retaining pre-domestication alleles (Hasan et al., 2023). This genetic isolation provides valuable insights into the impact of domestication on the rice genome and highlights the importance of selective pressures in the domestication process.

5 Linkage Drag in Rice Breeding

5.1 Occurrence of linkage drag

Linkage drag refers to the co-inheritance of undesirable traits along with desirable ones due to their close proximity on the chromosome. In rice breeding, this phenomenon is often observed when attempting to introduce beneficial traits from wild relatives into cultivated varieties. For instance, the study (Xiong et al., 1999) identified that genetic factors controlling domestication-related traits are concentrated in a few chromosomal blocks. This clustered distribution of genes can lead to linkage drag, as undesirable traits from wild species may be inherited along with beneficial traits. Similarly, the research on the molecular population genetics of rice domestication highlights the existence of highly polymorphic linkage blocks that are much older than the speciation between wild species, which can contribute to linkage drag during breeding programs (Tang et al., 2007).

Inter subspecies (*indica* and *japonica*) hybrids are usually sterile, limiting gene exchange. The study identified that a killer-protector system at the *S5* locus encoded by three tightly linked genes [Open Reading Frame 3 *(ORF3)* to *ORF5*] regulates fertility in *indica-japonica* hybrids (Yang et al., 2012). During female sporogenesis, the action of ORF5+ (killer) and ORF4+ (partner) causes endoplasmic reticulum (ER) stress. ORF3+ (protector) prevents ER stress and produces normal gametes, but ORF3− cannot prevent ER stress, resulting in premature programmed cell death and leads to embryo-sac abortion. Preferential transmission of *ORF3+* gametes results in segregation distortion in the progeny (Figure 2).

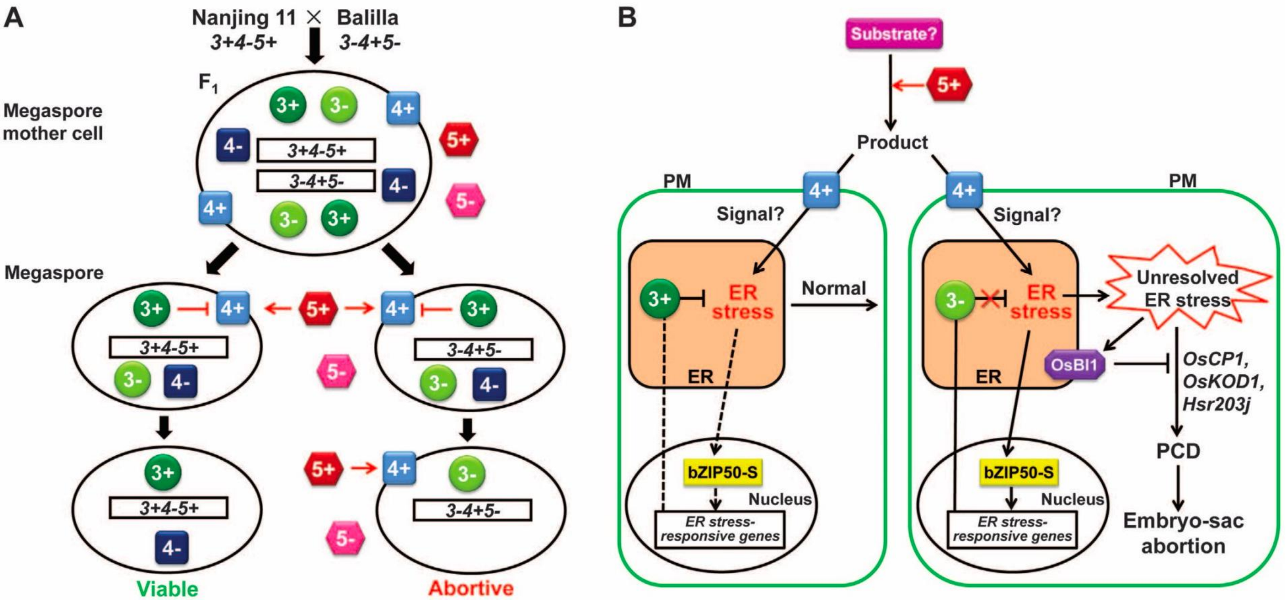


Figure 2 Schematic representation of the killer-protector system in an *indica-japonica* hybrid regulated by the *S5* locus. (A) A genetic model depicting the process of megaspore formation and effects of the three genes, where 3+, 3-, 4+, 4-, 5+, and 5- represent ORF3+, ORF3-, ORF4+, ORF4-, ORF5+, and ORF5-, respectively, and colored blocks and circles represent the proteins. In the megaspore mother cell and daughter cells immediately after meiotic division, killing would not occur because of the presence of ORF3+. Killing would occur in the daughter cell carrying ORF3- and ORF4+ at a later stage of megaspore development. (B) Hypothetical molecular processes involving ER-stress and PCD. bZIP50-S, spliced bZIP50; ER, endoplasmic reticulum; PM, plasma membrane (Adapted from Yang et al., 2012)

The impact of linkage drag on agronomic traits can be significant, often resulting in reduced yield, poor grain quality, or susceptibility to diseases. For example, the deletion in the *qSW5* gene, which is associated with increased grain size, also highlights how changes in DNA regulating agronomically important traits can be linked with other undesirable traits due to linkage drag (Shomura et al., 2008). Additionally, the study on recombination patterns in tomato, which shares similarities with rice, found that loss of recombination hotspots due to domestication can lead to linkage drag, affecting the overall genetic diversity and agronomic performance (Fuentes et al., 2021).

5.2 Strategies to mitigate linkage drag

Marker-assisted selection (MAS) is a powerful tool to mitigate linkage drag by allowing breeders to select for specific genetic markers associated with desirable traits while avoiding those linked with undesirable ones. The identification of QTLs (Quantitative Trait Loci) controlling domestication-related traits in rice provides a basis for MAS. For instance, the study (Xiong et al.1999) identified 44 QTLs associated with various traits, which can be used in MAS to selectively breed for beneficial traits while minimizing linkage drag. This approach can significantly enhance the efficiency of breeding programs by reducing the co-inheritance of undesirable traits.

Increasing recombination rates and employing gene editing technologies are other effective strategies to break linkage drag. Recombination can be enhanced through the use of wild relatives or induced mutations to create new genetic variations. The study on recombination patterns in tomato suggests that understanding the dynamics of recombination hotspots can help in designing strategies to increase recombination in specific genomic regions, thereby reducing linkage drag (Fuentes et al., 2021). Additionally, gene editing technologies like CRISPR/Cas9 offer precise tools to directly modify or remove undesirable genes linked with beneficial traits. This can be particularly useful in overcoming the limitations posed by linkage drag in traditional breeding methods.

Anyhow, linkage drag presents a significant challenge in rice breeding, but with the use of advanced genetic tools and techniques such as marker-assisted selection and gene editing, it is possible to mitigate its effects and enhance the efficiency of breeding programs.

6 Case Studies and Examples

6.1 Case study 1: overcoming linkage drag in disease resistance

Linkage drag, the phenomenon where undesirable traits are co-inherited with beneficial ones due to their close genetic proximity, poses a significant challenge in breeding disease-resistant rice varieties. One notable example is the effort to incorporate disease resistance genes from wild rice into cultivated varieties. The study (Hasan et al., 2023) highlights the genetic isolation of Australian wild rice populations, which have retained pre-domestication alleles, including those related to disease resistance. These wild populations exhibit a high level of natural variation at domestication loci, such as seed shattering and grain size, which are often linked to disease resistance genes. By leveraging the genetic diversity in these wild populations, breeders can potentially overcome linkage drag by identifying and selecting for alleles that confer disease resistance without the associated undesirable traits.

6.2 Case study 2: improving grain quality while managing linkage drag

Improving grain quality in rice, such as grain size and weight, while managing linkage drag is a critical goal in rice breeding programs. The study by Kumar et al. (2020) provides a comprehensive analysis of polymorphisms associated with grain size and weight in Indian rice germplasm. The researchers identified a contiguous ~6 Mb long low diversity region (LDR) on chromosome 5, which carries a major grain weight QTL (quantitative trait locus) harboring the *OsTOR* gene. This region has undergone significant positive selection and multiple selection sweeps, indicating its importance in domestication. By understanding the genetic basis of grain quality traits and their association with domestication-driven evolution, breeders can develop strategies to improve grain quality while minimizing the impact of linkage drag. For instance, the identification of six SNPs significantly associated with grain size/weight provides valuable markers for high-throughput genotyping and selection in breeding programs.

6.3 Case study 3: balancing yield and stress tolerance

Balancing yield and stress tolerance in rice is another area where linkage drag presents a challenge. The domestication process has often led to the selection of high-yielding varieties at the expense of stress tolerance traits. The study by Hasan et al. (2023） on Australian wild rice populations reveals that these populations have retained a high level of natural variation at domestication loci, including those related to stress tolerance. This genetic diversity offers a valuable resource for breeding programs aiming to enhance stress tolerance without compromising yield. By utilizing the allelic variations present in wild rice populations, breeders can identify and introgress stress tolerance genes into cultivated varieties, thereby achieving a balance between yield and stress tolerance. This approach not only helps in overcoming linkage drag but also ensures the development of resilient rice varieties capable of thriving under diverse environmental conditions.

7 Evolutionary Insights from Rice Domestication

7.1 Comparative genomics of wild and cultivated rice

The comparative genomics of wild and cultivated rice provides significant insights into the genetic factors that have driven the domestication process. A study conducted using an F_2 population derived from a cross between *O. sativa* (cultivated rice) and *O. rufipogon* (wild rice) identified numerous genetic loci associated with domestication-related traits. Specifically, 19 traits were analyzed, revealing that seven qualitative traits were each controlled by a single Mendelian locus, while 12 quantitative traits were associated with 44 putative QTLs (Xiong et al., 1999). This clustered distribution of genes in specific chromosomal blocks underscores the genetic basis of the “domestication syndrome” and highlights the challenges posed by “linkage drag” in breeding programs (Xiong et al., 1999).

7.2 Insights into adaptation and speciation

The process of rice domestication has also provided valuable insights into adaptation and speciation. The genetic factors identified in the comparative genomics studies suggest that both major and minor effect genes play a role in the differences between wild and cultivated rice (Xiong et al., 1999). This genetic diversity is crucial for understanding how rice has adapted to various environmental conditions over time. Moreover, the study of linkage drag in other cereal crops, such as wheat, reveals that strong selection for specific traits can inadvertently eliminate beneficial genetic variants, thereby constraining adaptation potential (Voss-Fels et al., 2017). This phenomenon underscores the importance of maintaining genetic diversity to ensure the adaptability and resilience of crop species in fluctuating environments (Voss-Fels et al., 2017).

7.3 Lessons for future breeding programs

The insights gained from the study of rice domestication have significant implications for future breeding programs. The identification of genetic loci associated with desirable traits in wild rice can facilitate the incorporation of these traits into cultivated varieties, thereby enhancing their performance and resilience (Xiong et al., 1999). Additionally, understanding the mechanisms of linkage drag and its impact on genetic diversity can help breeders develop strategies to mitigate its effects. For instance, reversing the inadvertent consequences of selection in wheat by recovering root diversity could be essential for future food production (Voss-Fels et al., 2017). These lessons highlight the importance of leveraging genetic insights from domestication studies to inform and improve modern breeding practices.

8 Challenges and Future Directions

8.1 Technological advances in genomics and breeding

Advancements in genomic technologies have significantly transformed rice breeding practices, allowing for more precise and efficient improvements. Techniques such as CRISPR/Cas9 and genomic selection are becoming integral to modern breeding programs. CRISPR/Cas9 facilitates targeted gene editing, enabling the direct modification of specific traits without introducing foreign DNA, which can help in avoiding linkage drag (Lenaerts et al., 2018). Additionally, genomic selection leverages genome-wide markers to predict the performance of breeding candidates, accelerating the development of new varieties with desired traits (Boersma et al., 2018).

8.2 Addressing complex traits and polygenic inheritance

One of the significant challenges in rice breeding is the manipulation of complex traits governed by multiple genes, known as polygenic traits. Traits such as yield, drought tolerance, and disease resistance often involve intricate genetic networks. Advances in high-throughput genotyping and phenotyping, coupled with bioinformatics tools, are aiding breeders in dissecting these complex traits. However, integrating these technologies into breeding programs requires substantial investment and expertise (Giordano et al., 2019). Understanding the polygenic basis of these traits and implementing marker-assisted selection (MAS) can significantly enhance breeding efficiency and outcome (Siegrist et al., 2016).

8.3 Policy and ethical considerations in genetic improvement

The rapid adoption of new genomic technologies in rice breeding raises several policy and ethical issues. Regulatory frameworks must adapt to the unique aspects of genomic editing techniques compared to traditional breeding. There is ongoing debate over the labeling and acceptance of genetically modified organisms (GMOs) and gene-edited crops, which impacts public perception and market acceptance (Delwaide et al., 2015). Ethical considerations also encompass the equitable distribution of the benefits of these technologies, ensuring that smallholder farmers and diverse communities can access and benefit from the advancements. Furthermore, there is a need for policies that balance innovation with safety, environmental sustainability, and socioeconomic factors (Hussain et al., 2020). In summary, the future of rice breeding lies in integrating advanced genomic technologies with a deep understanding of complex traits, while navigating the policy and ethical landscape to ensure sustainable and equitable advancements in rice production.

9 Conclusion

The genetic study of rice domestication has revealed significant insights into the differences between domesticated rice and its wild progenitor. Key findings include the identification of both major and minor genetic factors controlling domestication-related traits, with many of these factors clustered in specific chromosomal regions. This clustering is indicative of the "domestication syndrome" and explains the phenomenon of "linkage drag" observed in breeding programs. Additionally, the differentiation within the AA genome species, including the transition from wild to cultivated types and the *indica-japonica* differentiation, has been mapped to specific genomic locations, further elucidating the genetic basis of domestication.

The clustered distribution of genetic factors controlling domestication traits has significant implications for rice breeding. Understanding these clusters can help breeders more effectively utilize desirable traits from wild rice, despite the challenges posed by linkage drag. This knowledge can facilitate the development of new rice varieties with improved traits such as yield, disease resistance, and environmental adaptability. Furthermore, the insights gained from the genetic differentiation within the AA genome species can inform evolutionary studies, providing a clearer picture of the domestication process and the genetic mechanisms underlying it.

The genetic lessons from rice evolution underscore the complexity of domestication and the intricate interplay of genetic factors involved. The findings from these studies not only enhance our understanding of rice domestication but also offer practical applications for rice breeding programs. By leveraging the genetic information on domestication-related traits, breeders can overcome the challenges of linkage drag and develop superior rice varieties. Continued research in this field will undoubtedly yield further insights, contributing to the advancement of both rice breeding and evolutionary biology.

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Conflict of Interest Disclosure

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

References

Boersma R., Poortvliet P., and Gremmen B., 2018, The elephant in the room: how a technology's name affects its interpretation, Public Understanding of Science, 28: 218-233.
http://dx.doi.org/10.1177/0963662518812295s

Delwaide A., Nalley L., Dixon B., Danforth D., Nayga R., Loo E., and Verbeke W., 2015, Revisiting GMOs: are there differences in European consumers' acceptance and valuation for cisgenically vs transgenically bred rice, PLoS One, 10(5): e0126060.
https://doi.org/10.1371/journal.pone.0126060

Egorova A., Chalaya N., Fomin I., Barchuk A., and Gerasimova S., 2022, De novo domestication concept for potato germplasm enhancement, Agronomy, 12(2): 462.
https://doi.org/10.3390/agronomy12020462

Fuentes R., Ridder D., Dijk A., and Peters S., 2021, Domestication shapes recombination patterns in tomato, Molecular Biology and Evolution, 39(1): msab287.
https://doi.org/10.1093/molbev/msab287

Giovannoni J., 2018, Tomato multiomics reveals consequences of crop domestication and improvement, Cell, 172(1): 6-8.
https://doi.org/10.1016/j.cell.2017.12.036

Giordano J., Miller R., Levy B., Goldstein D., and Wapner R., 2019, Have genomic screening advances gone far enough, American Journal of Obstetrics and Gynecology, 220: S4.
https://doi.org/10.1016/j.ajog.2018.11.005

Jin J., Huang W., Gao J.P., Yang J., Shi M., Zhu M.Z., Luo D., and Lin H.X., 2008, Genetic control of rice plant architecture under domestication, Nature Genetics, 40: 1365-1369.
http://dx.doi.org/10.1038/ng.247

Lin Z., Li X., Shannon L., Yeh C., Wang M., Bai G., Peng Z., Li J., Trick H., Clemente T., Doebley J., Schnable P., Tuinstra M., Tesso T., White F., and Yu J., 2012, Parallel domestication of the *Shattering1* genes in cereals, Nature Genetics, 44: 720-724.
https://doi.org/10.1038/ng.2281

Hasan S., Furtado A., and Henry R., 2023, Analysis of domestication loci in wild rice populations, Plants, 12(3): 489.
https://doi.org/10.3390/plants12030489

Hussain S., Quittner A., Brown M., and Li-Rosi A., 2020, Understanding access to genomics in an ethnically diverse south Florida population: A comparison of demographics in odyssey and rapid whole genome sequencing programs, Journal of Genetic Counseling, 29(4): 553-561.
https://doi.org/10.1002/jgc4.1281

Izawa T., Konishi S., Shomura A., and Yano M., 2009, DNA changes tell us about rice domestication, Current Opinion in Plant Biology, 12(2): 185-192.
https://doi.org/10.1016/j.pbi.2009.01.004

Kumar A., Daware A., Kumar A., Kumar V., Krishnan S., Mondal S., Patra B., Singh A., Tyagi A., Parida S., and Thakur J., 2020, Genome-wide analysis of polymorphisms identified domestication-associated long low diversity region carrying important rice grain size/weight QTL, The Plant Journal, 103(4): 1525-1547.
https://doi.org/10.1111/tpj.14845

Lenaerts B., Collard B., and Demont M., 2018, Global survey of rice breeders to investigate characteristics and willingness to adopt alternative breeding methods, Agriculture & Food Security, 7: 40.
https://doi.org/10.1186/s40066-018-0191-3

Li C.B., Zhou A.L., and Sang T., 2006, Rice domestication by reducing shattering, Science, 311(5769): 1936-1939.
http://dx.doi.org/10.1126/science.1123604

Lv S., Wu W., Wang M., Meyer R., Ndjiondjop M., Tan L., Zhou H., Zhang J., Fu Y., Cai H., Sun C., Wing R., and Zhu Z., 2018, Genetic control of seed shattering during African rice domestication, Nature Plants, 4: 331-337.
https://doi.org/10.1038/s41477-018-0164-3

Poncet V., Martel E., Allouis S., Devos K., Lamy F., Sarr A., and Robert T., 2002, Comparative analysis of QTLs affecting domestication traits between two domesticated × wild pearl millet (*Pennisetum glaucum* L., Poaceae) crosses, Theoretical and Applied Genetics, 104: 965-975.
https://doi.org/10.1007/s00122-002-0889-1

Qiu J., Zhou Y., Mao L., Ye C., Wang W., Zhang J., Yu Y., Fu F., Wang Y., Qian F., Qi T., Wu S., Sultana M., Cao Y., Wang Y., Timko M., Ge S., Fan L., and Lu Y., 2017, Genomic variation associated with local adaptation of weedy rice during de-domestication, Nature Communications, 8: 15323.
https://doi.org/10.1038/ncomms15323

Shomura A., Izawa T., Ebana K., Ebitani T., Kanegae H., Konishi S., and Yano M., 2008, Deletion in a gene associated with grain size increased yields during rice domestication, Nature Genetics, 40: 1023-1028.
https://doi.org/10.1038/ng.169

Siegrist M., Hartmann C., and Sütterlin B., 2016, Biased perception about gene technology: how perceived naturalness and affect distort benefit perception, Appetite, 96: 509-516.
https://doi.org/10.1016/j.appet.2015.10.021

Sweeney M., Thomson M., Pfeil B., and McCouch S., 2006, Caught red-handed: Rc encodes a basic helix-loop-helix protein conditioning red pericarp in rice, Plant Cell, 18: 283-294.

Tang T., and Shi S., 2007, Molecular population genetics of rice domestication, Journal of Integrative Plant Biology, 49: 769-775.

Vaughan D., Lu B., and Tomooka N., 2008, The evolving story of rice evolution, Plant Science, 174: 394-408.
https://doi.org/10.1016/J.PLANTSCI.2008.01.016

Voss-Fels K., Qian L., Parra-Londono S., Uptmoor R., Frisch M., Keeble-Gagnère G., Appels R., and Snowdon R., 2017, Linkage drag constrains the roots of modern wheat, Plant, Cell Environment, 40(5): 717-725.
https://doi.org/10.1111/pce.12888

Wang E., Wang J., Zhu X., Hao W., Wang L., Li Q., Zhang L., He W., Lu B., Lin H., Ma H., Zhang G., and He Z., 2008, Control of rice grain-filling and yield by a gene with a potential signature of domestication, Nature Genetics, 40: 1370-1374.
https://doi.org/10.1038/ng.220

Wang H., Xu X., Vieira F., Xiao Y., Li Z., Wang J., Nielsen R., and Chu C., 2016, The power of Inbreeding: NGS-Based GWAS of rice reveals convergent evolution during rice domestication, Molecular Plant, 9(7): 975-985.
https://doi.org/10.1016/j.molp.2016.04.018

Wang M., Li W., Fang C., Xu F., Liu Y., Wang Z., Yang R., Zhang M., Liu S., Lu S., Lin T., Tang J., Wang Y., Wang H., Lin H., Zhu B., Chen M., Kong F., Liu B., Zeng D., Jackson S., Chu C., and Tian Z., 2018, Parallel selection on a dormancy gene during domestication of crops from multiple families, Nature Genetics, 50: 1435-1441.
https://doi.org/10.1038/s41588-018-0229-2

Wang Z., Guo Z., Zou T., Zhang Z., Zhang J., He P., Song R., Liu Z., Zhu H., Zhang G., and Fu X., 2023, Substitution mapping and allelic variations of the domestication genes from *O. rufipogon* and *O. nivara*, Rice, 16: 38.
http://dx.doi.org/10.1186/S12284-023-00655-Y

Wei X., Chen M.,Zhang Q., Gong J., Liu J., Yong K., Wang Q., Fan J., Chen S., Hua H., Luo Z., Zhao X., Wang X., Li W., Cong J., Yu X., Wang Z., Huang R., Chen J., Zhou X., Qiu J., Xu P., Murray J., Wang H., Xu Y., Xu C., Yang J., Han B., and Huang X., 2024, Genomic investigation of 18 421 lines reveals the genetic architecture of rice, Science, 385(6704): eadm8762.
http://dx.doi.org/10.1126/SCIENCE.ADM8762

Xiong L., Liu K., Dai X., Xu C., and Zhang Q., 1999, Identification of genetic factors controlling domestication-related traits of rice using an F_2 population of a cross between *Oryza sativa* and *O. rufipogon*, Theoretical and Applied Genetics, 98: 243-251.
https://doi.org/10.1007/s001220051064

Yang J., Zhao X., Cheng K., Du H.,Ouyang Y., Chen J., Qiu S., Huang J., Jiang Y., Jiang L., Ding J.,Wang J., Xu C., Li X., and Zhang Q., 2012, A killer-protector system regulates both hybrid sterility and segregation distortion in rice, Science, 337(6100): 1336-1340.
http://dx.doi.org/10.1126/science.1223702

Zhang L., Zhu Q., Wu Z., Ross-Ibarra J., Gaut B., Ge S., and Sang T., 2009, Selection on grain shattering genes and rates of rice domestication, The New Phytologist, 184(3): 708-720.
https://doi.org/10.1111/j.1469-8137.2009.02984.x

Zhang W., Tan L., Sun H., Zhao X., Liu F., Cai H., Fu Y., Sun X., Gu P., Zhu Z., and Sun C., 2019, Natural variations at *TIG1* encoding a TCP transcription factor contribute to plant architecture domestication in rice, Molecular Plant, 12(8): 1075-1089.

Zhu Y., Ellstrand N., and Lu B., 2012, Sequence polymorphisms in wild, weedy, and cultivated rice suggest seed-shattering locus *sh4* played a minor role in Asian rice domestication, Ecology and Evolution, 2(9): 2106-2113.
https://doi.org/10.1002/ece3.318

Zhu Z., Tan L., Fu Y., Liu F., Cai H., Xie D., Wu F., Wu J., Matsumoto T., and Sun C., 2013, Genetic control of inforescence architecture during rice domestication, Nature Communication, 4: 2200.
http://dx.doi.org/10.1038/ncomms3200